Curriculum Vitae
Andreas Wagner

Professor, University of Zürich
Institute of Evolutionary Biology
and Environmental Studies

Citizenship: Austria, U.S.A. (dual)

Winterthurerstrasse 190, Building Y27
CH-8057 Zürich
Switzerland

E-mail: andreas.wagner@ieu.uzh.ch
Phone: +41-44-635-6141
FAX: +41-44-635-6144

Academic Positions

2011-	**Professor** (full), **University of Zurich**, Dept. of Evolutionary Biology and Environmental Studies
2016-2020	Chairman, Univ. of Zürich, Dept. of Evolutionary Biology and Environmental Studies
1999 -	**External Professor, The Santa Fe Institute**, New Mexico, U.S.A.
2021	Fellow, Stellenbosch Institute for Advanced Study (STIAS), South Africa
2006-2010	Professor (full), Univ. of Zürich, Institute of Biochemistry
2012-2013	Consultant, A*Star Bioinformatics Institute, Singapore
2002-2012	Associate Professor (with tenure), Univ. of New Mexico, Department of Biology
2007-	Group Leader, Swiss Institute of Bioinformatics
2004-2005	Visiting Scientist, Institut des Hautes Études Scientifiques, Bures-sur-Yvette, France
1998-2002	Assistant Professor, University of New Mexico, Department of Biology
2000-2006	Associated Faculty Member, Albuquerque High Performance Computing Center
1998-2002	Adjunct Professor, University of New Mexico, Department of Biology
1996	Visiting Scientist, Los Alamos National Laboratory, U.S.A.
1996-1998	Postdoctoral Fellow, The Santa Fe Institute
1995-1996	Fellow, Institute for Advanced Study Berlin, Germany
1995	Postdoctoral Fellow with Leo W. Buss, Yale University

Education

1995	**Ph.D.**, Yale University, Dept. of Biology
1994	**M. Phil**, Yale University, Dept. of Biology
1990	**M.Sc.**, Univ. of Vienna, Dept. of Molecular Genetics, "with honors"

Honors

2018	Elected Corresponding Member, Austrian Academy of Sciences
2014	Elected Member, European Molecular Biology Organization (EMBO)
2011	Elected Fellow, American Association for the Advancement of Science
2010	Gold medal for *Paradoxical Life*, best Science books of 2009, Independent Publisher Book Awards 2010
2010	Silver medal for *Paradoxical Life*, best Philosophy books of 2009, by Foreword Magazine
2004-	Member, Faculty of 1000 Biology
1996-1998	Postdoctoral Fellow, The Santa Fe Institute
1995-1996	Fellow, Institute for Advanced Study Berlin, Germany
1995	J.S. Nicholas Prize for Best Dissertation, Yale University
1994	G. Evelyn Hutchinson Prize, Yale University
1991-1995	University Fellowship, Yale University

| 1991 | Fellowship for Research at the University of Chicago, Austrian Federal Science Ministry. |

Professional Service

Editorial Boards	Genome Biology and Evolution (2013-2016), Biology (2019-), Bioessays (2004-2013), BMC Ecology and Evolution (2004-), Journal of Experimental Zoology/Molecular and Developmental Evolution (1999-2016); The Open Evolution Journal (2007-2013); Santa Fe Institute Publications (2002-), Wiley Interdisciplinary Reviews: Systems Biology (2007-2011), Philosophy, Theory, and Practice in Biology (2010-), Molecular Genetics and Genomics (2007-2011), Advances in Complex Systems (2000-2008)
Steering Committees	Research Priority Program in Evolutionary Biology at the University of Zurich (2012-), Evolutionary Biology Ph.D. Program, University of Zurich (2009-), Research Priority Program in Systems Biology at the University of Zurich (2007-2012), Center for Advanced Studies, UNM (2002-2004)
Advisory Boards	Science Board, The Santa Fe Institute (2014-2020)
Juries	SIB Young Bioinformatician Award (2008 as Chair, 2010), Motoo Kimura Lifetime Contribution Award (SMBE, 2017)
Admission Committees	Computational Biology and Bioinformatics Master Program (2007-2016)
Program Coordinator	One of several coordinators for the research program in "Evolutionary Dynamics" funded by the W.M. Keck foundation, The Santa Fe Institute (1998-2001)
Conference Co-organization	"Origins of novelty in biological, social, and technological systems" at the Santa Fe Institute, Santa Fe, NM (October 2014); "Robustness in biological systems" at the Mathematical Biology Institute, Ohio State University (March 2012); Program Committee Member, International Conference for Systems Biology (ICSB), Barcelona, Spain (Sep. 2016), Lyon (Oct. 2018)
Journal Reviewing	*Science, Nature, Nature Genetics, Nature Reviews Genetics, Nature Ecology and Evolution, Proc. Natl. Acad. Sci. U.S.A., Nature Biotechnology, Genetics, Trends in Genetics, Trends in Ecology and Evolution, Trends in Microbiology, Trends in Biochemical Sciences, PloS Biology, PloS Computational Biology, PLoS Genetics, Genome Research, Genome Biology, Genetical Research, Brain and Behavior, Evolution, Journal of Theoretical Biology, Journal of Biological Chemistry, Evolution and Development, Journal of Molecular Biology, Molecular Biology and Evolution, Journal of Experimental Zoology/Molecular and Developmental Evolution, Molecular Genetics and Genomics, American Naturalist, Advances in Complex Systems, BioEssays, Bioinformatics, BMC Bioinformatics, BMC Evolutionary Biology, BMC Genomics, BioSystems, Proc. Roy. Soc. London, Journal of the Royal Society Interface, Philosophical Transactions of the Royal Society B, Perspectives on Psychological Science, Origins of Life and Evolution of the Biosphere, Mammalian Genome, Wiley Interdisciplinary Reviews, The Open Evolution Journal, Proteomics, Adaptive Behavior, Scientific Reports, Cell Systems*
Book and Grant Proposal Reviewing	*National Science Foundation, National Institutes of Health, Biotechnology and Biological Sciences Research Council (BBSRC), Swiss National Science Foundation,*

        Deutsche Forschungsgemeinschaft, Dutch Research Council (NWO), Templeton Foundation, European Molecular Biology Organization (EMBO), Wellcome Trust, Science Foundation Ireland, Conicyt (Chile) Human Frontier Science Program, Millenium Institute (Chile), Fonds zur Förderung der wissenschaftlichen Forschung (Austria), European Research Council (ERC), Austrian Academy of Sciences, Carl-Zeiss Stiftung, DBT Wellcome Trust India Alliance, AXA Research Foundation, India Alliance, the Santa Fe Institute Publication Series, Oxford University Press, Cambridge University Press, Springer Verlag, Wissenschaftskolleg (Berlin), Institut Pascal (France)

Review Panels   Swiss National Science Foundation Ambizione Fellowship (2013-2021), Univ. Zürich Standing Committee to Support Young Scientists (2020-), Review of Centers of Excellence in Complex Biomedical Systems Research, NIH Study Section (2003), Comité d'Evaluation laboratoire De Vienne, Gif-sur-Yvette, France (2004), Center for Genomic Regulation (CRG), Barcelona (2010)

Habil. Committee   Daniel Rankin (2011-2012, chair)

Teaching Experience
<u>Classroom Teaching</u>

2013-	Lecture Course "Evolution" (multiple instructors)
2013-	Laboratory Course "Practical Bioinformatics" (multiple instructors)
2008-	Lecture Course "Functional Genomics"
2007-2017	Lecture Course "Computational Biology" (with C. von Mering, K. Shimizu)
2007-2012	Lecture Course "Foundations of Molecular Evolution"
2007-2012	Lecture Course and Exercises "Bioinformatics I" (multiple lecturers)
2007	Lecture Course "Dynamical Systems Biology" (with A. Becskei, C. von Mering)
2004	Lecture Course "Evolution"
2002, 2005	Lecture Course "Genome and Computational Biology"
1999, 2000, 2001, 2003, 2006	Lecture Courses "Evolutionary Genetics" and "Introductory Genetics"
1999, 2000, 2003, 2004	Seminar Courses " Genome Biology" "Comparative Genomics", "Computational Genomics"
1995	Laboratory for Development and Reproduction, Yale University
1994	Laboratory for Genetics, Yale University.
1992	Laboratory for Ecology and Evolution, Yale University.
1992	Laboratory for Introductory Biology, Yale University.

<u>Postdoctoral Advisement </u>(chronological)

2000-2003	Susannah Green (with S. Ruby, UNM Health Sciences Center)
2002-2005	Michael Gilchrist
2008-2010	Bing Chen
2016-	Jordi van Gestel (with M. Ackermann, ETH Zürich)
2008-2011	Eric Hayden
2016-	Shraddha Karve
2011-2014	Adrian Lopez
2019-	Andrei Papkou
2011-2017	Joshua Payne
2008-2011	Karthik Raman
2008-2011	Daniel Rankin
2011-2014	Mariana Ricca
2008-2011	Elias Zamora-Silero
2012-2017	Kathleen Sprouffsky
2011-2015	Peter Szoevenyi

2010-2012	Niv Sabath
2014-2017	Athena Chu
2014-2019	Macarena Toll-Riera
2014-2017	Yolanda Schaerli
2015-2017	Charles de Santana
2016-2020	Jia Zheng
2017-2021	Gabriel Schweizer
2017-2020	Shraddha Karve
2017-2020	Bharat Ravi Iyengar
2018-2020	Carla Bello
2018-2020	Eugenio Azpeitia
2019-2022	Tess Brewer
2019-2022	Diego Pesce
2019-	Andrei Papkou
2019-2022	Pouria Dasmeh
2021-	Timothy Fuqua
2022-	Gopinath Chattopadhyay

Graduate Student Advisement (chronological)

1998-2004	Gavin C. Conant
1999-2004	Mike Fuller
2000-2007	Annette Evangelisti
2004-2012	Jeremiah Wright
2007-2015	Manuel Bichsel
2007-2011	Joao Rodriguez
2007-2010	Saurabh Polyphaly
2007-2011	Nicole de la Chaux
2007-2011	Marc Hafner (w. M. Hasler)
2007-2011	Evandro Ferrada
2008	Giovanni Bussotti
2008-2013	Riddhiman Dhar
2009-2014	Aditya Barve
2010-2014	Tugce Bilgin
2010-	Sinisa Bratulic
2010-2012	Vardan Andriasyan
2012-2018	Jose Aguilar Rodriguez
2012-2018	Ali Rezaee Vahdati
2013-2018	Rzgar Hosseini
2013-2018	Debbie Leigh (w. Lukas Keller)
2013-2017	Kasia Sluzek (w. Lukas Keller)
2014-2015	Malami Koletou
2015-2020	Maria Magdalena San Roman
2016-2020	Pierre Laye
2017-2021	Alexandre Figueiredo (w. Rolf Kümmerli)
2017-2021	Felix Moerman (w. Florian Altermatt)
2017-2022	Michael Schmutzer
2019-	Camille Jourdan
2019-	Caua Westmann
2019	Nadine Thierer
2020	Roman Doronin
2022-	Christian Ramos Uria
2022-	Leander Goldbach

Publications

Books

Wagner, A. (2023) Sleeping Beauties. The mystery of dormant innovations in nature and culture. One World (in press).

Wagner, A. (2019) Life Finds a Way. What Evolution Can Teach us About Creativity. Basic Books.

Wagner, A. (2014) The Arrival of the Fittest. How Nature Innovates. Penguin Random House.

Wagner, A. (2011) The Origins of Evolutionary Innovations. Oxford University Press.

Wagner, A. (2009) Paradoxical Life. Yale University Press.

Wagner, A. (2005) Robustness and Evolvability in Living Systems. Princeton University Press.

Patents

Wagner, A. (2006) "Method for reconstructing pathways in large genetic networks from genetic perturbations." United States Patent 7,124,032.

Articles and Book Chapters

Submitted and in press

245. Schmutzer, M., **Wagner, A.** Not quite lost in translation: Mistranslation alters adaptive landscape topography and the dynamics of evolution (submitted).

244. Papkou, A., **Wagner, A.** A rugged yet easily navigable fitness landscape of antibiotic resistance (submitted).

243. **Wagner, A.** Evolvability-enhancing mutations in the fitness landscape of an RNA and a protein (submitted).

242. Dasmeh. P., Zheng, J., **Wagner, A.** Rapid evolutionary change in trait correlations of a single protein. (submitted)

241. Wagner, A. Mutational robustness and evolvability. In *Evolvability*: *A unifying concept in evolutionary biology?* Hansen, T., Houle, D. Pavlicev, M., Pelabon, C. (Eds.) MIT Press, Cambridge MA. (submitted)

Appeared

240. Karve, S., Dasmeh, P., Zheng, J., **Wagner, A.** (2022) Low protein expression enhances phenotypic evolvability by intensifying selection on folding stability. *Nature Ecology and Evolution* **6**, 1155—1164.

239. Wagner, A. (2022) AI predicts the effectiveness and evolution of gene promoter sequences. *Nature* **603**, 399-400.

238. Karve, S., **Wagner, A.** (2022) Environmental complexity is more important than mutation in driving the evolution of latent novel traits in *E. coli. Nature Communications* **13,** 5904.

237. Toll-Riera, M., Olombrada, M., Castro-Giner, F., **Wagner, A.** (2022) A limit on the evolutionary rescue of an Antarctic bacterium from rising temperatures. *Science Advances* **8**, eabk3511

236. Wagner, A. (2022) Nutrient competition increases invasion resistance during assembly of microbial communities. *Molecular Ecology* **31**:4188-4203.

235. Iyengar, B.R., **Wagner, A.** (2022) Bacterial Hsp90 predominantly buffers but does not potentiate the phenotypic effects of deleterious mutations during fluorescent protein evolution. *Genetics* **222**, iyac154.

234. Iyengar, B.R., **Wagner, A**. (2022) GroEL/S helps to purge deleterious mutations and reduce genetic diversity during adaptive protein evolution. *Molecular Biology and Evolution* **39**: msac047.

233. Brewer, T.E., **Wagner, A.** (2022) Translation stalling proline motifs are enriched in slow-growing, thermophilic, and multicellular bacteria. *The ISME Journal* **16**, 1065-1073

232. Moerman, F., Fronhofer, E.A., Altermatt, F. **Wagner, A**. (2022) Selection on growth rate and local adaptation drive genomic adaptation during experimental range expansions in the protist *Tetrahymena thermophila*. *Journal of Animal Ecology* **91**, 1088-1103.

231. Van Gestel, J., **Wagner, A.** (2021) Cryptic surface-associated multicellularity emerges through cell adhesion and its regulation. *PLoS Biology* **19(5),** e3001250.

230. Karve, S., **Wagner, A.** (2021) Multiple novel traits without immediate benefits originate in bacteria evolving on single antibiotics. *Molecular Biology and Evolution* msab341

229. San Roman, M., **Wagner, A.** (2021) Diversity begets diversity during community assembly until ecological limits impose a diversity ceiling. *Molecular Ecology* **30**, 5874-5887

228. Dasmeh, P., **Wagner, A.** (2021) Yeast proteins may reversibly aggregate like amphiphilic molecules. *Journal of Molecular Biology* **434**, 167352

227. Schweizer, G., **Wagner, A.** (2021) Both binding strength and evolutionary accessibility affect the population frequency of transcription factor binding sequences in *Arabidopsis thaliana. Genome Biology and Evolution* **13***, evab273*

226. Wagner, A. Adaptive evolvability through direct selection instead of indirect, second-order selection. (2021) *Journal of Experimental Zoology Part B: Molecular and Developmental Evolution* **338**: 395–404.

225. Dasmeh, P., Doronin, R., **Wagner, A.** (2021) The length scale of multivalent interactions is evolutionarily conserved in fungal and vertebrate phase-separating protein. *Genetics* **220**, iyab184.

224. Figueiredo, A.R.T, **Wagner, A.,** Kümmerli, R. (2021) Ecology drives the evolution of diverse social strategies in *Pseudomonas aeruginosa. Molecular Ecology* **30**, 5214-5228

223. Zheng, J., Bratulic, S., Lischer, H.E.L., **Wagner, A.** (2021) Mistranslation can promote the exploration of alternative evolutionary trajectories in enzyme evolution. *Journal of Evolutionary Biology* **34**: 1302-1315.

222. Zheng, J., Guo, N., **Wagner, A.** (2021) Mistranslation reduces mutation load in evolving proteins through negative epistasis with DNA mutations. *Molecular Biology and Evolution* **38**, 4792-4804

221. **Wagner, A.** (2021) Adaptive gene misregulation. *Genetics* **217**, iyaa044 (https://doi.org/10.1093/genetics/iyaa044).

220. Dasmeh, P., **Wagner, A.** (2021) Natural selection on the phase-separation properties of FUS during 160 million years of mammalian evolution. *Molecular Biology and Evolution* **38**, 940-951.

219. Zheng, J., Guo, N., **Wagner, A.** (2020) Strong selection enhances protein evolvability by increasing mutational robustness and foldability. *Science* **370**, 6521

218. San Roman, M., **Wagner, A.** (2020) Acetate and glycerol are not uniquely suited for the evolution of cross-feeding in *E. coli. PLoS Computational Biology* **16 (11)**, e1008433

217. Schweizer, G., **Wagner, A.** (2020) Genotype networks of 80 quantitative *Arabidopsis thaliana* phenotypes reveal substantial phenotypic evolvability despite pervasive epistasis. *PLoS Computational biology* **16 (8)**, e1008082.

216. Schmutzer, M., **Wagner, A.** (2020) Gene expression noise can promote the fixation of beneficial mutations in fluctuating environments. *PLoS Computational Biology* **16 (10)**, e1007727

215. Azpeitia, E., **Wagner, A.** (2020) Signaling pathways have an inherent need for noise to acquire information. *BMC Bioinformatics* **21***, 1-21

214. Wagner, A. (2020) Information theory can help quantify the potential of new phenotypes to originate as exaptations. *Frontiers of Ecology and Evolution* **8**: 564071

213. Azpeitia, E., **Wagner, A.** (2020) Short residence times of DNA-bound transcription factors can reduce gene expression noise and increase the transmission of information in a gene regulation system. *Frontiers in Molecular Biosciences* **7**: 67

212. Moerman, F., Fronhofer, E.A., **Wagner, A**. Altermatt, F. (2020) Gene swamping alters evolution during range expansions in the protist *Tetrahymena thermophile. Biology Letters* **16**, 20200244.

211. Moerman, F., Arquint, A., Merkli, S. **Wagner, A.,** Altermatt F., Fronhofer, E.A. (2020) Evolution under pH stress and high population densities leads to increased density-dependent fitness in the protest *Tetrahymena thermophile. Evolution* **74**, 573-586.

210. Zheng, J., Payne, J.L., **Wagner, A**. (2019) Cryptic genetic variation accelerates adaptive evolution by opening alternative paths towards diverse adaptive peaks. *Science* **365**, 347-353

209. van Gestel, J., Ackermann, M., **Wagner, A.** (2019) Microbial life cycles link global modularity in regulation to mosaic evolution. *Nature Ecology and Evolution* **3**, 1184-1196

208. Payne, J.L., **Wagner, A.** (2019) The causes of evolvability and their evolution. *Nature Reviews Genetics* **20**, 24–38.

207. Libby, E., Hebert-Dufresne, L., Hosseini, S.-R., **Wagner, A**. (2019) Syntrophy emerges spontaneously in complex metabolic systems. *PLoS Computational Biology* **15** (7), e1007169

206. Aguilar-Rodriguez, J., Fares, M.,A., **Wagner, A.** (2019) Chaperonin overproduction and metabolic erosion caused by mutation accumulation in Escherichia coli. *FEMS microbiology letters* **366** (10), fnz121.

205. Payne, J.L., Khalid, F., **Wagner, A.** (2018) RNA-mediated gene regulation is less evolvable than transcriptional regulation. *Proceedings of the National Academy of Sciences of the U.S.A.* **115**, E3481-E3490

204. Hosseini, S.-R., **Wagner, A**. (2018) Genomic organization underlying deletional robustness in bacterial metabolic systems. *Proceedings of the National Academy of Sciences of the U.S.A.* **115**, 7075-7080.

203. Sprouffske, K., Aguilar-Rodriguez, J., Sniegowski, P., **Wagner, A.** (2018) High mutation rates limit evolutionary adaptation in Escherichia coli. *PLoS Genetics* **14**, e1007324.

202. Schaerli, Y., Jimenez, A., Duarte, J.M., Mihajlovic, L., Renggli, J., Isalan, M., Sharpe, J., **Wagner, A.** (2018) Mechanistic causes of constrained phenotypic variation revealed by synthetic gene regulatory circuits. *Molecular Systems Biology* **14**, e8102.

201. San Roman, M., **Wagner, A.** (2018) An enormous potential for niche construction through bacterial cross-feeding in a homogeneous environment. *PLoS Computational Biology* **14**, e1006340

200. Aguilar Rodriguez, J., Peel, L., Stella, M., **Wagner, A.** Payne., J.A. (2018) The architecture of an empirical genotype-phenotype map. *Evolution* **72**, 1242-1260.

199. Aguilar-Rodriguez, J., **Wagner, A.** (2018) Metabolic determinants of enzyme eolution in a genome-scale bacterial metabolic network. *Genome Biology and Evolution* **10**, 3076-3088.

198. Bichsel, M., Barbour, A.D., **Wagner, A.** (2018) Dynamics of an insertion sequence infection in a spatially structured environment. *Journal of Biological Systems* **26**, 133-166.

197. Chu, H.-Y., Sprouffske, K., **Wagner, A.** (2018) Assessing the benefits of horizontal gene transfer by laboratory evolution and genome sequencing. *BMC evolutionary biology* **18**, 54

196. Catalan, P., **Wagner, A.,** Manrubia, S., Cuesta, J.A. (2018) Adding levels of complexity enhances robustness and evolvability in a multi-level genotype-phenotype map. *Journal of the Royal Society Interface* **15**, 20170516.

195. Vahdati, A.R., **Wagner, A.** (2018) Population size affects adaptation in complex ways: simulations on empirical adaptive landscapes. *Evolutionary Biology* **45**, 156-169,
https://doi.org/10.1007/s11692-017-9440-9

194. Bratulic, S., Toll-Riera, M., **Wagner, A.** (2017) Mistranslation benefits adaptive evolution through purging of deleterious mutations. *Nature Communications* 8, 15410.

193. Aguilar Rodriguez, J., Payne., J.A., **Wagner, A.** (2017) 1000 empirical adaptive landscapes and their navigability. *Nature Ecology and Evolution* 1, 0045 (doi: 10.1038/s41559-016-0045)

192. Fortuna, M.A., Zaman, L., Ofria, C., **Wagner, A.** (2017) The genotype-phenotype map of an evolving digital organism. *PLoS Computational Biology* **13** (2), e1005414

191. **Wagner, A.** (2017) The White Knight hypothesis, or does the environment limit evolutionary innovations? *Trends in Ecology and Evolution* **32**, 131-140.

190. Hochberg, M. E., Marquet, P.A., Boyd, R., **Wagner, A.** (2017) Innovation: an emerging focus from cells to societies. *Philosophical Transactions of the Royal Society B* **372**: 20160414.

189. Chu, H.-Y., Sprouffske, K., **Wagner, A.** (2017) The role of recombination in evolutionary adaptation of *Escherichia coli* to a novel nutrient. *Journal of Evolutionary Biology* **30**: 1692–1711.

188. Hosseini, S.-R., **Wagner, A.** (2017) Constraint and contingency pervade the emergence of novel phenotypes in complex metabolic systems. *Biophysical Journal* **113**, 690-701

187. **Wagner, A.** (2017) Information theory, evolutionary innovations, and evolvability. *Philosophical Transactions of the Royal Society B* **372**: 20160416.

186. Fortuna, M.A., Zaman, L., **Wagner, A.,** Bascompte, J. (2017) Non-adaptive origins of evolutionary innovations increase network complexity in interacting digital organisms. *Philosophical Transactions of the Royal Society B* **372**: 20160431.

185. Vahdati, A.R., Sprouffske, K., **Wagner, A.** (2017) Effect of population size and mutation rate on the evolution of RNA sequences on an adaptive landscape determined by RNA folding. *International Journal of Biological Sciences* **13**: 1138.

184. Hosseini, S.-R., Martin, O.C., **Wagner, A.** (2016) Phenotypic innovation through recombination in genome-scale metabolic networks. *Proceedings of the Royal Society B: Biological Sciences* **283**: 20161536 (http://dx.doi.org/10.1098/rspb.2016.1536)

183. Toll-Riera, M., San Millan, A., **Wagner, A.**, MacLean, R.C. (2016) The genomic basis of metabolic evolutionary innovation in Pseudomonas aeruginosa. *PLoS Genetics* **12**(5), e1006005.

182. **Wagner, A.,** Ortman, S., Maxfield, R. (2016) From the primordial soup to self-driving cars: standards and their role in natural and technological innovation. *Journal of the Royal Society Interface* **13**, 20151086.

181. Aguilar-Rodríguez, J., Sabater-Muñoz, B., Montagud-Martínez, R. Berlanga, V. Alvarez-Ponce, D., **Wagner, A.,** Fares, M.A. The molecular chaperone DnaK is a source of mutational robustness. (2016) *Genome Biology and Evolution* 8: 2979-2991.

180. Sprouffske, K., Aguilar-Rodriguez, J., **Wagner, A**. (2016) How archiving by freezing alters the genome-scale diversity of Escherichia coli populations. *Genome Biology and Evolution* **8** (5), 1290-1298.

179. Hosseini, S.-R., Martin, O.C., **Wagner, A.** (2016) The potential for non-adaptive origins of evolutionary innovations in central carbon metabolism. *BMC Systems Biology* 10 (1), 97

178. Vahdati, A.R., **Wagner, A.** (2016) Parallel or convergent evolution in human population genomic data revealed by genotype networks. *BMC Evolutionary Biology* **16**, 1.

177. Khalid, F., Aguilar-Rodríguez, J., **Wagner, A.,** Payne, J.L. (2016) Genonets server – A web server for the construction, analysis, and visualization of genotype networks. *Nucleic Acids Research*, **44**: W70-W76.

176. Sprouffske, K., **Wagner, A.** (2016) Growthcurver: An R package for obtaining interpretable metrics from microbial growth curves. *BMC Bioinformatics* **17**, 1.

175. Blattner, A.C., Aguilar-Rodriguez, J., Kränzlin, M., **Wagner, A.,** Lehner, C.F. (2016) Drosophila Nnf1 paralogs are partially redundant for somatic and germ line kinetochore function. *Chromosoma.,* 1-19. doi:10.1007/s00412-016-0579-4.

174. Wagner, A., Payne, J. L. (2016) Robustness and Evolvability in Molecular Evolution. In *Encyclopedia of Evolutionary Biology*, Elsevier, pp. 484 - 488.

173. Hayden, E., Bendixsen, D.P., **Wagner, A.** (2015) Intramolecular phenotypic capacitance in a modular RNA molecule. *Proceedings of the National Academy of Sciences* **112**, 12444-12449

172. Bratulic, S., Gerber, F., **Wagner, A.** (2015) Mistranslation drives the evolution of robustness but not translational accuracy in TEM-1 β-lactamase. *Proceedings of the National Academy of Sciences* **112** , 12758-12763.

171. Hosseini, S.-R., Barve, A., **Wagner, A.** (2015) Exhaustive analysis of a genotype space comprising 10^{15} central carbon metabolisms reveals an organization conducive to metabolic innovation. *PLoS Computational Biology* **11** (8), e1004329.

170. Bilgin Sonay, T., Carvalho, T., Robinson, M., Greminger, M., Krutzen, M., Comas, D., Highnam, G., Mittelman, D.A., Sharp., A.J., Marques-Bonet, T., **Wagner, A.** (2015) Tandem repeat variation in human and great ape populations, and its impact on gene expression divergence. *Genome Research* **25**, 1591-1599.

169. Sabater-Muñoz, B., Prats-Escriche, M., Montagud-Martínez, R., López-Cerdán, A., Toft, C., Aguilar-Rodríguez, J., **Wagner, A.,** Fares, M.A. (2015) Fitness trade-offs determine the role of the molecular chaperonin GroEL in buffering mutations. *Molecular Biology and Evolution* **32**, 2681-2693.

168. **Wagner, A.** (2015) Causal drift, robust signaling, and complex disease. *PLoS ONE* **10**(3), e0118413.

167. Payne, J.L., **Wagner, A.** (2015) Mechanisms of mutational robustness in transcriptional regulation. *Frontiers in Genetics* **6**, 322, doi: 10.3389/fgene.2015.00322.

166. Payne, J.L., **Wagner, A.** (2015) Function does not follow form in gene regulatory circuits. *Scientific Reports* **5**, 13015, doi:10.1038/srep13015.

165. Calcott, B., Levy, A., Siegal, M.L., Soyer, O.S., **Wagner, A.** (2015) Engineering and biology: Counsel for a continued relationship. *Biological Theory* **10**, 50-59.

164. Dall'Olio, G.M., Vahdati, A.R., Bertranpetit, J. **Wagner, A.** Hafid, L. (2015) VCF2Networks: applying genotype networks to single nucleotide variants data. *Bioinformatics* **31**, 438-439.

163. Bilgin Sonay, T., Koletou, M., **Wagner, A.** (2015) A survey of tandem repeat instabilities and associated gene expression changes in 35 colorectal cancers. *BMC Genomics* **16** (1), 702.

162. Payne, J.L., **Wagner, A**. (2014) The robustness and evolvability of transcription factor binding sites. *Science* **343**, 875-877.

161. Wagner, A. (2014) A genotype network reveals homoplastic cycles of convergent evolution in influenza A (H3N2) evolution. P*roceedings of the Royal Society B: Biological Sciences* **281**, 20132763.

160. Szovényi, P., Devos, N., Weston, D.J., Yang, X., Hock, Z., Shaw, J.A., Shimizu, K.K., McDaniel, S., **Wagner, A.** (2014) Efficient purging of deleterious mutations in plants with haploid selfing. *Genome Biology and Evolution* **6**, 1238-1252.

159. **Wagner, A.**, Rosen, W. (2014) Spaces of the possible: universal Darwinism and the wall between technological and biological innovation. *Journal of the Royal Society Interface* **11**, 20131190.

158. Payne, J.L., **Wagner, A.** (2014) Latent phenotypes pervade gene regulatory circuits. *BMC Systems Biology* **8** (1), 64.

157. Dhar, R., Bergmiller, T., **Wagner, A.** (2014) Increased gene dosage plays a predominant role in the initial stages of evolution of duplicate TEM-1 beta lactamase genes. *Evolution* **68**, 1775-1791.

156. Hayden, E., Bratulic, S., Konig, I., Ferrada, E., **Wagner, A.** (2014) The effects of stabilizing and directional selection on phenotypic and genotypic variation in a population of RNA enzymes. *Journal of Molecular Evolution* **78**, 101-108.

155. Barve, A., Hosseini, S.-R., Martin, O.C**., Wagner, A**. (2014). Historical contingency and the gradual evolution of metabolic properties in central carbon and genome-scale metabolisms. *BMC Systems Biology* 2014, **8**:48.

154. **Wagner, A**. (2014) Mutational robustness accelerates the origin of novel RNA phenotypes through phenotypic plasticity. *Biophysical Journal* **106**, 955-965.

153. Sunnaker, M., Zamora-Sillero, E., Garcia de Lomana, A.L., Rudroff, F., Sauer, U., Stelling, J., **Wagner, A.** (2014) Topological augmentation to infer hidden processes in biological systems. *Bioinformatics* **30**, 221-227.

152. Dall'Olio, G.M., Bertranpetit, J. **Wagner, A.** Hafid, L. (2014) Human genome variation and the concept of genotype networks. *PLoS ONE* **9**(6), e99424. doi:10.1371/journal.pone.0099424.

151. **Wagner, A.,** Andriasyan, V., Barve, A. (2014) The organization of metabolic genotype space facilitates adaptive evolution in nitrogen metabolism. *Journal of Molecular Biochemistry* **3**: 2-13.

150. Payne, J.L., Moore, J.H., **Wagner, A.** (2014) Robustness, evolvability, and the

logic of genetic regulation. *Artificial Life* **20**, 111-126.

149. Barve, A., **Wagner, A**. (2013) A latent capacity for evolutionary innovation through exaptation in metabolic systems. *Nature* **500**, 203-206.

148. Sunnaker, M., Zamora-Sillero, E., Dechant, R., Ludwig, C., Busetto, A.G., **Wagner, A.,** Stelling, J.(2013) Automatic generation of predictive dynamic models reveals nuclear phosphorylation as the key Msn2 control mechanism. *Science Signaling* **6**, ra41

147. Szovenyi, P., Ricca, M., Hock, Z., Shaw, J.A., Shimizu, K.K., **Wagner, A.** (2013) Selection is no more efficient in haploid than in diploid life stages of an angiosperm and a moss. *Molecular Biology and Evolution* **30**: 1929-1939

146. Payne, J.A**., Wagner, A.** (2013) Constraint and contingency in multifunctional gene regulatory circuits. *PLoS Computational Biology* **9** (6), e1003071.

145. Dhar, R., Sägesser, R., Weikert, C., **Wagner, A.** (2013) Yeast adapts to a changing stressful environment by evolving cross-protection and anticipatory gene regulation. *Molecular Biology and Evolution* 30, 573-588.

144. Sabath, N., Ferrada, E., Barve, A., **Wagner, A.,** (2013) Growth temperature and genome size in bacteria are negatively correlated, suggesting genomic streamlining during thermal adaptation. *Genome Biology and Evolution* **5**, 966-977.

143. Bilgin, T., Kurnaz, I.A., **Wagner, A.** (2013) Selection shapes the robustness of ligand-binding amino acids. *Journal of Molecular Evolution* **76,** 343-349

142. Bichsel, M., Barbour, A.D., **Wagner, A**. (2013) Estimating the fitness effect of insertion sequences. *Journal of Mathematical Biology* **66***,* 95-114.

141. **Wagner, A.** (2013) Genotype networks and evolutionary innovations in biological systems. In *Handbook of Systems Biology*. Eds: Walhout, A.J.M., Vidal, M., Dekker, J., Academic Press, London, p 251-264.

140. **Wagner, A.** (2013) Metabolic networks and their evolution. In *Encyclopedia of Systems Biology*; p 1256-1259; Dubitzky, W., Wolkenhauer, O., Yokota, H., Cho, K.-H. (eds) Springer, New York.

139. Barve, A., Rodrigues, J.F.M., **Wagner, A.** (2012) Superessential reactions in metabolic networks. *Proceedings of the National Academy of Sciences of the U.S.A.* **109** (18), E1121-E1130.

138. **Wagner, A.** (2012) The role of robustness in phenotypic adaptation and innovation. *Proceedings of the Royal Society B: Biological Sciences* **279**, 1249-1258.

137. Hayden, E.J., **Wagner, A**. (2012) Environmental change exposes beneficial epistatic interactions in a catalytic RNA. *Proceedings of the Royal Society B: Biological Sciences* **279**, 3418-3425.

136. Chen, B., **Wagner, A.** (2012) Hsp90 is important for fecundity, longevity, and buffering of cryptic deleterious variation in wild fly populations. *BMC Evolutionary Biology* **12**, 25

135. Sabath, N., **Wagner, A.,** Karlin, D. (2012) Evolution of viral proteins originated de novo by overprinting. *Molecular Biology and Evolution* **29**, 3767-3780

134. **Wagner, A.** (2012) The role of randomness in Darwinian evolution. *Philosophy of Science* **79**, 95-119

133. Guo, B., Zuo, M., **Wagner, A.** (2012) Pervasive indels and their evolutionary dynamics after the fish-specific genome duplication. *Molecular Biology and Evolution.* 29, 3005-3022.

132. Bragg, J.G., Quigg, A., Raven, J.A., **Wagner, A.** (2012) Protein elemental sparing and codon usage bias are correlated among bacteria. *Molecular Ecology* **21***, 2480–248.*

131. Ferrada, E., **Wagner, A.** (2012) A comparison of genotype-phenotype maps for RNA and proteins. *Biophysical Journal* **102**, 1916-1925.

130. Matias Rodrigues, J.F., Rankin, D., Rossetti, V., **Wagner, A.**, Bagheri, H.C. (2012) Differences in cell division rates drive the evolution of terminal and differentiation in microbes. *PLoS Computational Biology* **8** (4), e1002468.

129. De la Chaux, N., Tsuchimatsu, T., Shimizu, K.K., **Wagner, A.** (2012) The predominantly selfing plant *Arabidopsis thaliana* experienced a recent reduction in transposable element abundance compared to its outcrossing relative *Arabidopsis lyrata*. *Mobile DNA* **3**, 2.

128. Bilgin, T., **Wagner, A.** (2012) Design constraints on a synthetic metabolism. *PLoS ONE* **7**(6): e39903

127. **Wagner, A.** (2012) Metabolic networks and their evolution. *Evolutionary Systems Biology/Advances in Experimental Medicine and Biology* **751**: 29-52

126. **Wagner, A.** (2012) High dimensional adaptive landscapes facilitate evolutionary innovation p271-282 *in* Svensson, E.I., Calsbeek, R. (eds) The adaptive landscape in evolutionary biology. Oxford University Press, Oxford, UK.

125. Wagner, A., Weikert, C. (2012) Phenotypic constraints and phenotypic hitchhiking in a promiscuous enzyme. *The Open Evolution Journal* **6**, 14-28.

124. Hayden, E., **Wagner, A.** (2012) Directional selection causes decanalization in a catalytic RNA*. PLoS ONE* 7(9), e45351.

123. Hayden, E.J., Ferrada, E., **Wagner, A.** (2011) Cryptic genetic variation promotes rapid evolutionary adaptation in an RNA enzyme. *Nature* **474**, 92-95.

122. **Wagner, A.** (2011) The molecular origins of evolutionary innovations. *Trends in Genetics* **27**, 397-410.

121. Dhar, R., Sägesser, R., Weikert, C., Yuan, J., **Wagner, A**. (2011) Adaptation of *Saccharomyces cerevisiae* to saline stress through laboratory evolution. *Journal of Evolutionary Biology* **5**, 1135-1153.

120. Wagner, A. (2011) Genotype networks shed light on evolutionary constraints. *Trends in Ecology and Evolution* **26**, 577-584.

119. Samal, A., **Wagner, A.,** Martin, O.C. (2011) Environmental versatility promotes modularity in large scale metabolic networks. *BMC Systems Biology* **5**,135.

118. Raman, K., **Wagner, A.** (2011) Evolvability and robustness in a complex signaling circuit. *Molecular BioSystems* **7**, 1081-1092

117. Zamora-Sillero, E. Hafner, M., Ibig, A., Stelling, J., **Wagner, A.** (2011) Efficient characterization of high-dimensional parameter spaces for systems biology. *BMC Systems Biology* **5**, 142.

116. De la Chaux, N., **Wagner, A.** (2011) BEL/Pao retrotransposons in metazoan genomes. *BMC Evolutionary Biology* **11** :154

115. Raman, K., **Wagner, A.** (2011) The evolvability of programmable hardware. *Journal of the Royal Society Interface* **8**: 269-281

114. Espinosa-Soto, C. Martin, O.C., **Wagner, A**. (2011) Phenotypic plasticity can facilitate adaptive evolution in gene regulatory circuits. *BMC Evolutionary Biology* **11:5**, doi:10.1186/1471-2148-11-5

113. Rodrigues, J.F.M., **Wagner, A.** (2011) Genotype networks, innovation, and robustness in sulfur metabolism. *BMC Systems Biology* **5:39**.

112. **Wagner, A.** (2011) The low cost of recombination in creating novel phenotypes. *Bioessays* **33**, 636-646.

111. Wright, J., Bellissimi, E., de Hulster, E., **Wagner, A.,** Pronk, J.T., van Maris, A.J.A. (2011) Batch and continuous culture-based selection strategies for acetic acid tolerance in xylose-fermenting *Saccharomyces cerevisiae. FEMS Yeast Research* **11**, 299–306

110. Espinosa-Soto, C., Martin, O.C., **Wagner, A.** (2011) Phenotypic plasticity can increase phenotypic variability after non-genetic perturbations in gene regulatory circuits. *Journal of Evolutionary Biology* **24**, 1284-1297.

109. Guo, B., **Wagner, A.,** He, S. (2011) Duplicated gene evolution following whole-genome duplication in teleost fish. pp. 27-36. In: Friedberg, F. (ed.), Gene duplication. InTech, Rijeka, Croatia

108. Espinosa-Soto, C., **Wagner, A.** (2010) Specialization can drive the evolution of modularity. *PloS Computational Biology* **6**: e1000719.

107. Samal, A., Matias Rodrigues, J.F., Jost, J., Martin, O.C., **Wagner, A.** (2010) Genotype networks in metabolic reaction spaces. *BMC Systems Biology* **4**:30.

106. Rankin, D.J., Bichsel, M. **Wagner, A.** (2010) Mobile DNA can drive lineage extinction in bacterial populations. *Journal of Evolutionary Biology* **23**, 2422-2431

105. Ferrada, E., **Wagner, A.** (2010) Evolutionary innovation and the organization of protein functions in genotype space. *PLoS ONE* 5(11): e14172.

104. **Wagner, A.** (2010) On the energy and material cost of gene duplication. In: Dittmar, K., Liberles, D. *Evolution after gene duplication*. Wiley-Blackwell, Hoboken, NJ, p 207-214.

103. Bragg, JG**, Wagner, A.** (2010) The evolution of protein material costs. In: *Evolutionary genomics and systems biology*, Caetano-Anolles, G., Ed., Wiley, NY, p 203-211.

102. Bichsel, M., Barbour, A.D., **Wagner, A.** (2010) The early phase of an insertion sequence infection. *Theoretical Population Biology* 78, 278-288.

101. Sulc, P., **Wagner, A.,** Martin, O.C. (2010) Quantifying slow evolutionary dynamics in RNA fitness landscapes. *Journal of Bioinformatics and Computational Biology* **8***, 1027-1040.*

100. Bragg, JG**, Wagner, A.** (2009) Protein material costs: single atoms can make an evolutionary difference**.** *Trends in Genetics* **25***, 5-8.*

99. Martin, O.C.M., **Wagner, A.** (2009) Effects of recombination on complex regulatory circuits. *Genetics* **183**, 673-684.

98. Wagner, A. (2009) Evolutionary constraints permeate large metabolic networks. *BMC Evolutionary Biology* **9:**231

97. Rodrigues, J., **Wagner, A.** (2009) Evolutionary plasticity and innovations in complex metabolic reaction networks. *PloS Computational Biology* 5(12).

96. Hafner, M., Koeppl, H., Hasler, M., **Wagner, A**. (2009) "Glocal" robustness analysis and model discrimination for circadian oscillators. *PloS Computational Biology* 5(10): e1000534.

95. de la Chaux, N., **Wagner, A.** (2009) Evolutionary dynamics of the LTR retrotransposon roo inferred from twelve complete Drosophila genomes. *BMC Evolutionary Biology* **9:**205

94. **Wagner, A**. (2009) Transposable elements as genomic diseases. *Molecular Biosystems*, **5** 32.

93. Wagner, A. (2009) Networks in molecular evolution. In: Meyers, R.A. (ed.) Encyclopedia of Complexity and System Science. Springer, Heidelberg.

92. **Wagner, A.**. (2009) Andreas Wagner. *In* Oftedal, G., Olsen, J.K.B., Rossell, P., Norup, M.S. (eds.) Evolutionary theory: 5 Questions. p 223-229. Automatic Press / VIP, Copenhagen.

91. Hafner, M., Koeppl, H., **Wagner, A.** (2009) Evolution of feedback loops in oscillatory systems. Proceedings of the Third International Conference on Foundations of Systems Biology in Engineering (FOSBE 2009), Denver, CO, August 9-12, 2009.

90. Wagner, A. (2008) Neutralism and selectionism: A network-based reconciliation. *Nature Reviews Genetics* **9**, 965-974.

89. Wagner, A. (2008) Robustness and evolvability: A paradox resolved. *Proc. Roy. Soc. London Series. B* **275***,* 91-100.

88. Ferrada, E., **Wagner, A.** (2008) Protein robustness promotes evolutionary innovations on large evolutionary time scales *Proc. Roy. Soc. London Series. B* **275**:1595-602.

87. Wright, J., **Wagner, A.** (2008) The systems biology research tool: Evolvable open-source software. *BMC Systems Biology* **2**:55.

86. Martin, OC, **Wagner, A**. (2008) Multifunctionality and robustness tradeoffs in model genetic circuits. *Biophysical Journal* **94**, 2927-2937.

85. Jörg, T., Martin, OC, **Wagner, A.** (2008) Neutral network sizes of biological RNA molecules can be computed and are atypically large. *BMC Bioinformatics* **9**:464.

84. Wagner, A. (2008) Gene duplications, robustness, and evolutionary innovations. *Bioessays* **30**, 367-373.

83. Wagner, A., de la Chaux, N. (2008) Distant horizontal gene transfer is rare for mobile prokaryotic DNA. *Molecular Genetics and Genomics* **280,** 397-408.

82. Felix, M-A, **Wagner, A**. (2008) Robustness and evolution: concepts, insights, and challenges from a developmental model system. *Heredity* **100**, 132-140

81. Wright, J., **Wagner, A.** (2008) Exhaustive identification of steady state cycles in large stoichiometric networks. *BMC Systems Biology*, **2**:61.

80. Fuller, M., **Wagner, A.** , Enquist, J. (2008) Using network analysis to characterize forest structure. *Natural Resources Modeling* **21**, 225-247.

79. Ciliberti, S., Martin, OC, **Wagner, A**. (2007) Innovation and robustness in complex regulatory gene networks. *Proc. Natl. Acad. Sci. U.S.A*. **104**, 13591-13596

78. Ciliberti, S, Martin, OC, **Wagner, A**. (2007) Robustness can evolve gradually in complex regulatory networks with varying topology. *PLoS Computational Biology* **3(2)**: e15

77. **Wagner, A.** (2007) Rapid detection of positive selection in genes and genomes through variation clusters. *Genetics* **176**: 2451–2463.

76. Bragg, JG**, Wagner, A.** (2007) Protein carbon content evolves in response to carbon availability and may influence the fate of duplicated genes. *Proc. Roy. Soc. London Series. B* **274**, 1063-1070.

75. Wagner, A., Lewis, C., Bichsel, M. (2007) A survey of transposable elements using IScan. *Nucleic Acids Research* **35**, 5284-5293

74. Wagner, A. (2007) From bit to it: The transformation of information into living matter by metabolic networks. *BMC Systems Biology* **1**: 33.

73. Wagner, A. (2007) Gene networks and natural selection: Is there a network biology?
In Pagel, M. Pomiankowski, A. (eds.) Evolutionary Genomics and Proteomics, Sinauer Associates, Sunderland, MA, USA

72. Sumedha, Martin, OC, **Wagner, A**. (2007) New structural variation in evolutionary searches of RNA neutral networks. *Biosystems* **90**: 475-485.

71. Wagner, A. (2007) Energy costs constrain the evolution of gene expression. *Journal of Experimental Zoology (Molecular and Developmental Evolution)* **308B**:322–324

70. Wagner, A., Wright, J. (2007) Alternative routes and mutational robustness in complex regulatory networks. *Biosystems* **88**, 163-172.

69. **Wagner A** (2006) Cooperation is Fleeting in the World of Transposable Elements. *PLoS Computational Biology* **2**(12): e162

68. Wagner, A. (2006) Periodic extinctions of transposable elements in bacterial lineages: Evidence from intragenomic variation in multiple genomes. *Molecular Biology and Evolution* **23**, 723-733.

67. Vitkup, D, Kharchenko, P., **Wagner, A**. (2006) Influence of metabolic network structure and function on enzyme evolution. *Genome Biology* **7**(5):R39.

66. Gilchrist, MA, **Wagner, A.** (2006) A model of protein translation including codon bias, nonsense errors,and ribosome recycling. *Journal of Theoretical Biology* **239,** 417-434

65. Wagner, A. (2005) Circuit topology and the evolution of robustness in two-gene circadian oscillators. *Proc. Natl. Acad. Sci. U.S.A.* **102,** 11775-11780

64. Wagner, A. (2005) Energy constraints on the evolution of gene expression. *Molecular Biology and Evolution* **22**:1365–1374.

63. Wagner, A. (2005) Distributed robustness and redundancy as causes of mutational robustness**.** *Bioessays* **27**,176–188

62. Conant, GC, **Wagner, A.** (2005) The rarity of gene shuffling in conserved genes. *Genome Biology* **6**(6), R50

61. Wagner, A. (2005) Robustness, Neutrality, and Evolvability. *FEBS Letters* **579**: 1772–1778.

60. Wagner, A. (2005) The structure of large genetic networks: design, history, or (mere) chemistry? In: Koonin, EV (ed.) Power laws, scale-free networks and genome biology. Landes Bioscience, Georgetown, TX

59. Wagner, A., Wright, J **(**2005). Compactness and cycles in signal transduction and transcriptional regulation networks: a signature of natural selection? *Advances in Complex Systems* **7**, 419-432.

58. Wagner, A. (2005) Lessons from a genetic network about the evolution of dominance. In: Veitia R. (ed.) The biology of genetic dominance. Landes Bioscience, Georgetown, TX

57. Conant, G.C., **Wagner, A.** (2004) Duplicate genes and robustness to transient gene knockouts in *Caenorhabditis elegans Proc. Roy. Soc. London Series.* B **271**, 89-96.

56. Hahn, M., Conant, G.C., **Wagner, A.** (2004) Evolution in large genetic networks: connectivity does not equal importance. *Journal of Molecular Evolution* **58**, 203-211

55. Gilchrist, M.A., Salter, L.A., **Wagner, A.** Gilchrist, MA, Salter, L., **Wagner, A**. (2004) A statistical framework for combining and interpreting proteomic datasets. *Bioinformatics* **20**, 689-700

54. **Wagner, A**. (2004) Reconstructing pathways in large genetic networks from genetic perturbations. *Journal of Computational Biology* **11**, 53-60.

53. Tringe, SG, **Wagner, A.**, Ruby, S.W. (2004) Enriching for direct regulatory targets in perturbed gene expression profiles. *Genome Biology* **5**, 109

52. Evangelisti, A, **Wagner, A**. (2004) Molecular evolution in the transcriptional regulation network of yeast. *Journal of Experimental Zoology Part B – Molecular and Developmental Evolution 302B*, 392-411.

51. Conant, G.C., **Wagner, A.** (2004) A fast algorithm for determining the longest combination of local alignments to a query sequence. *BMC Bioinformatics* **5**, 62

50. Berg, J. Lässig, M., **Wagner, A.**, (2004) Structure and evolution of protein interaction networks: a statistical model for link dynamics and gene duplication. *BMC Evolutionary Biology* 2004, **4**:51.

49. Conant, G.C. **Wagner, A.** (2003) Convergent evolution in gene circuits. *Nature Genetics* **34**, 264-266

48. Wagner, A. (2003) How large protein interaction networks evolve. *Proc. R. Soc. Lond.* B **270**, 457–466

47. Wagner, A. Does natural selection mold molecular networks? (2003) *Science* STKE, pe 41-43.

46. Wagner, A. Risk management in biological evolution. (2003) *Journal of Theoretical Biology* **225**, 45-47

45. de Visser, J.A.G.M, Hermisson, J., Wagner, G.P., Ancel, L.W., Bagheri, H., Blanchard, J.L., Chao, L., Cheverud, J.M., Elena, S.F., Fontana, W., Gibson, G., Hansen, T., Krakauer, D., Lewontin, R.C., Ofria, C., Rice, S.H., von Dassow, G., **Wagner, A**., and Whitlock, M.C. Evolution and detection of genetic robustness. (2003) *Evolution* **57**, 1959-1972

44. Conant, G.C., **Wagner, A**. (2003) Asymmetric sequence divergence of duplicate genes. *Genome Research* **13**, 2052-2058

43. Wagner, A. (2003) Evolution: Neutralist view. In *Nature Encyclopedia of the Human Genome;* vol. 2; pp 379; David Cooper (ed.) Nature Publishing Group: London, UK. (http://www.ehgonline.net/)

42. Wagner, A. (2003) Evolution: Selectionist view. In *Nature Encyclopedia of the Human Genome;* vol 2; pp 380; David Cooper (ed.) Nature Publishing Group: London, UK.

41. Wagner, A. (2003) Protein networks. In *Complex Systems Science in Biomedicine*. Deisboeck, TS, Kresh, JY, Kepler, TB (eds.) Kluwer, New York.

40. Conant, G.C., Plimpton, S.J. Old, W., **Wagner, A**., Fain, P.R., Pacheco, T.R. and Heffelfinger, G. (2003) Parallel Genehunter: Implementation of a Linkage Analysis Package for Distributed-Memory Architectures, *Journal of Parallel and Distributed Computing* **63**, 674-682.

39. Wagner, A. (2002) Asymmetric functional divergence of duplicate genes. *Mol. Biol. Evol.* **19**, 1760–1768.

38. Conant, G.C., **Wagner, A.** (2002) GenomeHistory: a software tool and its application to fully sequenced genomes. *Nucleic Acids Research* **30**, 1-10.

37. Wagner, A. (2002) Estimating coarse gene network structure from large-scale gene perturbation data. *Genome Research* **12***,* 309-315.

36. Wagner, A. (2002) Selection after gene duplication: a view from the genome. *Genome Biology* **3**, reviews 1012.1-1012.3

35. Wagner, A. (2002) The large-scale structure of metabolic networks: a glimpse at life's origin? *Complexity* **8**, 15-19

34. Wagner, A. (2002) Gene duplications and gene redundancy. In: Encyclopedia of Life Sciences. *Nature* Publishing Group: London, UK. (http://www.els.net/)

33. Wagner, A., Fell, D. (2001) The small world inside large metabolic networks. *Proc. Roy. Soc. London Series B*, **268**, 1803-1810.

32. Wagner, A. (2001) How to reconstruct a large genetic network from *n* gene perturbation in n^2 easy steps. *Bioinformatics* **17,** 1183-1197.

31. Wagner, A. (2001) The yeast protein interaction network evolves rapidly and has few redundant duplicate genes. *Molecular Biology and Evolution* **18**, 1283-1292

30. Wagner, A. (2001) Birth and death of duplicate genes in fully sequenced eukaryotes. *Trends in Genetics* **17**, 237-239**.**

29. Gleiss, P.M., Stadler, P.F**., Wagner, A**., Fell, D.A. (2001) Relevant cycles in chemical reaction networks. *Advances in Complex Systems* **4**, 207-226.

28. Conant, G., Plimpton, S., Old, W., **Wagner, A**., Fain, P., and Heffelfinger, G. (2001). Parallel Genehunter: Implementation of a Linkage Analysis Package for Distributed-Memory Architectures, Proceedings of the First IEEE Workshop on High Performance Computational Biology. (http://www.hicomb.org/HiCOMB2002/)

27. Wagner, A. (2000) Mutational robustness in genetic networks of yeast. *Nature Genetics* **24**, 355 – 361.

26. Fell, D., **Wagner, A**. (2000) The small world of metabolism. *Nature Biotechnology* **18,** 1121-1122.

25. Wagner, A. (2000) The role of pleiotropy, population size fluctuations, and fitness effects of mutations in the evolution of redundant gene functions. *Genetics* **154**, 1389-1401

24. Wagner, A. (2000) Decoupled evolution of coding region and expression patterns after gene duplications: implications for the neutralist-selectionist debate. *Proc. Natl. Acad. Sci. U.S.A.* **97**, 6579-6584.

23. Wagner, A. (2000) Inferring life style from gene expression patterns. *Molecular Biology and Evolution* **17**, 1985-1987.

22. Fell, D.A. and **Wagner, A**. (2000) Structural properties of metabolic networks: implications for evolution and modelling of metabolism. In: J.-H. S. Hofmeyr, J. M. Rohwer and J. L. Snoep (eds) Animating the cellular map. Stellenbosch University Press, Stellenbosch. pp. 79-85.

21. Wagner, A. (1999) Genes regulated cooperatively by one or more transcription factors and their identification in whole eukaryotic genomes. *Bioinformatics* **15**, 776-784.

20. Wagner, A., Stadler, P. (1999) Viral RNA and evolved mutational robustness. *Journal of Experimental Zoology* **285**, 119-127

19. Wagner, A. (1999) Redundant gene functions and natural selection. *Journal of Evolutionary Biology* **12** , 1-16

18. Wagner, A. (1999) Causality in complex systems. *Biology and Philosophy* **14**, 83-101

17. Dudgeon, S., **Wagner, A**., Vaisnys, J.R., Buss, L.W. (1999) Dynamics of gastrovascular circulation in the hydrozoan Podocoryne carnea: the one-polyp case. *Biological Bulletin* **196**, 1-17

16. Wagner, A. (1998) A computational "genome walk" technique to identify regulatory interactions in gene networks. In: Altman, R.B., Dunker, K.A., Hunter, L., Klein, T.E. (eds.), *Proceedings of the Pacific Symposium for Biocomputing* 1998, 264-278.

15. Wagner, A., Dudgeon, S., Vaisnys, R., and L.W. Buss. (1998) Non-linear oscillations in the marine invertebrate *Podocoryne carnea. Naturwissenschaften* **85**, 117-120.

14. Wagner, A. (1998) Distribution of transcription factor binding sites in the yeast genome suggests abundance of coordinately regulated genes. *Genomics* **50,** 293-295

13. Wagner, A. (1998) The fate of duplicated genes: loss or diversification? *BioEssays* **20**, 785-788

12. Lavorgna, G., Boncinelli, E., **Wagner, A**. and T. Werner (1998) Detection of potential target genes in silico? *Trends in Genetics* 14, 375-376

11. Wagner, A. (1997) Models in the biological sciences. *In* Falkenburg, B., Hauser, S. (eds.) *Dialektik* , 1997/1, Felix Meiner, Hamburg

10. Wagner, A. (1997) A computational genomics approach to the identification of gene networks. *Nucleic Acids Research* **25**, 3594-3604.

9. Wagner, A. (1996) Does evolutionary plasticity evolve? *Evolution* **50**, 1008-1023.

8. Wagner, A. (1996) Can nonlinear epigenetic interactions obscure causal relations between genotype and phenotype? *Nonlinearity* **9**, 607-629.

7. Wagner, A. (1996) Genetic redundancy and its evolution in networks of transcriptional regulators. *Biological Cybernetics* **74**, 559-569.

6. Wagner, A., Blackstone, N., Cartwright, P., Dick, M., Misof, B., Snow, P., Wagner, G.P., Bartels, J., Murtha, M. and J. Pendleton. (1994) Surveys of gene families using polymerase chain reaction: PCR selection and PCR drift. *Systematic Biology* **43**,250-261.

5. Wagner, A. (1994) Evolution of gene networks by gene duplications: a mathematical model and its implications on genome organization. *Proc. Natl. Acad. Sci. USA*. **91**, 4387-4391.

4. Wagner, A. (1994) Reductionism in Evolutionary Biology: A Perceptional Artifact? in *1993 Lectures in Complex Systems,* eds. D. Stein and L. Nagel, Santa Fe Institute Studies in the Sciences of Complexity, Lect. Vol. X, Reading, MA:Addison-Wesley.

3. Wagner, A., Wagner, G.P. and P. Similon. (1994) Epistasis can facilitate the evolution of reproductive isolation by peak shifts: a two-locus two-allele model. *Genetics* **138**, 533-545.

2. Belazzi, T., **Wagner, A.**, Wieser, R., Schanz, M., Adam, G., Hartig, A. and H. Ruis. (1991) Negative regulation of transcription of the *Saccharomyces cerevisiae* catalase T (*CTT1*) gene by cAMP is mediated by a positive control element. *EMBO J.* **10**, 585-592.

1. Wieser, R., Adam, G., **Wagner, A.**, Schueller, C., Marchler, G., Ruis, H., Krawiec, Z. and T. Bilinski. (1991) Heat shock factor-independent heat control of transcription of the *CTT1* gene encoding the cytosolic catalase T of *Saccharomyces cerevisiae*. *J. Biol. Chem.*, **19**, 12406-12411.

Invited Lectures (since 2000)

2022

199 Dept. of Bioinformatics, University of Texas Southwestern, Dallas, TX, USA
198 Complex Systems Summer School, Santa Fe, NM, USA
197 Institute for Biochemistry and Biology, University of Potsdam, GERMANY
196 Distinguished Speaker Seminar Series, MPI for biology, Tübingen, GERMANY
195 "Peregrí Casanova" Honorary Lecture, University of Valencia, SPAIN

2019
194 ETH Zurich, Department of Biology PhD lecture series, Zurich, SWITZERLAND
193 Center for Advanced Study, Oslo, NORWAY
192 European Molecular Biology Laboratory, Heidelberg, GERMANY
191 The Santa Fe Institute, Santa Fe, NM, USA
190 Institute for Biodiversity and Ecosystems Dynamics, Univ. of Amsterdam, THE NETHERLANDS
189 Complex Systems Summer School, Santa Fe, NM, USA
188 Molecular evolution workshop, Jyväskylä, FINLAND

2018
187 The Santa Fe Institute, Santa Fe, NM
186 Department of Genetics, Cambridge University, Cambridge, UK
185 Institute for New Economic Thinking (INET), Oxford University, Oxford, UK
184 Oxford Martin School, Oxford University, Oxford, UK
183 MRC London Institute of Medical Sciences LMS/Imperial College London, UK
182 Complex Systems Summer School, Santa Fe, NM, USA
181 Indo Swiss primer Symposium, University of Zurich, SWITZERLAND

2017
180 Keynote, European Society of Evolutionary Biology (ESEB) 2017, Groningen, THE NETHERLANDS
179 The Santa Fe Institute, Santa Fe, NM, USA
178 Complex Systems Summer School, Santa Fe, NM, USA
177 Gordon Research Conference "Molecular Mechanisms in Evolution", Easton, MA, USA
176 Department of Biology, University of Konstanz, GERMANY
175 Workshop "Quantifying Biological Complexity", Arizona State University, Tempe, AZ, USA

2016
174 British Ecological Society meeting, Liverpool, UK
173 Zoological Institute, University of Basel, SWITZERLAND
172 The Santa Fe Institute, Santa Fe, NM, USA

171 XXI Population Genetics and Evolution Seminar, Sitges, SPAIN
170 Lake Como School of Adanced Studies, Como ITALY
169 EMBO Member's meeting, Heidelberg, GERMANY
168 Workshop "Understanding Life", University of Bern, SWITZERLAND
167 Conference "Evolutionary Systems Biology", Hinxton, UK,
166 Department of Molecular Evolution and Development, University of Vienna, AUSTRIA

2015
165 Complex Systems Winter School, IISER Mohali, INDIA
164 Winter School on Quantitative Systems Biology, Intl. Centre for Theoretical Sciences, Bangalore, INDIA
163 Workshop "From Genome to Gene", Jacques Loeb Centre, Ben-Gurion University of the Negev, Beer-Sheva, ISRAEL
162 Keynote lecture, LyonSysBio Systems Biology Conference, Villeurbanne, FRANCE
161 BioFrontiers Institute, University of Colorado, Boulder, CO, U.S.A.
160 Workshop "Innovation as Search on a Space
of Possibilities", Santa Fe Institute, Santa Fe, NM, USA
159 Laboratoire de Biologie Moléculaire et Cellulaire des Eucaryotes, CNRS, Université Pierre et Marie Curie, Paris, FRANCE
158 Institute of Biotechnology, University of Helsinki, Helsinki, FINLAND

2014
157 The Royal Institution, London, UK
156 Institute for Population Genetics, Vienna, AUSTRIA
155 Conference "From functional genomics to systems biology", EMBL, Heidelberg, GERMANY
154 Workshop "Origins of novelty in biological, social, and technological systems", The Santa Fe, Institute, Santa Fe, NM, USA
153 VIBes in biosciences Ph.D student symposium, Antwerp, BELGIUM
152 NTNU Biotechnology Distinguished Speaker Series, Trondheim, NORWAY
151 European Conference on Complex Systems 2014, Lucca, ITALY
150 Symposium "Is Innovation Evolutionary?", Millbank House, House of Lords, London, ENGLAND
149 Summer School, Santa Fe Institute, Santa Fe, NM, USA
148 Faculdad de Ciencias, UNAM, Mexico City, MEXICO
147 Instituto de Fisiología Celular, UNAM, Mexico City, MEXICO

2013

146 Department of Biology, Université Laval, Québec, CANADA
145 Workshop "Out of the box thinking", Santa Fe Institute, Santa Fe, NM, USA
144 FEBS Congress 2013, Bioinformatics Symposium (keynote), St. Petersburg, RUSSIA
143 Summer School, Santa Fe Institute, Santa Fe, NM, USA
142 Dept. of Bionanoscience, Delft University, The NETHERLANDS
141 Centre for Ecological and Evolutionary Studies, Univ. of Groningen, the NETHERLANDS
140 Systems Biology Program, Centro Nacional de Biotecnologia (CNB), Madrid, SPAIN
139 Evolutionary Systems Biology Workshop, Konrad Lorenz Institute, Vienna, AUSTRIA
138 Dept of Genetics & Evolution, University of Geneva, SWITZERLAND
137 Synthetic and Systems Biology Center, University of Edinburgh, SCOTLAND

2012

136 SMBE 2012 - Annual Meeting of the Society for Molecular Biology and Evolution, Dublin, IRELAND
135 Workshop "Robustness in biological systems", MBI, Ohio State University, Columbus, Ohio, U.S.A.
134 Department of Genetics, Harvard University, Boston, MA, U.S.A.
133 Institute for Molecular and Cellular Biology of Plants (IBMCP), Valencia, SPAIN
132 Laboratory of Theoretical Physics and Statistical Models (LPTMS), Univ. Paris 11, Orsay, FRANCE

2011

131 John Innes Centre, Norwich, UK
130 The Santa Fe Institute, Santa Fe, NM, USA
129 Mathematical Models in Ecology and Evolution 2011 (Keynote), Groningen, The NETHERLANDS
128 13th Congress of the European Society of Evolutionary Biology (ESEB), Tuebingen, GERMANY
127 13th joint PhD retreat of the MDC and FMP (Keynote), Berlin, GERMANY
126 University of Basel, BC² Seminar Series, Basel, SWITZERLAND
125 Workshop "Trends and Controversies in Evol. Developmental Biology", Ringberg Castle, GERMANY
124 Institute of Molecular Biology, Academia Sinica, Taipei, TAIWAN
123 Institute Seminar, A*star Bioinformatics Institute (BII), SINGAPORE

2010
122 Seminar on Modeling in Life Sciences, Clusters de Recherche Rhone-Alpes, Lyon, FRANCE
121 Research Priority Program Symposium in Systems Biology, Monte Verita, Ascona, SWITZERLAND
120 Santa Fe Institute, Santa Fe, NM, USA
119 Berlin Summer Meeting 2010, Max Delbrueck Center for Molecular Medicine, Berlin, GERMANY
118 10th SMBE 2010 - Annual Meeting of the Society for Molecular Biology and Evolution, Lyon, FRANCE
117 1st EMBL/CRG Systems Biology Workshop on "The Evolution of Biological Networks", Center for Genomic Regulation, Barcelona, SPAIN
116 Keynote lecture, XXVII European Society for Biochemistry and Physiology (ESCBP) meeting, Alessandria, ITALY
115 Frontiers of Multidisciplinary Research: Mathematics, Engineering and Biology, University of Exeter, UK
114 Indo-Swiss Bioinformatics Symposium, IIT Delhi, INDIA
113 Jawaharlal Nehru University (JNU), Delhi, INDIA
112 Ludwig Maximilians University Munich, Dept. of Evolutionary Biology, Munich, GERMANY
111 Forschungsmuseum Alexander Koenig, Bonn, GERMANY
110 Westfälische Wilhelms University, Institute for Evolution and Biodiversity, Münster, GERMANY

2009
109 The Abdus Salam International Center for Theoretical Physics, Conference "From biological networks to cellular function", Trieste, ITALY
108 Santa Fe Institute, Science Board Meeting and Symposium, "Foundations of Molecular Evolution", NM, USA
107 Imperial College, Ctr. for Complexity Science, "On the relationship between robustness and evolutionary innovation", London, UK
106 The Abdus Salam International Center for Theoretical Physics, Summer School, Trieste, ITALY
105 International Symposium on Complex Systems Biology, Tokyo, JAPAN
104 2009 Meeting of the European Society for Evolutionary Biology (ESEB), Turin, ITALY
103 Institute of Developmental Biology and Cancer, University of Nice Sophia-Antipolis, Nice, FRANCE
102 The 10th International Conference on Systems Biology (ICSB), Stanford University, Palo Alto, CA, USA
101 Keynote lecture, 60th Panhellenic Congress on Molecular Biology & Biochemistry, Athens, GREECE
100 Institute of Computational Science, ETH Zurich, Molecular Evolution Seminar Series, Zurich, SWITZERLAND
99 Keynote lecture, 11th Annual Congress of the Italian Life Sciences Federation, Riva del Garda, ITALY
98 Institut Pasteur, Paris, FRANCE

2008
97 BiRC, University of Aarhus, Denmark
96 National Academies Keck Foundation Initiative on Complex Systems, Beckman Center, Irvine, CA
95 Complex Systems Summer School, Santa Fe Institute, Santa Fe, NM
94 Centre de Regulacio Genomica, Barcelona, Spain
93 9th International Conference on Systems Biology (ICSB 2008), Goeteborg, Sweden
92 COMPLEX Meeting on Evolution and Development, University College London, UK
91 Keynote lecture, Early career scientist symposium, University of Michigan, Ann Arbor, MI
90 The Santa Fe Institute, Santa Fe, NM

2007

89 Gordon Research Conference "Microbial Population Ecology", Andover, New Hampshire, USA
88 The Santa Fe Institute, Santa Fe, New Mexico, USA
87 Workshop "Evolvability", Varenna, ITALY
86 Zoology Department, University of Cambridge, ENGLAND
85 Department of Anthropology, University of Zurich, Zurich, SWITZERLAND
84 Kavli Institute for Theoretical Physics, Santa Barbara, California, USA
83 Department of Physical Chemistry, University of Zurich, Zurich, SWITZERLAND
82 Department of Biology, California State University, Northridge, California, USA
81 URPP Systems Biology Retreat, Braunwald, SWITZERLAND
80 Swiss Institute of Bioinformatics Meeting, Grindelwald, SWITZERLAND
79 Department of Biology, Indiana University, Bloomington, IN, USA
78 Biozentrum Basel, Basel, SWITZERLAND
77 Workshop "Biology without borders", CoSBi, Trento, ITALY
76 Department of Ecology and Evolution, University of Lausanne, Lausanne, SWITZERLAND

2006
75 NESCent workshop on genetic networks. National Evolutionary Synthesis Center, Marathon, FL, USA
74 Workshop "Evolution of gene regulatory logic" The Santa Fe Institute, Santa FE, NM, USA
73 Gordon Research Conference "Biology of Aging", Ventura, CA, USA
72 Complex Systems Summer School, Santa Fe, NM, USA
71 Systems Biology Research Priority Program, Inst. for Cancer Biology, University of Zurich, SWITZERLAND
70 Division of Biological Science, Ecology and Evolution, University of Chicago, Chicago, IL, USA
69 Department of Organismal and Evolutionary Biology. Harvard University, Cambridge, MA, USA
68 Biochemistry Department, University of Zurich, Zurich, SWITZERLAND
67 Biotechnology Research Institute, Montreal, CANADA
66 Complex Systems Summer School, Beijing, CHINA
65 Department of Zoology, University of Bern, Bern, SWITZERLAND

2005
64 Workshop "Complex biomolecular networks: structure, evolution, and function" Montauk, LI, USA
63 Genopole Complexity Advanced Course, Evry, FRANCE
62 Workshop "Technology of Nature, Nature of Technology", UNM, NM, USA
61 Institut Jacques Monod, Paris, FRANCE
60 Institut National de la Recherche Agronomique (INRA), Versailles, FRANCE
59 Department of Ecology and Evolutionary Biology, Tucson, AZ
58 Workshop "Stochastic phenomena in gene regulation", Rice University, Houston, TX, USA
57 Biocomplexity Seminar, UNM Biology, NM USA
56 Institut Curie, Paris, FRANCE
55 Conference "Bioinformatics 2005", Soc. for Bioinformatics in the Nordic Countries, Tartu, ESTONIA
54 Spring School "Modelisation de systemes biologiques complexes ", Montpellier, FRANCE

2004
53 University of Pennsylvania, Bioinformatics Forum at the Penn Center for Bioinformatics, PA, U.S.A.
52 University of Illinois at Urbana-Champaign, Symposium "Understanding Complex Systems",IL, U.S.A.
51 Gordon Research Conference on Molecular Evolution, Ventura, CA, USA
50 Department of Genetics, University of Georgia, Athens, GA, USA
49 Center for Nonlinear Studies, Los Alamos National Laboratory, Los Alamos, NM, USA
48 ETH Zurich, SWITZERLAND
47 Max Planck Institut für Physik Complexer Systeme, Workshop "Molecules, networks, populations", Dresden, GERMANY
46 INRIA and Universite Claude Bernard, Seminar on Computational Biology, Lyon, FRANCE
45 UMR de Génétique Végétale INRA/CNRS/UPS/INAPG, Ferme du Moulon, Gif-sur-Yvette, FRANCE
44 University of Zurich Medical School, SWITZERLAND
43 Institut Pasteur, Paris, FRANCE

2003
42 Erwin Schrödinger Institute for Mathematical Physics, Vienna, AUSTRIA
41 Institute of Biochemistry, Technical University Graz, AUSTRIA

40 Insituto de Ecología, Universidad Autónoma de México, Mexico City, MEXICO
39 Lorne Genome Conference, Lorne, AUSTRALIA
38 Center For Advanced Study, University of New Mexico, Albuquerque, U.S.
37 Genopole, Evry, FRANCE
36 Center for Nonlinear Studies, Los Alamos National Laboratory, 23rd annual conference;
   "Networks: structure, dynamics, and function", Santa FE, New Mexico, U.S.
35 Institut Henri Poincaré, Paris, FRANCE
34 Virtual Conference on Genomics and Bioinformatics, North Dakota State University, Fargo, N.D., U.S.
33 International Conference on Bioinformatics, Atlanta, U.S.
32 Aegaean Conference "Pathways, networks, and systems: theory and experiments", Santorini, GREECE

2002
31 Department of Physiology, Johns Hopkins Univ., Baltimore, MD, U.S.A.
30 Workshop "Statistical mechanics of complex networks", Asia-Pacific Ctr. for Theoret. Phys.,Pohang, KOREA
29 Inaugural New Mexico Genomics Symposium, Univ. New Mexico, NM, U.S.A.
28 Workshop "Robustness and Evolvability of Molecules and Microbes", Santa Fe Institute, U.S.A
27 Symposium on Macromolecular Networks, Institut Pasteur, Paris, FRANCE
26 Workshop "Genetics of phenotypic robustness", Santa Fe Institute, U.S.A
25 Advanced Materials Laboratory, Sandia National Laboratory, New Mexico, U.S.A.
24 Dept. of Genetics and Ctr. for Comput. Genomics , Case Western Reserve Univ. Cleveland, OH, U.S.A.
23 Santa Fe Institute Summer School, U.S.A.
22 Center for Nonlinear Studies, Los Alamos National Laboratory, New Mexico, U.S.A.
21 Symposium "Complex Regulation Across Species Boundaries", Harvard University, U.S.A.

2001
20 Centre for Cellular and Molecular Biology, Hyderabad, INDIA
19 Gordon Research Conference on "Quantitative Genetics and Genomics", Ventura, California, U.S.A.
18 Business Network Meeting on "Network Dynamics", Santa Fe Institute, New Mexico, U.S.A.
17 Cologne Spring Meeting on Evolutionary Genomics and Bioinformatics, Cologne, GERMANY
16 Center for Interdisplinary Research, Bielefeld, GERMANY
15 Program in Proteomics and Bioinformatics, University of Toronto, CANADA
14 Institute for Theoretical Physics, University of Santa Barbara, U.S.A.
13 Workshop on mathematical models in molecular biology, The Santa Fe Institute, New Mexico, U.S.A.
12 VIIIth international congress of the European Society for Evolutionary Biology, Aarhus, DENMARK.
11 Symposium on the evolution of genetic networks, University of Oregon, Eugene, Oregon, U.S.A.
10 Division of Biological Sciences, UC Davis, California, U.S.A.
9 DOE Workshop "Beyond the identification of transcribed sequences" Washington D.C., U.S.A.

2000
8 Southwest Genomics and Biotechnology Alliance Workshop, Sandia Natl. Lab., New Mexico, U.S.A.
7 Department of Biology, Arizona State University, Tempe, Arizona, U.S.A.
6 Symposium on the consequences of gene duplications; Univ. of Oregon, Eugene, U.S.A.
5 Charles Darwin Research Station, Galápagos, ECUADOR
4 Workshop "Structure and Dynamics of Complex Interactive Networks", The Santa Fe Institute, NM, U.S.A.
3 National Center for Genome Research, Santa Fe, New Mexico, U.S.A.
2 Center for the Study of Complex Systems, University of Michigan, Michigan, U.S.A.
1 University of New Mexico School of Medicine, New Mexico, U.S.A.