

Peter F. Stadler: List of Publications

- [1] Peter F Stadler and Peter Schuster. Dynamics of small autocatalytic reaction networks I: Bifurcations, permanence and exclusion. *Bull. Math. Biol.*, 52:485–508, 1990.
- [2] Peter F Stadler. Dynamics of small autocatalytic reaction network IV: Inhomogeneous replicator equations. *BioSystems*, 26:1–19, 1991.
- [3] Peter F Stadler. Complementary replication. *Math. Biosc.*, 107:83–109, 1991.
- [4] Walter Fontana, Thomas Griesmacher, Wolfgang Schnabl, Peter F Stadler, and Peter Schuster. Statistics of landscapes based on free energies, replication and degradation rate constants of RNA secondary structures. *Monatsh. Chem.*, 122:795–819, 1991.
- [5] Wolfgang Schnabl, Peter F Stadler, Christian V Forst, and Peter Schuster. Full characterization of a strange attractor. chaotic dynamics in low dimensional replicator systems. *Physica D*, 48:65–90, 1991.
- [6] Bärbel M R Stadler and Peter F Stadler. Dynamics of small autocatalytic reaction networks III: Monotonous growth functions. *Bull. Math. Biol.*, 53:469–485, 1991.
- [7] Peter F Stadler and Peter Schuster. Mutation in autocatalytic networks — an analysis based on perturbation theory. *J. Math. Biol.*, 30:597–631, 1992.
- [8] Peter F Stadler and Wolfgang Schnabl. The landscape of the travelling salesman problem. *Phys. Lett. A*, 161:337–344, 1992.
- [9] Peter F Stadler and Robert Happel. Correlation structure of the landscape of the graph-bipartitioning-problem. *J. Phys. A:Math. Gen.*, 25:3103–3110, 1992.
- [10] Peter F Stadler. Correlation in landscapes of combinatorial optimization problems. *Europhys. Lett.*, 20:479–482, 1992.
- [11] Peter F Stadler and Robert Happel. The probability for permanence. *Math. Biosc.*, 113:25–50, 1993.
- [12] Peter F Stadler, Walter Fontana, and John H Miller. Random catalytic reaction networks. *Physica D*, 63:378–392, 1993.
- [13] Peter F Stadler and Walter Grüner. Anisotropy in fitness landscapes. *J. Theor. Biol.*, 165:373–388, 1993.
- [14] Sebastian Bonhoeffer, John S McCaskill, Peter F Stadler, and Peter Schuster. RNA multi-structure landscapes. a study based on temperature dependent partition functions. *Eur. Biophys. J.*, 22:13–24, 1993.
- [15] Sebastian Bonhoeffer and Peter F Stadler. Errorthreshold on complex fitness landscapes. *J. Theor. Biol.*, 164:359–372, 1993.

- [16] Walter Fontana, Peter F Stadler, Erich G Bornberg-Bauer, Thomas Griesmacher, Ivo L Hofacker, Manfred Tacker, Pedro Tarazona, Edward D Weinberger, and Peter Schuster. RNA folding landscapes and combinatorial landscapes. *Phys. Rev. E*, 47:2083–2099, 1993.
- [17] Walter Fontana, Daniella A M Konings, Peter F Stadler, and Peter Schuster. Statistics of RNA secondary structures. *Biopolymers*, 33:1389–1404, 1993.
- [18] Edward D Weinberger and Peter F Stadler. Why some fitness landscapes are fractal. *J. Theor. Biol.*, 163:255–275, 1993.
- [19] Peter F Stadler. Linear operators on correlated landscapes. *J. Phys. I France*, 4:681–696, 1994.
- [20] Peter F Stadler and Juan Carlos Nuño. The influence of mutation on autocatalytic reaction networks. *Math. Biosci.*, 122:127–160, 1994.
- [21] Peter F Stadler, Peter Schuster, and Alan S Perelson. Immune networks modelled by replicator equations. *J. Math. Biol.*, 33:111–137, 1994.
- [22] Ivo L Hofacker, Walter Fontana, Peter F Stadler, L Sebastian Bonhoeffer, Manfred Tacker, and Peter Schuster. Fast folding and comparison of RNA secondary structures. *Monatsh. Chem.*, 125:167–188, 1994.
- [23] Peter Schuster, Walter Fontana, Peter F Stadler, and Ivo L Hofacker. From sequences to shapes and back: A case study in RNA secondary structures. *Proc. Roy. Soc. Lond. B*, 255:279–284, 1994.
- [24] Peter Schuster and Peter F Stadler. Landscapes: Complex optimization problems and biopolymer structures. *Computers & Chem.*, 18:295–314, 1994.
- [25] Manfred Tacker, Walter Fontana, Peter F Stadler, and Peter Schuster. Statistics of RNA melting kinetics. *Eur. Biophys. J.*, 23:29–38, 1994.
- [26] see Technical Reports.
- [27] Catherine A. Macken and Peter F. Stadler. Evolution on fitness landscapes. In L. Nadel and D. L. Stein, editors, *1993 Lectures in Complex Systems*, volume VI of *SFI Studies in the Sciences of Complexity*, pages 43–86. Addison-Wesley, Reading MA, 1995.
- [28] Manfred Tacker and Peter F. Stadler. RNA: Genotype and phenotype. In L. Nadel and D. L. Stein, editors, *1993 Lectures in Complex Systems*, volume VI of *SFI Studies in the Sciences of Complexity*, pages 579–589. Addison-Wesley, Reading MA, 1995.
- [29] Peter F Stadler, Wolfgang Schnabl, Christian V Forst, and Peter Schuster. Dynamics of small autocatalytic reaction networks II: Replication, mutation, and catalysis. *Bull. Math. Biol.*, 57:21–61, 1995.
- [30] Peter F Stadler. Random walks and orthogonal functions associated with highly symmetric graphs. *Discr. Math.*, 145:229–238, 1995.
- [31] Peter F. Stadler. Towards a theory of landscapes. In R. López-Peña, R. Capovilla, R. García-Pelayo, H. Waelbroeck, and F. Zertuche, editors, *Complex Systems and Binary Networks*, volume 461 of *Lecture Notes in Physics*, pages 77–163, Berlin, New York, 1995. Springer Verlag. SFI preprint 95-03-030.

- [32] Peter F. Stadler. RNA: Genotype and phenotype. In J. Chela-Flores, M. Chadha, A. Negron-Mendoza, and T. Oshima, editors, *Chemical Evolution: Self-Organization of the Macromolecules of Life*, pages 159–176, 1995. Proceedings of the Second Trieste Conference on Chemical Evolution: Self Organization of the Macromolecules of Life 25-29 October 1993.
- [33] see Technical Reports.
- [34] Walter Gruener, Robert Giegerich, Dirk Strothmann, Christian Reidys, Jacqueline Weber, Ivo L. Hofacker, Peter F. Stadler, and Peter Schuster. Analysis of RNA sequence structure maps by exhaustive enumeration. I. neutral networks. *Monath. Chem.*, 127:355–374, 1996. SFI preprint 95-10-099.
- [35] Walter Gruener, Robert Giegerich, Dirk Strothmann, Christian Reidys, Jacqueline Weber, Ivo L. Hofacker, Peter F. Stadler, and Peter Schuster. Analysis of RNA sequence structure maps by exhaustive enumeration. II. structures of neutral networks and shape space covering. *Monath. Chem.*, 127:375–389, 1996. SFI preprint 95-10-099.
- [36] Christian Reidys and Peter F. Stadler. Bio-molecular shapes and algebraic structures. *Computers & Chem.*, 20:85–94, 1996. SFI preprint 95-10-098.
- [37] Andreas Schwienhorst, Andreas Schober, Rolf Guenther, and Peter F. Stadler. Hamming chromatography. *Molecular Diversity*, 1:187–192, 1996. SFI preprint 95-10-090.
- [38] Ivo L. Hofacker, Martijn A. Huynen, Peter F. Stadler, and Paul E. Stolorz. Knowledge discovery in RNA sequence families of HIV using scalable computers. In Evangelos Simoudis, Jiawei Han, and Usama Fayyad, editors, *Proceedings of the 2nd International Conference on Knowledge Discovery and Data Mining, Portland, OR*, pages 20–25, Menlo Park, CA, 1996. AAAI Press.
- [39] Subbiah Baskaran, Peter F. Stadler, and Peter Schuster. Approximate scaling properties of RNA free energy landscapes. *J. Theor. Biol.*, 181:299–310, 1996. SFI preprint 95-10-083.
- [40] Peter F. Stadler and Bärbel Krakhofer. Local minima of p-spin models. *Rev. Mex. Fis.*, 42:355–363, 1996. SFI preprint 95-09-076.
- [41] Peter F. Stadler. Landscapes and their correlation functions. *J. Math. Chem.*, 20:1–45, 1996. SFI preprint 95-07-067.
- [42] Robert Happel and Peter F. Stadler. Canonical approximation of fitness landscapes. *Complexity*, 2:53–58, 1996. SFI preprint 95-07-068.
- [43] Robert Happel, Robert Hecht, and Peter F. Stadler. Autocatalytic networks with translation. *Bull. Math. Biol.*, 58:877–905, 1996. SFI preprint 95-07-063.
- [44] Martijn A. Huynen, Peter F. Stadler, and Walter Fontana. Smoothness within ruggedness: the role of neutrality in adaptation. *Proc. Natl. Acad. Sci. (USA)*, 93:397–401, 1996. SFI preprint 95-01-006, LAUR-94-3763.
- [45] Martijn A. Huynen, Alan S. Perelson, Wayne A. Vieira, and Peter F. Stadler. Base pairing probabilities in a complete HIV-1 RNA. *J. Comp. Biol.*, 3:253–274, 1996. SFI preprint 95-07-057, LAUR-95-1613.

- [46] Peter F. Stadler and Peter Schuster. Permanence of sparse autocatalytic networks. *Math. Biosc.*, 131:111–134, 1996. SFI Preprint 94-05-028.
- [47] Bärbel Krakhofer and Peter F. Stadler. Local minima in the graph bipartitioning problem. *Europhys. Lett.*, 34:85–90, 1996. SFI preprint 96-02-005.
- [48] Manfred Tacker, Peter F. Stadler, Erich G. Bornberg-Bauer, Ivo L. Hofacker, and Peter Schuster. Algorithm independent properties of RNA structure prediction. *Eur. Biophys. J.*, 25:115–130, 1996. Santa Fe Institute Preprint 96-04-016.
- [49] J. Cupal, I. L. Hofacker, and P. F. Stadler. Dynamic programming algorithm for the density of states of RNA secondary structures. In R. Hofstädt, T. Lengauer, M. Löffler, and D. Schomburg, editors, *Computer Science and Biology 96 (Proceedings of the German Conference on Bioinformatics)*, pages 184–186, Leipzig, Germany, 1996. Universität Leipzig.
- [50] Jan Cupal, Christoph Flamm, Alexander Renner, and Peter F. Stadler. Density of states, metastable states, and saddle points. Exploring the energy landscape of an RNA molecule. In T. Gaasterland, P. Karp, K. Karplus, Ch. Ouzounis, Ch. Sander, and A. Valencia, editors, *Proceedings of the ISMB-97*, pages 88–91, Menlo Park, CA, 1997. AAAI Press.
- [51] Robert Hecht, Robert Happel, Peter Schuster, and Peter F. Stadler. Autocatalytic networks with intermediates I: Irreversible reactions. *Math. Biosc.*, 140:33–74, 1997. Santa Fe Institute preprint 96-05-024.
- [52] Christian Reidys, Peter F. Stadler, and Peter Schuster. Generic properties of combinatorial maps: Neutral networks of RNA secondary structures. *Bull. Math. Biol.*, 59:339–397, 1997. SFI preprint 95-07-058.
- [53] Peter Schuster, Peter F. Stadler, and Alexander Renner. RNA structures and folding: From conventional to new issues in structure predictions. *Curr. Opinions Structural Biol.*, 7:229–235, 1997.
- [54] Ricardo García-Pelayo and Peter F. Stadler. Correlation length, isotropy, and meta-stable states. *Physica D*, 107:240–254, 1997. Santa Fe Institute Preprint 96-05-034.
- [55] Susanne Rauscher, Christoph Flamm, Christian Mandl, Franz X. Heinz, and Peter F. Stadler. Secondary structure of the 3'-non-coding region of flavivirus genomes: Comparative analysis of base pairing probabilities. *RNA*, 3:779–791, 1997. Santa Fe Institute Preprint 97-02-010.
- [56] Aderonke Babajide, Ivo L. Hofacker, Manfred J. Sippl, and Peter F. Stadler. Neutral networks in protein space: A computational study based on knowledge-based potentials of mean force. *Folding & Design*, 2:261–269, 1997. Santa Fe Institute Preprint 96-12-085.
- [57] Peter Schuster and Peter F. Stadler. Sequence redundancy in biopolymers: A study on RNA and protein structures. In Gerald Myers, editor, *Viral Regulatory Structures*, volume XXVIII of *Santa Fe Institute Studies in the Sciences of Complexity*, pages 163–186. Addison-Wesley, Reading MA, 1998. Santa Fe Institute Preprint 97-07-67.
- [58] Peter F. Stadler and Günter P. Wagner. The algebraic theory of recombination spaces. *Evol. Comp.*, 5:241–275, 1998. Santa Fe Institute Preprint 96-07-046.

- [59] Christian W. Mandl, Heidemarie Holzmann, Tamara Meixner, Susanne Rauscher, Peter F. Stadler, Steven L. Allison, and Franz X. Heinz. Spontaneous and engineered deletions in the 3'-noncoding region of tick-borne encephalitis virus: Construction of highly attenuated mutants of flavivirus. *J. Virology*, 72:2132–2140, 1998.
- [60] Josef Leydold and Peter F. Stadler. Minimal cycle basis of outerplanar graphs. *Elec. J. Comb.*, 5:209–222 [R16: 14 p.], 1998. See <http://www.combinatorics.org/R16> and Santa Fe Institute Preprint 98-01-011.
- [61] Ivo L. Hofacker, Martin Fekete, Christoph Flamm, Martijn A. Huynen, Susanne Rauscher, Paul E. Stolorz, and Peter F. Stadler. Automatic detection of conserved RNA structure elements in complete RNA virus genomes. *Nucl. Acids Res.*, 26:3825–3836, 1998. Santa Fe Institute Preprint 98-03-020.
- [62] Wim Hordijk and Peter F. Stadler. Amplitude spectra of fitness landscapes. *J. Complex Systems*, 1:39–66, 1998. Santa Fe Institute Preprint 98-03-021.
- [63] Peter F. Stadler. Generic properties of the sequence-structure relations of biopolymers. In J. Chela-Flores and F. Raulin, editors, *Exobiology: Matter, Energy, and Information in the Origin of Life in the Universe*, pages 149–156, Dordrecht, 1998. Kluwer.
- [64] John H. Miller and Peter F. Stadler. The dynamics of adaptive parties under spatial voting. *J. Econ. Dyn. & Control*, 171–189:23, 1998. Santa Fe Institute Preprint 94-06-042.
- [65] Robert Happel and Peter F. Stadler. The evolution of diversity in replicator networks. *J. Theor. Biol.*, 195:329–338, 1998. Santa Fe Preprint 97-07-61.
- [66] Peter R. Wills, Stuart A. Kauffman, Bärbel M.R. Stadler, and Peter F. Stadler. Selection dynamics in autocatalytic systems: Templates replicating through binary ligation. *Bull. Math. Biol.*, 60:1073–1098, 1998. Santa Fe Institute Preprint 97-07-065.
- [67] Ivo L. Hofacker, Peter Schuster, and Peter F. Stadler. Combinatorics of RNA secondary structures. *Discr. Appl. Math.*, 88:207–237, 1998. SFI preprint 94-04-026.
- [68] Peter F. Stadler. Fitness landscapes arising from the sequence-structure maps of biopolymers. *J. Mol. Struct. (THEOCHEM)*, 463:7–19, 1999. Santa Fe Institute Preprint 97-11-082.
- [69] Ivo L. Hofacker and Peter F. Stadler. Automatic detection of conserved base pairing patterns in RNA virus genomes. *Comp. & Chem.*, 23:401–414, 1999. Santa Fe Institute preprint 98-06-058.
- [70] Christoph Flamm, Ivo L. Hofacker, and Peter F. Stadler. RNA *in silico*: The computational biology of RNA secondary structures. *Adv. Complex Syst.*, 2:65–90, 1999.
- [71] Robert Happel and Peter F. Stadler. Autocatalytic replication in a CSTR and constant organization. *J. Math. Biol.*, 38:422–434, 1999. SFI preprint 95-07-062.
- [72] Peter F. Stadler and Robert Happel. Random field models for fitness landscapes. *J. Math. Biol.*, 38:435–478, 1999. SFI preprint 95-07-069.
- [73] Christian Haslinger and Peter F. Stadler. RNA structures with pseudo-knots: Graph-theoretical and combinatorial properties. *Bull. Math. Biol.*, 61:437–467, 1999. Santa Fe Institute Preprint 97-03-030.

- [74] Peter Schuster and Peter F. Stadler. Nature and evolution of early replicons. In E. Domingo, R. Webster, and J. Holland, editors, *Origin and Evolution of Viruses*, pages 1–24. Academic Press, London, UK, 1999. Santa Fe Preprint 98-11-098.
- [75] Andreas Wagner and Peter F. Stadler. Viral RNA and evolved mutational robustness. *J. Exp. Zool./ MDE*, 285:119–127, 1999. Santa Fe Institute preprint 99-02-010.
- [76] Günter P. Wagner and Peter F. Stadler. Complex adaptations and the structure of recombination spaces. In Chrystopher Nehaniv and Misami Ito, editors, *Algebraic Engineering*, pages 96–115, Singapore, 1999. World Scientific. (Proceedings of the Conference on Semi-Groups and Algebraic Engineering, University of Aizu, Japan); Santa Fe Institute Preprint 97-03-029.
- [77] Jan Cupal, Peter Schuster, and Peter F. Stadler. Topology in phenotype space. In *Computer Science in Biology*, pages 9–15, Bielefeld, D, 1999. Univ. Bielefeld. Proceedings of the GCB’99, Hannover, D.
- [78] Roman Stocsits, Ivo L. Hofacker, and Peter F. Stadler. Conserved secondary structures in hepatitis B virus RNA. In *Computer Science in Biology*, pages 73–79, Bielefeld, D, 1999. Univ. Bielefeld. Proceedings of the GCB’99, Hannover, D.
- [79] Günter Weberndorfer, Ivo L. Hofacker, and Peter F. Stadler. An efficient potential for protein sequence design. In *Computer Science in Biology*, pages 107–112, Bielefeld, D, 1999. Univ. Bielefeld. Proceedings of the GCB’99, Hannover, D.
- [80] Peter F. Stadler and Gottfried Tinhofer. Equitable partitions, coherent algebras and random walks: Applications to the correlation structure of landscapes. *MATCH*, 40:215–261, 1999.
- [81] Viviane M. de Oliveira, José Fernando Fontanari, and Peter F. Stadler. Metastable states in high order short-range spin glasses. *J. Phys. A: Math. Gen.*, 32:8793–8802, 1999. SFI preprint 99-09-62; xxx.lanl.gov/abs/physics/9908439/.
- [82] Paulo Roberto Araújo Campos, José Fernando Fontanari, and Peter F. Stadler. Error propagation in the hypercycle. *Phys. Rev. E*, 61:2996–3002, 2000. SFI preprint 99-09-63; xxx.lanl.gov/abs/physics/9907049/.
- [83] Petra M. Gleiss, Josef Leydold, and Peter F. Stadler. Interchangeability of relevant cycles in graphs. *Elec. J. Comb.*, 7:R16 [16pages], 2000. Santa Fe Institute preprint 99-07-046.
- [84] Katharina Wimmer, Markus Eckart, Peter F. Stadler, Helga Rehder, and Christa Fonatsch. Three different premature stop codones lead to skipping of exon 7 in Neurofibromatosis type I patients. *Human Mutation*, 16:90–91, 2000. Full Text: *Mutations in Brief #341* (7 pages) <http://humu.edoc.com/mutbr1.html>.
- [85] Peter F. Stadler, Rudi Seitz, and Günter P. Wagner. Evolvability of complex characters: Population dependent Fourier decomposition of fitness landscapes over recombination spaces. *Bull. Math. Biol.*, 62:399–428, 2000. Santa Fe Institute Preprint 99-01-001.
- [86] Martin Fekete, Ivo L. Hofacker, and Peter F. Stadler. Prediction of RNA base pairing probabilities using massively parallel computers. *J. Comp. Biol.*, 7:171–182, 2000. Santa Fe Institute preprint 98-06-057.
- [87] Jan Cupal, Stefan Kopp, and Peter F. Stadler. RNA shape space topology. *Alife*, 6:3–23, 2000. SFI Preprint 99-03-022.

- [88] Bärbel M. R. Stadler, Peter F. Stadler, and Peter Schuster. Dynamics of autocatalytic replicator networks based on higher order ligation reactions. *Bull. Math. Biol.*, 62:1061–1086, 2000. SFI preprint 99-09-65.
- [89] Fernando F. Ferreira, José F. Fontanari, and Peter F. Stadler. Landscape statistics of the low autocorrelated binary string problem. *J. Phys. A: Math. Gen.*, 33:8635–8647, 2000. Santa Fe Institute Preprint 00-07-033.
- [90] Christian M. Reidys and Peter F. Stadler. Neutrality in fitness landscapes. *Appl. Math. & Comput.*, 117:321–350, 2001. Santa Fe Institute preprint 98-10-089.
- [91] Christoph Flamm, Ivo L. Hofacker, Sebastian Maurer-Stroh, Peter F. Stadler, and Martin Zehl. Design of multi-stable RNA molecules. *RNA*, 7:254–265, 2000. Santa Fe Institute Preprint 00-05-027.
- [92] Aderonke Babajide, Robert Farber, Ivo L. Hofacker, Jeff Inman, Alan S. Lapedes, , and Peter F. Stadler. Exploring protein sequence space using knowledge based potentials. *J. Theor. Biol.*, 212:35–46, 2001. Santa Fe Preprint 98-11-103.
- [93] E. Brian Davies, Graham M. L. Gladwell, Josef Leydold, and Peter F. Stadler. Discrete nodal domain theorems. *Lin. Alg. Appl.*, 336:51–60, 2001. Archive: math.SP/0009120.
- [94] Petra M. Gleiss, Peter F. Stadler, Andreas Wagner, and David A. Fell. Relevant cycles in chemical reaction network. *Adv. Complex Syst.*, 4:207–226, 2001.
- [95] Bärbel M. R. Stadler, Peter F. Stadler, Günter Wagner, and Walter Fontana. The topology of the possible: Formal spaces underlying patterns of evolutionary change. *J. Theor. Biol.*, 213:241–274, 2001. SFI preprint 00-12-070.
- [96] Christina Witwer, Susanne Rauscher, Ivo L. Hofacker, and Peter F. Stadler. Conserved RNA secondary structures in picornaviridae genomes. *Nucl. Acids Res.*, 29:5079–5089, 2001. SFI preprint 01-08-040.
- [97] Peter F. Stadler, Anita Mehta, and Jean-Marc Luck. Shaking a box of sand. *Europhys. Lett.*, 57:46–52, 2001.
- [98] Peter F. Stadler, Anita Mehta, and Jean-Marc Luck. Glassy states in a shaken sandbox. *Adv. Complex Syst.*, 4:429–439, 2001. Presented at the research workshop on *Challenges in Granular Physics*, ICTP Trieste, Italy, Aug 07-11 (2001).
- [99] Dan Rockmore, Peter Kostelec, Wim Hordijk, and Peter F. Stadler. Fast fourier transform for fitness landscapes. *Appl. Comput. Harmonic Anal.*, 12:57–76, 2002. Santa Fe Institute preprint 99-10-068.
- [100] Bärbel M. R. Stadler, Peter F. Stadler, and Peter R. Wills. Evolution in systems of ligation-based replicators. *Z. Phys. Chem.*, 21-33:216, 2001.
- [101] Bärbel M. R. Stadler, Peter F. Stadler, Max Shpak, and Günter P. Wagner. Recombination spaces, metrics, and pretopologies. *Z. Phys. Chem.*, 216:217–234, 2002. SFI preprint 01-02-011.
- [102] Christoph Flamm, Ivo L. Hofacker, Peter F. Stadler, and Michael T. Wolfinger. Barrier trees of degenerate landscapes. *Z. Phys. Chem.*, 216:155–173, 2002.

- [103] José Fernando Fontanari and Peter F. Stadler. Fractal geometry of spin-glass models. *J. Phys. A: Math. Gen.*, 35:1509–1516, 2002. SFI preprint 01-06-034.
- [104] Christian M. Reidys and Peter F. Stadler. Combinatorial landscapes. *SIAM Review*, 44:3–54, 2002. SFI preprint 01-03-14.
- [105] Bärbel M. R. Stadler and Peter F. Stadler. Generalized topological spaces in evolutionary theory and combinatorial chemistry. *J. Chem. Inf. Comput. Sci.*, 42:577–585, 2002. Proceedings MCC 2001, Dubrovnik.
- [106] Peter F. Stadler. Fitness landscapes. In Michael Lässig and Angelo Valleriani, editors, *Biological Evolution and Statistical Physics*, pages 187–207, Berlin, 2002. Springer-Verlag.
- [107] Ivo L. Hofacker, Martin Fekete, and Peter F. Stadler. Secondary structure prediction for aligned RNA sequences. *J. Mol. Biol.*, 319:1059–1066, 2002. SFI Preprint 01-11-067.
- [108] Oliver Bastert, Dan Rockmore, Peter F. Stadler, and Gottfried Tinhofer. Landscapes on spaces of trees. *Appl. Math. Comput.*, 131:439–459, 2002. SFI preprint 01-01-006.
- [109] Wilfried Imrich and Peter F. Stadler. Minimal cycle bases of product graphs. *Australasian J. Comb.*, 26:233–244, 2002. SFI preprint 01-08-044.
- [110] Ulrike Mückstein, Ivo L. Hofacker, and Peter F. Stadler. Stochastic pairwise alignments. *Bioinformatics*, S153-S160:18, 2002. ECCB 2002.
- [111] Peter F. Stadler. Spectral landscape theory. In J. P. Crutchfield and P. Schuster, editors, *Evolutionary Dynamics—Exploring the Interplay of Selection, Neutrality, Accident, and Function*, pages 231–272. Oxford University Press, 2002.
- [112] Peter Schuster and Peter F. Stadler. Networks in molecular evolutions. *Complexity*, 8:34–42, 2002.
- [113] Peter F. Stadler and Christoph Flamm. Barrier trees on poset-valued landscapes. *Genetic Prog. Evol. Mach.*, 7-20:4, 2003.
- [114] Günter Wagner and Peter F. Stadler. Quasi-independence, homology and the unity of type: A topological theory of characters. *J. Theor. Biol.*, 220:505–527, 2003.
- [115] Wim Hordijk, José F. Fontanari, and Peter F. Stadler. Shapes of tree representations of spin-glass landscapes. *J. Phys. A: Math. Gen.*, 36:3671–3681, 2003.
- [116] Peter F. Stadler. Minimal cycle bases of Halin graphs. *J. Graph Theory*, 43:150–155, 2003.
- [117] Peter F. Stadler, Wim Hordijk, and José F. Fontanari. Phase transition and landscape statistics of the number partitioning problem. *Phys. Rev. E*, 67:056701,1–6, 2003.
- [118] Stefan Wuchty and Peter F. Stadler. Centers of complex networks. *J. Theor. Biol.*, 223:45–53, 2003.
- [119] Bärbel M. R. Stadler and Peter F. Stadler. Molecular replicator dynamics. *Adv. Complex Syst.*, 6:47–77, 2003. presented at *Emergence in Chemical Systems*, Anchorage AK, June 2002; SFI # 02-09-049.

- [120] Petra M. Gleiss, Josef Leydold, and Peter F. Stadler. Circuit bases of strongly connected digraphs. *Discussiones Mathematicae: Graph Theory*, 23:241–260, 2003. Presented at: Recent Trends in Graph Theory, Algebraic Combinatorics, and Graph Algorithms, Bled (Slovenia) Sep 24-27 2001.
- [121] Gil Benkő, Christoph Flamm, and Peter F. Stadler. A graph-based toy model of chemistry. *J. Chem. Inf. Comput. Sci.*, 43:1085–1093, 2003. presented at *MCC 2002*, Dubrovnik CRO, June 2002; SFI # 02-09-045.
- [122] Peter F. Stadler and Christopher R. Stephens. Landscapes and effective fitness. *Comments on Theoretical Biology*, 8:389–431, 2003.
- [123] Günter Weberndorfer, Ivo L. Hofacker, and Peter F. Stadler. On the evolution of primitive genetic codes. *Origins Life Evol. Biosph.*, 33:491–514, 2003. SFI preprint #02-08-034.
- [124] Gil Benkő, Christoph Flamm, and Peter F. Stadler. Generic properties of chemical networks: Artificial chemistry based on graph rewriting. In W. Banzhaf, T. Christaller, P. Dittrich, J. T. Kim, and J. Ziegler, editors, *Advances in Artificial Life*, volume 2801 of *Lecture Notes in Computer Science*, pages 10–20, Heidelberg, Germany, 2003. Springer-Verlag. 7th European Conference, ECAL 2003, Dortmund, Germany, September 14-17, 2003, Proceedings.
- [125] Claudia Fried, Sonja J. Prohaska, and Peter F. Stadler. Independent hox-cluster duplications in lampreys. *J. Exp. Zool., Mol. Dev. Evol*, 299B:18–25, 2003.
- [126] Ingrid Abfalter, Christoph Flamm, and Peter F. Stadler. Design of multi-stable nucleic acid sequences. In H.-W. Mewes, V. Heun, D. Frishman, and S. Kramer, editors, *Proceedings of the German Conference on Bioinformatics. GCB 2003*, volume 1, pages 1–7, München, D, 2003. belleville Verlag Michael Farin.
- [127] Ivo L. Hofacker, Roman Stocsits, and Peter F. Stadler. Conserved RNA secondary structures in viral genomes: A survey. *Bioinformatics*, 20:1495–1499, 2004. **also**: Proceedings of the German Conference on Bioinformatics. GCB 2003 vol. 1; Mewes, H.-W., Heun, V., Frishman, D. and Kramer, S. (eds.); belleville Verlag Michael Farin, München, D (2003), pp. 57-62.
- [128] Lukas C. Faulstich, Peter F. Stadler, Caroline Thurner, and Christina Witwer. **litsift**: Automated text categorization in bibliographic search. In Tobias Scheffer and Ulf Leser, editors, *Data Mining and Text Mining for Bioinformatics: Proceedings of the European Workshop*, pages 20–25, Berlin, 2003. Humboldt University. <http://www.informatik.hu-berlin.de/%7Escheffer/publications/ProceedingsWS2003.pdf>.
- [129] Bärbel M. R. Stadler and Peter F. Stadler. Higher separation axioms in generalized closure spaces. *Commentationes Math. Warszawa, Ser. I*, 43:257–273, 2003.
- [130] Chi-Hua Chiu, Ken Dewar, Günter P. Wagner, Kazuhiko Takahashi, Frank Ruddle, Christina Ledje, Peter Bartsch, Jean-Luc Scemama, Edmund Stellwag, Claudia Fried, Sonja J. Prohaska, Peter F. Stadler, and Chris T. Amemiya. Bichir *HoxA* cluster sequence reveals surprising trends in ray-finned fish genomic evolution. *Genome Res.*, 14:11–17, 2004.
- [131] Steen Rasmussen, Liaohai Chen, Bärbel M. R. Stadler, and Peter F. Stadler. Proto-organism kinetics: Evolutionary dynamics of lipid aggregates with genes and metabolism. *Orig. Life Evol. Biosph.*, 34:171–180, 2004.

- [132] Ivo L. Hofacker, Barbara Priwitzer, and Peter F. Stadler. Prediction of locally stable RNA secondary structures for genome-wide surveys. *Bioinformatics*, 20:191–198, 2004.
- [133] Steen Rasmussen, Liaohai Chen, David Deamer, David C. Krakauer, Peter F. Packard, Norman H. and Stadler, and Mark A. Bedau. Transitions from nonliving to living matter. *Science*, pages 963–965, 2004. Perspectives.
- [134] Sonja J. Prohaska, Claudia Fried, Chris T. Amemiya, Frank H. Ruddle, Günter P. Wagner, and Peter F. Stadler. The shark HoxN cluster is homologous to the human HoxD cluster. *J. Mol. Evol.*, page 58, 2004. 212-217.
- [135] Claudia S. Copeland, Oliver Heyers, Bernd H. Kalinna, Andreas Bachmair, Peter F. Stadler, Ivo L. Hofacker, and Paul J. Brindley. Structural and evolutionary analysis of the transcribed sequence of *Boudicca*, a *Schistosoma mansoni* retrotransposon. *Gene*, 329:103–114, 2004.
- [136] Franziska Berger, Christoph Flamm, Petra M. Gleiss, Josef Leydold, and Peter F. Stadler. Counterexamples in chemical ring perception. *J. Chem. Inf. Comput. Sci.*, 44:323–331, 2004.
- [137] Claudia Fried, Wim Hordijk, Sonja J. Prohaska, Claus R. Stadler, and Peter F. Stadler. The footprint sorting problem. *J. Chem. Inf. Comput. Sci.*, 44:332–338, 2004.
- [138] Claudia Fried, Sonja J. Prohaska, and Peter F. Stadler. Exclusion of repetitive DNA elements from gnathostome Hox clusters. *J. Exp. Zool., Mol. Dev. Evol.*, 302B:165–173, 2004.
- [139] Sonja Prohaska, Claudia Fried, Christoph Flamm, Günter Wagner, and Peter F. Stadler. Surveying phylogenetic footprints in large gene clusters: Applications to Hox cluster duplications. *Mol. Phyl. Evol.*, 31:581–604, 2004. SFI preprint #03-02-011.
- [140] Michael T. Wolfinger, W. Andreas Svrcek-Seiler, Christoph Flamm, Ivo L. Hofacker, and Peter F. Stadler. Exact folding dynamics of RNA secondary structures. *J. Phys. A: Math. Gen.*, 37:4731–4741, 2004.
- [141] Martin Beck, Gil Benkö, Gunther Eble, Christoph Flamm, Stefan Müller, and Peter F. Stadler. Graph grammars as models for the evolution of developmental pathways. In H. Schaub, F. Detje, and U. Brüggemann, editors, *The Logic of Artificial Life: Abstracting and Synthesizing the Principles of Living Systems*, pages 8–15, Berlin, 2004. IOS Press, Akademische Verlagsgesellschaft. presented at GWAL, Bamberg 14-16 April 2004.
- [142] Gil Benkö, Christoph Flamm, and Peter F. Stadler. Multi-phase artificial chemistry. In H. Schaub, F. Detje, and U. Brüggemann, editors, *The Logic of Artificial Life: Abstracting and Synthesizing the Principles of Living Systems*, pages 16–22, Berlin, 2004. IOS Press, Akademische Verlagsgesellschaft. presented at GWAL, Bamberg 14-16 April 2004.
- [143] Caroline Thurner, Christine Witwer, Ivo Hofacker, and Peter F. Stadler. Conserved RNA secondary structures in Flaviviridae genomes. *J. Gen. Virol.*, 85:1113–1124, 2004.
- [144] Andrea Tanzer and Peter F. Stadler. Molecular evolution of a microRNA cluster. *J. Mol. Biol.*, 339:327–335, 2004.
- [145] Ivo L. Hofacker and Stadler Peter F. The partition function variant of Sankoff’s algorithm. In Marian Bubak, Geert Dick van Albada, Peter M. A. Sloot, and Jack J. Dongarra, editors, *Computational Science - ICCS 2004*, volume 3039 of *Lecture Notes in Computer Science*, pages 728–735, 2004. Kraków, June 6-9, 2004.

- [146] Christoph Flamm, Ivo L. Hofacker, and Peter F. Stadler. RNA folding *in silico*. In Susanne Brakmann and Andreas Schwienhost, editors, *Evolutionary Methods in Biotechnology*, pages 177–190. Wiley-VCH, Weinheim, Germany, 2004.
- [147] Bärbel M. R. Stadler and Peter F. Stadler. The topology of evolutionary biology. In Ciobanu, editor, *Modeling in Molecular Biology*, Natural Computing Series, 267–286, 2004. Springer Verlag.
- [148] Max Shpak, Peter F. Stadler, Günter P. Wagner, and Joachim Hermisson. Aggregation of variables and system decomposition: Applications to fitness landscape analysis. *Th. Biosci.*, 123:33–68, 2004.
- [149] Sonja J. Prohaska and Peter F. Stadler. The duplication of the hox gene clusters in teleost fishes. *Th. Biosci.*, 123:89–110, 2004.
- [150] Peter F. Stadler, Claudia Fried, Sonja J. Prohaska, Wendy J. Bailey, Bernhard Y. Misof, Frank H. Ruddle, and Günter P. Wagner. Evidence for independent *Hox* gene duplications in the hagfish lineage: A PCR-based gene inventory of *Eptatretus stoutii*. *Mol. Phylog. Evol.*, 32:686–692, 2004.
- [151] Christoph Flamm, Ivo L. Hofacker, and Peter F. Stadler. Computational chemistry with RNA secondary structures. *Kemija u industriji*, 53:315–322, 2004. (Proceedings CECM-2 Varaždin 2003).
- [152] Max Shpak, Peter F. Stadler, Günter P. Wagner, and Lee Altenberg. Simon ando decomposability and fitness landscapes. *Th. Biosci.*, 123:139–180, 2004.
- [153] Paulo R. A. Campos, Viviane M. de Olivera, Günter P. Wagner, and Peter F. Stadler. Gene phylogenies and protein-protein interactions: Possible artifacts resulting from shared protein interaction partners. *J. Theor. Biol.*, 231:197–202, 2004.
- [154] Türker Bıyıkoglu, Wim Hordijk, Josef Leydold, Tomaž Pisanski, and Peter F. Stadler. Graph laplacians, nodal domains, and hyperplane arrangements. *Lin. Alg. Appl.*, 390:155–174, 2004. SFI # 02-09-046.
- [155] Ivo L. Hofacker, Stephan H. F. Bernhart, and Peter F. Stadler. Alignment of RNA base pairing probability matrices. *Bioinformatics*, 20:2222–2227, 2004.
- [156] Burkhard Morgenstern, Sonja J. Prohaska, Nadine Werner, Jan Weyer-Menkhoff, Isabelle Schneider, Amarendran R. Subramanian, and Peter F. Stadler. Multiple sequence alignment with user-defined constraints. In Robert Giegerich and Jens Stoye, editors, *Proceedings of the GCB 2004 (Bielefeld)*, volume P-53 of *Lecture Notes in Informatics*, pages 25–36, 2004.
- [157] Caroline Thurner, Ivo L. Hofacker, and Peter F. Stadler. Conserved RNA pseudoknots. In Robert Giegerich and Jens Stoye, editors, *Proceedings of the GCB 2004 (Bielefeld)*, volume P-53 of *GI-Edition: Lecture Notes in Informatics*, pages 207–216, 2004.
- [158] Günter P. Wagner, Claudia Fried, Sonja J. Prohaska, and Peter F. Stadler. Divergence of conserved non-coding sequences: Rate estimates and relative rate tests. *Mol. Biol. Evol.*, 21:2116–2121, 2004.

- [159] Christina Witwer, Ivo L. Hofacker, and Peter F. Stadler. Prediction of consensus RNA secondary structures including pseudoknots. *IEEE/ACM Trans. Comp. Biol. Bioinf.*, 1:65–77, 2004.
- [160] Hans Binder, Toralf Kirsten, Markus Löffler, and Peter F. Stadler. The sensitivity of microarray oligonucleotide probes — variability and the effect of base composition. *J. Phys. Chem.*, 108:18003–18014, 2004.
- [161] Hans Binder, Toralf Kirsten, Ivo L. Hofacker, Peter F. Stadler, and Markus Löffler. Interactions in oligonucleotide hybrid duplexes on microarrays. *J. Phys. Chem.*, 108:18015–18025, 2004.
- [162] Allan Force, Cooduvalli Shashikant, Peter F. Stadler, and Chris T. Amemiya. Comparative genomics, *cis*-regulatory elements, and gene duplication. In H. Detrich III, Leonard Zon, and Monte Westerfield, editors, *The Zebrafish*, volume 77 of *Methods in Cell Biology*, pages 545–561. Elsevier, New York, 2004.
- [163] Peter Schuster and Peter F. Stadler. Discrete models of biopolymers. In M. James C. Crabbe and Andrzej Konopka, editors, *Handbook of Computational Chemistry and Biology*, pages 187–221. Marcel Dekker, New York, 2004.
- [164] Andrea Tanzer, Chris T. Amemiya, Chang-Bae Kim, and Peter F. Stadler. Evolution of microRNAs located within *Hox* gene clusters. *J. Exp. Zool.: Mol. Dev. Evol.*, 304B:75–85, 2005.
- [165] Jörg Hackermüller, Nicole-Claudia Meisner, Manfred Auer, Markus Jaritz, and Peter F. Stadler. The effect of RNA secondary structures on RNA-ligand binding and the modifier RNA mechanism: A quantitative model. *Gene*, 345:3–12, 2005.
- [166] Stefan Washietl, Ivo L. Hofacker, and Peter F. Stadler. Fast and reliable prediction of non-coding RNAs. *Proc. Natl. Acad. Sci. USA*, 102:2454–2459, 2005.
- [167] Burkhard Morgenstern, Nadine Werner, Sonja J. Prohaska, Rasmus Steinkamp, Isabelle Schneider, Amarendran R. Subramanian, Peter F. Stadler, and Jan Weyer-Menkhoff. Multiple sequence alignment with user-defined constraints gobics. *Bioinformatics*, 7:1271–1273, 2004.
- [168] Christoph Dieterich, Steffen Grossmann, Andrea Tanzer, Stefan Ropcke, Peter F. Arndt, Peter F. Stadler, and Martin Vingron. Comparative promoter region analysis powered by CORG. *BMC Genomics*, 6:24 [10 pages], 2005. <http://www.biomedcentral.com/1471-2164/6/24>.
- [169] Athanasius F. Bompfünnewerer, Christoph Flamm, Claudia Fried, Guido Fritsch, Ivo L. Hofacker, Jörg Lehmann, Kristin Missal, Axel Mosig, Bettina Müller, Sonja J. Prohaska, Bärbel M. R. Stadler, Peter F. Stadler, Andrea Tanzer, Stefan Washietl, and Christina Witwer. Evolutionary patterns of non-coding RNAs. *Th. Biosci.*, 123:301–369, 2005.
- [170] Günter P. Wagner, Kazuhiko Takahashi, Vincent Lynch, Sonja J. Prohaska, Claudia Fried, Peter F. Stadler, and Chris T. Amemiya. Molecular evolution of duplicated ray finned fish *hoxa* clusters: Increased synonymous substitution rate and asymmetrical co-divergence of coding and non-coding sequences. *J. Mol. Evol.*, pages 665–676, 2005.
- [171] Gudrun Böhmendorfer, Ivo L. Hofacker, Srečko Garber, Karin Jelenic, Viktoria Nizhynska, Hirohiko Hirochika, Peter F. Stadler, and Andreas Bachmair. Unorthodox mRNA start site

- to extend the highly structured leader of retrotransposon Tto1 mRNA increases transposition rate. *RNA*, 11:1181–1191, 2005.
- [172] Roman R. Stocsits, Ivo L. Hofacker, Claudia Fried, and Peter F. Stadler. Multiple sequence alignments of partially coding nucleic acid sequences. *BMC Bioinformatics*, 6:160 [epub], 2005.
- [173] Petra M. Gleiss, Josef Leydold, and Peter F. Stadler. Minimum path bases and relevant paths. *Networks*, 46:119–123, 2005. Recent Trends in Graph Theory, Algebraic Combinatorics, and Graph Algorithms, Bled (Slovenia) Sep 24-27 2001; SFI Preprint 01-10-056.
- [174] Camille Stephan-Otto Attolini, Peter F. Stadler, and Christoph Flamm. **CelloS**: a multi-level approach to evolutionary dynamics. In Mathieu S. Capcarrere, Alex A. Freitas, Peter J. Bentley, Colin G. Johnson, and Jon Timmis, editors, *Advances in Artificial Life: 8th European Conference, ECAL 2005*, volume 3630 of *Lect. Notes Comp. Sci.*, pages 500–509. Springer Verlag, 2005. Canterbury, UK, September 5-9, 2005.
- [175] Gil Benkő, Christoph Flamm, and Peter F. Stadler. Explicit collision simulation of chemical reactions in a graph based artificial chemistry. In Mathieu S. Capcarrere, Alex A. Freitas, Peter J. Bentley, Colin G. Johnson, and Jon Timmis, editors, *Advances in Artificial Life: 8th European Conference, ECAL 2005*, volume 3630 of *Lect. Notes Comp. Sci.*, pages 725–733. Springer Verlag, 2005. Canterbury, UK, September 5-9, 2005.
- [176] Ivo L. Hofacker and Peter F. Stadler. RNA secondary structures. In Robert A. Meyers, editor, *Encyclopedia of Molecular Cell Biology and Molecular Medicine*, volume 12, pages 581–603. Wiley-VCH, Weinheim, 2nd edition, 2005.
- [177] Ulrike Mückstein, Hakim Tafer, Jör Hackermüller, Stephan Bernhard Bernhard, Peter F. Stadler, and Ivo L Hofacker. Thermodynamics of RNA-RNA binding. *Bioinformatics*, 22:1177–1182, 2006. Earlier version in: *German Conference on Bioinformatics 2005*, Torda, Andrew and Kurtz, Stefan and Rarey, Matthias (eds.), *Lecture Notes in Informatics P-71*, pp 3-13, Gesellschaft f. Informatik, Bonn 2005.
- [178] Ivo L. Hofacker and Peter F. Stadler. Memory efficient folding algorithms for circular RNA secondary structures. *Bioinformatics*, 22:1172–1176, 2006. Earlier version in: *German Conference on Bioinformatics 2005*, Torda, Andrew and Kurtz, Stefan and Rarey, Matthias (eds.), *Lecture Notes in Informatics P-71*, pp 3-13, Gesellschaft f. Informatik, Bonn 2005.
- [179] Kristin Missal, Dominic Rose, and Peter F. Stadler. Non-coding RNAs in *Ciona intestinalis*. *Bioinformatics*, 21 S2:i77–i78, 2005. Proceedings ECCB/JBI'05, Madrid.
- [180] Stefan Washietl, Ivo L. Hofacker, Melanie Lukasser, Alexander Hüttenhofer, and Peter F. Stadler. Mapping of conserved RNA secondary structures predicts thousands of functional non-coding RNAs in the human genome. *Nature Biotech.*, 23:1383–1390, 2005.
- [181] Türker Bıyıkoğlu, Josef Leydold, and Peter F. Stadler. Nodal domain theorems and bipartite subgraphs. *Elec. J. Lin. Algebra*, 13:344–351, 2005.
- [182] Camille Stephan-Otto Attolini and Peter F. Stadler. Neutral networks of interacting RNA secondary structures. *Adv. Complex Syst.*, 8:275–284, 2005.

- [183] Karen D. Crow, Peter F. Stadler, Vincent J. Lynch, Chris T. Amemiya, and Günter P. Wagner. The fish specific Hox cluster duplication is coincident with the origin of teleosts. *Mol. Biol. Evol.*, 23:121–136, 2006.
- [184] Wei-Che Hsu, Hsien-Da Huang, Sheng-Da Hsu, Li-Zen Lin, Ann-Ping Tsou, Ching-Ping Tseng, Peter F. Stadler, Stefan Washietl, and Ivo L. Hofacker. **miRNAMap**: Genomic maps of microRNA genes and their target genes in mammalian genomes. *Nucl. Acids Res.*, 34:D135–D139, 2006. Database issue.
- [185] Jana Hertel, Manuela Lindemeyer, Kristin Missal, Claudia Fried, Andrea Tanzer, Christoph Flamm, Ivo L. Hofacker, Peter F. Stadler, and The Students of Bioinformatics Computer Labs 2004 and 2005. The expansion of the metazoan microRNA repertoire. *BMC Genomics*, 7:15 [epub], 2006.
- [186] Christian V. Forst, Christoph Flamm, Ivo L. Hofacker, and Peter F. Stadler. Algebraic comparison of metabolic networks, phylogenetic inference, and metabolic innovation. *BMC Bioinformatics*, 7:67 [epub], 2006.
- [187] Konstantin Klemm and Peter F. Stadler. Statistics of cycles in large networks. *Phys. Rev. E*, 73:025101, 2006. cond-mat/0506493.
- [188] Stephan Bernhart, Ivo L. Hofacker, and Peter F. Stadler. Local RNA base pairing probabilities in large sequences. *Bioinformatics*, 22:614–615, 2006.
- [189] Wilfried Imrich and Peter F. Stadler. A prime factor theorem for a generalized direct product. *Discussiones Math. Graph Th.*, 26:135–140, 2006.
- [190] Stephan H. Bernhart, Hakim Tafer, Ulrike Mückstein, Christoph Flamm, Peter F. Stadler, and Ivo L. Hofacker. Partition function and base pairing probabilities of RNA heterodimers. *Algorithms Mol. Biol.*, 1:3 [epub], 2006.
- [191] Ivo L. Hofacker and Peter F. Stadler. Modeling RNA folding. In Thomas S. Deisboeck and J. Yasha Kresh, editors, *Complex Systems Science in BioMedicine*, pages 227–245. Springer, New York, 2006.
- [192] Axel Mosig, Katrin Sameith, and Peter F. Stadler. **fragrep**: Efficient search for fragmented patterns in genomic sequences. *Geno. Prot. Bioinfo.*, 4:56–60, 2005.
- [193] Burkhard Morgenstern, Sonja J Prohaska, Dirk Pohler, and Peter F Stadler. Multiple sequence alignment with user-defined anchor points. *Algo. Mol. Biol.*, 1:6 [epub], 2006. Updated version of the GCB contribution [?].
- [194] Michael T. Wolfinger, Sebastian Will, Ivo L. Hofacker, Rolf Backofen, and Peter F. Stadler. Exploring the lower part of discrete polymer model energy landscapes. *Europhys. Lett.*, 74:726–732, 2006.
- [195] Guido Fritzsche, Martin Schlegel, and Peter F. Stadler. Alignments of mitochondrial genome arrangements: Applications to metazoan phylogeny. *J. Theor. Biol.*, 240:511–520, 2006.
- [196] Camille Stephan-Otto Attolini and Peter F. Stadler. Evolving towards the hypercycle: A spatial model of molecular evolution. *Physica D*, 217:134–141, 2006.

- [197] Kirstin Missal, Xiaopeng Zhu, Dominic Rose, Wei Deng, Geir Skogerbø, Runsheng Chen, and Peter F. Stadler. Prediction of structured non-coding RNAs in the genome of the nematode *Caenorhabditis elegans*. *J. Exp. Zool.: Mol. Dev. Evol.*, 306B:379–392, 2006.
- [198] Jana Hertel and Peter F. Stadler. Hairpins in a haystack: Recognizing microRNA precursors in comparative genomics data. *Bioinformatics*, 22:e197–e202, 2006. ISMB 2006 contribution.
- [199] Andrea Tanzer and Peter F. Stadler. Evolution of microRNAs. In Shao Yao Ying, editor, *MicroRNA Protocols*, volume 342 of *Methods in Molecular Biology*, pages 335–350. Humana Press, Totowa, NJ, 2006.
- [200] Sonja J. Prohaska and Peter F. Stadler. Evolution of the vertebrate parahox clusters. *J. Exp. Zool.: Mol. Dev. Evol.*, 306B:481–487, 2006.
- [201] Christian Heine, Gerik Scheuermann, Christoph Flamm, Ivo L. Hofacker, and Peter F. Stadler. Visualization of barrier tree sequences. *IEEE Trans. Vis. Comp. Graphics*, 12:781–788, 2006. *Info-Vis 2006 contribution*.
- [202] Sebastian Pötsch, Gerik Scheuermann, Michael T. Wolfinger, Christoph Flamm, and Peter F. Stadler. Visualization of lattice-based protein folding simulations. In Ebad Banissi, editor, *Tenth International Conference on Information Visualization (IV’06)a*, pages 89–94, Los Alamitos, CA, 2006. IEEE Computer Society Press. doi: 10.1109/IV.2006.127.
- [203] Axel Mosig, Ivo L. Hofacker, and Peter F. Stadler. Comparative analysis of cyclic sequences: Viroids and other small circular RNAs. In Robert Giegerich and Jens Stoye, editors, *Proceedings GCB 2006*, volume P-83 of *Lecture Notes in Informatics*, pages 93–102, 2006.
- [204] Peter F. Stadler and Bärbel M. R. Stadler. Genotype phenotype maps. *Biological Theory*, 3:268–279, 2006. Konrad Lorenz Institute Workshop on Biological Information organized by Werner Callebaut in 2002.
- [205] Gavin C. Conant, Günter P. Wagner, and Peter F. Stadler. Patterns of amino acid substitution in orthologous and paralogous genes. *Mol. Phylog. Evol.*, 42:298–307, 2007.
- [206] Sonja J. Prohaska, Peter F. Stadler, and Günter P. Wagner. Evolutionary genomics of *Hox* gene clusters. In Spyros Papageorgiou, editor, *HOX Gene Expression*, pages 68–90. Landes Bioscience & Springer, New York, 2006.
- [207] The Athanasius F. Bompfünewerer RNA Consortium:, Rolf Backofen, Christoph Flamm, Claudia Fried, Guido Fritzsich, Jörg Hackermüller, Jana Hertel, Ivo L. Hofacker, Kristin Missal, Sonja J. Mosig, Axel Prohaska, Domininc Rose, Peter F. Stadler, Andrea Tanzer, Stefan Washietl, and Will Sebastian. RNAs everywhere: Genome-wide annotation of structured RNAs. *J. Exp. Zool. B: Mol. Dev. Evol.*, 308B:1–25, 2007.
- [208] Ivo L. Hofacker and Peter F. Stadler. RNA secondary structures. In Thomas Lengauer, editor, *Bioinformatics: From Genomes to Therapies*, volume 1, pages 439–489. Wiley-VCH, Weinheim, Germany, 2007.
- [209] Michael D. Woodhams, Peter F. Stadler, David Penny, and Lesley J. Collins. RNase MRP and the RNA processing cascade in the eukaryotic ancestor. *BMC Evol. Biol.*, 7:S13, 2007.

- [210] Sebastian Will, Kristin Missal, Ivo L. Hofacker, Peter F. Stadler, and Rolf Backofen. Inferring non-coding RNA families and classes by means of genome-scale structure-based clustering. *PLoS Comp. Biol.*, 3:e65, 2007.
- [211] Jing Luo, Peter F. Stadler, Shunping He, and Axel Meyer. PCR survey of Hox genes in the Goldfish *Carassius auratus auratus*. *J. Exp. Zool. B: (Mol. Devel. Evol.)*, 308B:250–258, 2007.
- [212] Axel Mosig, Meng Guofeng, Bärbel M. R. Stadler, and Peter F. Stadler. Evolution of the vertebrate Y RNA cluster. *Th. Biosci.*, 126:9–14, 2007.
- [213] Madleen Perseke, Thomas Hankeln, Bettina Weich, Guido Fritzsche, Peter F. Stadler, Detlef Bernhard, and Martin Schlegel. The mitochondrial DNA of *Xenoturbella bocki*: Genomic architecture and phylogenetic analysis. *Th. Biosci.*, 126:35–42, 2007.
- [214] P Kapranov, J Cheng, S. Dike, D Nix, R. Dutttagupta, A. T. Willingham, P. F. Stadler, J. Hertel, J. Hackermüller, I. L. Hofacker, I. Bell, E. Cheung, J. Drenkow, E. Dumais, S. Patel, G. Helt, G. Madhavan, A Piccolboni, V Sementchenko, H. Tammana, and T. R. Gingeras. RNA maps reveal new RNA classes and a possible function for pervasive transcription. *Science*, 316:1484–1488, 2007.
- [215] Kristin Reiche and Peter F. Stadler. **RNAstrand**: Reading direction of structured RNAs in multiple sequence alignments. *Alg. Mol. Biol.*, 1:6, 2007.
- [216] Stefan Washietl, Jakob S. Pedersen, Jan O. Korbel, Andreas Gruber, Jörg Hackermüller, Jana Hertel, Manja Lindemeyer, Kristin Reiche, Claudia Stocsits, Andrea Tanzer, Catherine Ucla, Carine Wyss, Stylianos E. Antonarakis, France Denoeud, Julien Lagarde, Jorg Drenkow, Philipp Kapranov, Thomas R. Gingeras, Roderic Guigó, Michael Snyder, Mark B. Gerstein, Alexandre Reymond, Ivo L. Hofacker, and Peter F. Stadler. Structured RNAs in the ENCODE selected regions of the human genome. *Gen. Res.*, 17:852–864, 2007.
- [217] The ENCODE Project Consortium. Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. *Nature*, 447:799–816, 2007.
- [218] Günter P. Wagner, Wolfgang Otto, Vincent Lynch, and Peter F. Stadler. The transient probability distribution of $m/m/\infty$: a stochastic model for transcription factor binding site evolution. *J. Theor. Biol.*, 247:544–553, 2007.
- [219] Stephan Steigele, Wolfgang Huber, Claudia Fried, Peter F. Stadler, and Kay Nieselt. Comparative analysis of structured RNAs in *S. cerevisiae* indicates a multitude of different functions. *BMC Biology*, 5v:25, 2007.
- [220] Dennis Löffler, Katja Brocke-Heidrich, Gabriele Pfeifer, Claudia Stocsits, Jörg Hackermüller, Antje Kretzschmar, Renate Burger, Martin Gramatzki, Conny Blumert, Kay Bauer, Helena Cvijic, Kerstin Ullmann, Peter F. Stadler, and Friedemann Horn. Interleukin-6dependent survival of multiple myeloma cells involves the Stat3-mediated induction of microRNA-21 through a highly conserved enhancer. *Blood*, 110:1330–1333, 2007.
- [221] Matthias Kruspe and Peter F. Stadler. Progressive multiple sequence alignments from triplets. *BMC Bioinformatics*, 8:254, 2007. doi: doi:10.1186/1471-2105-8-254.

- [222] Christoph Flamm, Bärbel M. R. Stadler, and Peter F. Stadler. Saddles and barrier in landscapes of generalized search operators. In C. R. Stephens, M. Toussaint, D. Whitley, and P. F. Stadler, editors, *Foundations of Genetic Algorithms IX*, volume 4436 of *Lecture Notes Comp. Sci.*, pages 194–212, Berlin, Heidelberg, 2007. Springer. 9th International Workshop, FOGA 2007, Mexico City, Mexico, January 8-11, 2007.
- [223] Peter Schuster and Peter F. Stadler. Modeling conformational flexibility and evolution of structure: RNA as an example. In Ugo Bastolla, Markus Porto, H. Eduardo Roman, and Michele Vendruscolo, editors, *Structural Approaches to Sequence Evolution: Molecules, Networks, Populations*, pages 3–36. Springer Verlag, Berlin, 2007.
- [224] Axel Mosig, Julian L. Chen, and Peter F. Stadler. Homology search with fragmented nucleic acid sequence patterns. In R. Giancarlo and S. Hannenhalli, editors, *Algorithms in Bioinformatics (WABI 2007)*, volume 4645 of *Lecture Notes in Computer Science*, pages 335–345, Berlin, Heidelberg, 2007. Springer Verlag.
- [225] Sonja J. Prohaska, Axel Mosig, and Peter F. Stadler. Regulatory signals in genomic sequences. In Jianfeng Feng, Jürgen Jost, and Minping Qian, editors, *Networks: From Biology to Theory*, pages 191–220. Springer, New York, 2007.
- [226] Peter Menzel, Peter F. Stadler, and Axel Mosig. Tanimoto’s Best Barbecue: Discovering regulatory modules using tanimoto scores. In Claudia Falter, Alexander Schliep, Joachim Selbig, Martin Vingron, and Dirk Walther, editors, *German Conference on Bioinformatics (GCB 2007)*, volume 115 of *Lecture Notes in Informatics*, pages 68–77, Bonn, 2007. Gesellschaft f. Informatik.
- [227] Stefan E. Seemann, Michael J. Gilchrist, Ivo L. Hofacker, Peter F. Stadler, and Jan Gorodkin. Detection of RNA structures in porcine EST data and related mammals. *BMC Genomics*, 8:316, 2007.
- [228] Matthias Bernt, Daniel Merkle, Kai Rasch, Guido Fritzsche, Marleen Perseke, Detlef Bernhard, Martin Schlegel, Peter F. Stadler, and Martin Middendorf. CREx: Inferring genomic rearrangements based on common intervals. *Bioinformatics*, 23:2957–2958, 2007.
- [229] Dominic Rose, Jörg Hackermüller, Stefan Washietl, Sven Findeiß, Kristin Reiche, Jana Hertel, Peter F. Stadler, and Sonja J. Prohaska. Computational RNomics of drosophilids. *BMC Genomics*, 8:406, 2007.
- [230] Manja Marz, Axel Mosig, Bärbel M. R. Stadler, and Peter F. Stadler. U7 snRNAs: A computational survey. *Geno. Prot. Bioinf.*, 5:187–195, 2007.
- [231] Christian Heine, Geric Scheuermann, Christoph Flamm, Ivo Hofacker, and Peter F. Stadler. Visualization of barrier tree sequences revisited. In Lars Linsen, Hans Hagen, and Bernd Hamann, editors, *Visualization in Medicine and Life Sciences*, pages 275–290. Springer, Berlin, Heidelberg, 2007.
- [232] Athanasius F. Bompfünnewerer, Rolf Backofen, Stephan H. Berhart, Jana Hertel, , Ivo L. Hofacker, Peter F. Stadler, and Sebastian Will. Variations on RNA folding and alignment: Lessons from Benasque. *J. Math. Biol.*, 56:129–144, 2008.
- [233] Jana Hertel, Ivo L. Hofacker, and Peter F. Stadler. snoReport: Computational identification of snoRNAs with unknown targets. *Bioinformatics*, 24:158–164, 2008.

- [234] Mingyi Xie, Axel Mosig, Xiaodong Qi, Yang Li, Peter F. Stadler, and Julian J.-L. Chen. Size variation and structural conservation of vertebrate telomerase RNA. *J. Biol. Chem.*, 283:2049–2059, 2008.
- [235] Andreas R. Gruber, Dorota Koper-Emde, Manja Marz, Hakim Tafer, Stephan Bernhart, Gregor Obernosterer, Axel Mosig, Ivo L. Hofacker, Peter F. Stadler, and Bernd-Joachim Benecke. Invertebrate 7SK snRNAs. *J. Mol. Evol.*, 107-115:66, 2008.
- [236] Guido Fritzscht, Manja U. Böhme, Mike Thorndyke, Hiroaki Nakano, Olle Israelsson, Thomas Stach, Martin Schlegel, Thomas Hankeln, and F. Stadler, Peter. A PCR survey of *Xenoturbella bocki* *Hox* genes. *J. Exp. Zool: Mol. Dev. Evol.*, 310B:278–284, 2008.
- [237] Veiko Krauss, Christian Thümmler, Franziska Georgi, Jörg Lehmann, Peter F. Stadler, and Carina Eisenhardt. Near intron positions are reliable phylogenetic markers: An application to Holometabolous Insects. *Mol. Biol. Evol.*, 25:821–830, 2008.
- [238] Marleen Perseke, Guido Fritzscht, Kai Ramsch, Matthias Bernt, Daniel Merkle, Martin Middendorf, Detlef Bernhard, Peter F. Stadler, and Martin Schlegel. Evolution of mitochondrial gene orders in echinoderms. *Mol. Phylog. Evol.*, 47:855–864, 2008.
- [239] Christoph Jöchel, Mathieu Rederstorff, Jana Hertel, Peter F. Stadler, Ivo L. Hofacker, Markus Schrettl, Hubertus Haas, and Alexander Hüttenhofer. Small ncRNA transcriptome analysis from *Aspergillus fumigatus* suggests a novel mechanism for regulation of protein-synthesis. *Nucleic Acids Res.*, 36:2677–2689, 2008.
- [240] Michael Geis, Christian Flamm, Michael T. Wolfinger, Andrea Tanzer, Ivo L. Hofacker, Martin Middendorf, Christian Mandl, Peter F. Stadler, and Caroline Thurner. Folding kinetics of large RNAs. *J. Mol. Biol.*, 379:160–173, 2008.
- [241] Sonja J. Prohaska, Guido Fritzscht, and Peter F. Stadler. Rate variations, phylogenetics, and partial orders. In Miika Ahdesmäki, Korbinian Strimmer, Nicole Radde, Jörg Rahnenführer, Konstantin Klemm, Harri Lähdesmäki, and Olli Yli-Harja, editors, *Fifth International Workshop on Computational Systems Biology, WCSB 2008*, pages 133–136, Tampere, FI, 2008. TU Tampere.
- [242] Chris T Amemiya, Sonja J Prohaska, Alicia Hill-Force, April Cook, Jessica Wasserscheid, Juan Ferrier David E. K., Pascual-Anaya, Jordi Garcia-Fernández, Ken Dewar, and Peter F. Stadler. The amphioxus *Hox* cluster: characterization, comparative genomics, and evolution. *J. Exp. Zool. B: Mol. Dev. Evol.*, 310B:465–477, 2008.
- [243] Dominic Rose, Jana Hertel, Kristin Reiche, Peter F. Stadler, and Jörg Hackermüller. NcDNAalign: Plausible multiple alignments of non-protein-coding genomic sequences. *Genomics*, 92:65–74, 2008.
- [244] Konstantin Klemm, Christoph Flamm, and Peter F. Stadler. Funnels in energy landscapes. *Eur. Phys. J. B*, 63:387–391, 2008. ECCS 2007 contribution.
- [245] Andreas W. M. Dress, Christoph Flamm, Guido Fritzscht, Stefan Grünewald, Matthias Kruspe, Sonja J. Prohaska, and Peter F. Stadler. Identification of homoplastic characters in multiple sequence alignments. *Alg. Mol. Biol.*, 3:7, 2008. extended abstract accepted at ICMSB 2008.

- [246] Sonja J. Prohaska and Peter F. Stadler. A story of growing confusion: Genes and their regulation. In Rubem P. Mondaini and Rui Dilão, editors, *BIOMAT-2007: International Symposium on Mathematical and Computational Biology*, pages 325–345, Singapore, 2007. World Scientific. Armação dos Búzios, RJ, Brazil, 24-29 November 2008.
- [247] Sonja J. Prohaska and Peter F. Stadler. “Genes”. *Th. Biosci.*, 127:215–221, 2008.
- [248] Steve Hoffmann, Sabine Cepok, Klaus Lehmann-Horn, Jörg Hackermüller, Peter F. Stadler, Hans-Peter Hartung, Achim Berthele, Florian Deisenhammer, Ralf Wasmuth, and Bernhard Hemmer. HLA-DRB1*0401 and HLA-DRB1*0408 are strongly associated with the development of antibodies against interferon-beta therapy in multiple sclerosis. *Amer. J. Hum. Genet.*, 83:219–227, 2008.
- [249] Andreas Gruber, Carsten Kilgus, Axel Mosig, Ivo L. Hofacker, Wolfgang Hennig, and Peter F. Stadler. Arthropod 7SK RNA. *Mol. Biol. Evol.*, 1923-1930:25, 2008.
- [250] Jörg Lehmann, Peter F. Stadler, and Sonja J. Prohaska. SynBlast: Assisting the analysis of conserved synteny information. *BMC Bioinformatics*, 9:351, 2008. doi:10.1186/1471-2105-9-351.
- [251] Ulrike Mückstein, Hakim Tafer, Stephan H. Bernhard, Maribel Hernandez-Rosales, Jörg Vogel, Peter F. Stadler, and Ivo L. Hofacker. Translational control by RNA-RNA interaction: Improved computation of RNA-RNA binding thermodynamics. In Mourad Elloumi, Josef Küng, Michal Linial, Robert F. Murphy, Kristan Schneider, and Cristian Toma Toma, editors, *Bioinformatics Research and Development — BIRD 2008*, volume 13 of *Comm. Comp. Inf. Sci.*, pages 114–127, Berlin, 2008. Springer.
- [252] Peter Schuster and Peter F. Stadler. Nature and evolution of early replicons. In E. Domingo, C. R. Parrish, and J. Holland, editors, *Origin and Evolution of Viruses*, pages 1–41. Academic Press, London, UK, 2nd edition, 2008. completely rewritten from [74].
- [253] Elisabeth Sonnleitner, Theresa Sorger-Domenigg, Monika J. Madej, Sven Findeiß, Jörg Hackermüller, Alexander Hüttenhofer, Peter F. Stadler, Udo Bläsi, and Isabella Moll. Detection of small non-coding RNAs in *Pseudomonas aeruginosa* by RNomics and structure-based bioinformatics tools. *Microbiology*, 154:3175–3187, 2008.
- [254] Peter F. Stadler and Bärbel M. R. Stadler. Replicator dynamics in protocells. In Steen Rasmussen, Mark A. Bedau, Liaohai Chen, David Deamer, David C. Krakauer, Norman H. Packard, and Peter F. Stadler, editors, *Protocells: Bridging Nonliving and Living Matter*, pages 317–336. MIT Press, 2008.
- [255] Andreas Heffel, Peter F. Stadler, Sonja J. Prohaska, Gerhard Kauer, and Jens-Peer Kuska. Process flow for classification and clustering of fruit fly gene expression patterns. In *Proceedings of the 15'th IEEE International Conference on Image Processing, ICIP 2008*, pages 721–724. IEEE, 2008. CD Proceedings; ISSN 978-1-4244-1764-3/08/.
- [256] Dominic Rose, Julian Jöris, Jörg Hackermüller, Kristin Reiche, Qiang Li, and Peter F. Stadler. Duplicated RNA genes in teleost fish genomes. *J. Bioinf. Comp. Biol.*, 6:1157–1175, 2008.
- [257] Stephan H Bernhart, Ivo L Hofacker, Sebastian Will, Andreas R Gruber, and Peter F Stadler. RNAalifold: improved consensus structure prediction for RNA alignments. *BMC Bioinformatics*, 9:474, 2008.

- [258] Manuela Marz, Toralf Kirsten, and Peter F. Stadler. Evolution of spliceosomal snRNA genes in metazoan animals. *J. Mol. Evol.*, 67:594–607, 2008.
- [259] Gil Benkő, Florian Centler, Peter Dittrich, Christoph Flamm, Bärbel M. R. Stadler, and Peter F. Stadler. A topological approach to chemical organizations. *Alife*, 15:71–88, 2009.
- [260] Frank Jühling, Mario Mörl, Roland K Hartmann, Mathias Sprinzl, Peter F Stadler, and Jörn Pütz. tRNAdb 2009: compilation of tRNA sequences and tRNA genes. *Nucleic Acids Res.*, 37:D159–D162, 2009.
- [261] T A Jones, Wolfgang Otto, Manja Marz, Sean R Eddy, and Peter F Stadler. A survey of nematode SmY RNAs. *RNA Biol.*, 6:5–8, 2009.
- [262] Bogumil Kaczkowski, Elfar Torarinsson, Kristin Reiche, Jakob Hull Havgaard, Peter F. Stadler, and Jan Gorodkin. Structural profiles of miRNA families from pairwise clustering. *Bioinformatics*, 25:291–294, 2009.
- [263] Jana Hertel, Danielle de Jong, Manja Marz, Dominic Rose, Hakim Tafer, Andrea Tanzer, Bernd Schierwater, and Peter F. Stadler. Non-coding RNA annotation of the genome of *Trichoplax adhaerens*. *Nucleic Acids Res.*, 37:1602–1615, 2009.
- [264] Karsten Scheibye-Alsing, Steve Hoffmann, Annett M. Frankel, Peter Jensen, Peter F. Stadler, Yuan Mang, Niels Tommerup, Mike J Gilchrist, Ann-Britt N. Hillig, Susanna Cirera, Claus B Jørgensen, Merete Fredholm, and Jan Gorodkin. Sequence assembly. *Comp. Biol. Chem.*, 33:121–136, 2009.
- [265] Andreas Heffel, Sonja J. Prohaska, Peter F. Stadler, Gerhard Kauer, and Jens-Peer Kuska. Automatic classification of embryonic fruit fly gene expression patterns. In H.-P. Meinzer, Th. M. Deserno, H. Handels, and Th. Tolxdorff, editors, *Bildverarbeitung für die Medizin 2009: Algorithmen – Systeme – Anwendungen*, pages 415–419, Heidelberg, 2009. Springer.
- [266] Marc Hellmuth, Wilfried Imrich, Werner Klöckl, and Peter F. Stadler. Approximate graph products. *Eur. J. Comb.*, 30:1119–1133, 2009.
- [267] Karen E Chambers, Ryan McDaniell, Jeremy D Raincrow, Maya Deshmukh, Peter F Stadler, and Chi-hua Chiu. Hox cluster duplication in the basal teleost *Hiodon alosoides* (Osteoglossomorpha). *Theory Biosci.*, 128:109–120, 2009.
- [268] Gavin C. Conant and Peter F. Stadler. Solvent exposure imparts similar selective pressures across a range of yeast proteins. *Mol. Biol. Evol.*, 26:1155–1161, 2009.
- [269] Konstantin Klemm and Peter F. Stadler. A note on fundamental, non-fundamental, and robust cycle bases. *Discr. Appl. Math.*, 157:2432–2438, 2009.
- [270] Axel Mosig, Türker Bıyıkoglu, Sonja J. Prohaska, and Peter F. Stadler. Discovering cis-regulatory modules by optimizing barbecues. *Discr. Appl. Math.*, 157:2458–2468, 2008.
- [271] Wolfgang Otto, Peter F. Stadler, Francesc López-Gialdéz, Jeffrey P. Townsend, Vincent J. Lynch, and Günter P. Wagner. Measuring transcription factor binding site turnover: A maximum likelihood approach using phylogenies. *Genome Biol. Evol.*, 1:85–98, 2009.

- [272] Michael Hiller, Sven Findeiß, Sandro Lein, Manja Marz, Claudia Nickel, Dominic Rose, Christine Schulz, Rolf Backofen, Sonja J. Prohaska, Gunter Reuter, and Peter F. Stadler. Conserved introns reveal novel transcripts in *Drosophila melanogaster*. *Genome Res.*, 19:1289–1300, 2009.
- [273] Markus Riester, Peter F. Stadler, and Konstantin Klemm. FRANz: Fast reconstruction of wild pedigrees. *Bioinformatics*, 25:2134–2139, 2009. Preliminary version in: *German Conference on Bioinformatics GCB 2008*, A. Beyer and M. Schroeder (eds.), Ges. f. Informatik, Bonn, *Lect. Notes Inf.* **136**, pp. 168–177.
- [274] Peter F. Stadler, Julian J.-L. Chen, Jörg Hackermüller, Steve Hoffmann, Friedemann Horn, Phillip Khaitovich, Antje K. Kretzschmar, Axel Mosig, Sonja J. Prohaska, Xiaodong Qi, Katharina Schutt, and Kerstin Ullmann. Evolution of vault RNAs. *Mol. Biol. Evol.*, 26:1975–1991, 2009.
- [275] David Langenberger, Clara Bermudez-Santana, Jana Hertel, Steve Hoffmann, Steve Khaitovich, and Peter F. Stadler. Evidence for human microRNA-offset RNAs in small RNA sequencing data. *Bioinformatics*, 25:2298–2301, 2009.
- [276] Andreea Munteanu and Peter F. Stadler. Mutate now, die later: Evolutionary dynamics with delayed selection. *J. Theor. Biol.*, 260:412–421, 2009.
- [277] Steve Hoffmann, Christian Otto, Stefan Kurtz, Cynthia Sharma, Philipp Khaitovich, Jörg Vogel, Peter F. Stadler, and Jörg Hackermüller. Fast mapping of short sequences with mismatches, insertions and deletions using index structures. *PLoS Comp. Biol.*, 5:e1000502, 2009.
- [278] Peter Menzel, Jan Gorodkin, and Peter F. Stadler. Maximum likelihood estimation of weight matrices for targeted homology search. In Ivo Grosse, Steffen Neumann, Stefan Posch, Falk Schreiber, and Peter F. Stadler, editors, *German Conference on Bioinformatics 2009*, volume 157 of *Lecture Notes in Informatics*, pages 211–220, Bonn, 2009. Gesellschaft f. Informatik.
- [279] Axel Mosig, Liang Zhu, and Peter F. Stadler. Customized strategies for discovering distant ncRNA homologs. *Brief. Funct. Genomics Proteomics*, 8:451–460, 2009.
- [280] Manja Marz, Alexander Donath, Nina Verstaete, Van Trung Nguyen, Peter F. Stadler, and Olivier Bensaude. Evolution of 7SK RNA and its protein partners in metazoa. *Mol. Biol. Evol.*, 26:2821–2830, 2009.
- [281] Claudia S. Copeland, Manja Marz, Dominic Rose, Jana Hertel, Paul J. Brindley, Clara Bermudez Santana, Stephanie Kehr, Camille Stephan-Otto Attolini, and Peter F. Stadler. Homology-based annotation of non-coding RNAs in the genomes of *Schistosoma mansoni* and *Schistosoma japonicum*. *BMC Genomics*, 10:464, 2009.
- [282] Roman R. Stocsits, Harald Letsch, Jana Hertel, Bernhard Misof, and Peter F. Stadler. Accurate and efficient reconstruction of deep phylogenies from structured RNAs. *Nucleic Acids Res.*, 37:6184–6193, 2009.
- [283] Peter F. Stadler, Sonja J. Prohaska, Christian V. Forst, and David C. Krakauer. Defining genes: A computational framework. *Th. Biosci.*, 128:165–170, 2009.

- [284] Fenix W. D. Huang, Jing Qin, Christian M. Reidys, and Peter F. Stadler. Partition function and base pairing probabilities for RNA-RNA interaction prediction. *Bioinformatics*, 25:2646–2654, 2009.
- [285] Peter Menzel, Jan Gorodkin, and Peter F. Stadler. The tedious task of finding homologous non-coding RNA genes. *RNA*, 15:2075–2082, 2009.
- [286] Jens-Philipp Ostermeier, Marc Helmuth, Konstantin Klemm, Josef Leydold, and Peter F. Stadler. A note on quasi-robust cycle bases. *Acta Math. Contemp.*, 2:231–240, 2009.
- [287] Manja Marz and Peter F. Stadler. Comparative analysis of eukaryotic U3 snoRNAs. *RNA Biol.*, 6:503–507, 2009.
- [288] Marc Hellmuth, Wilfried Imrich, Werner Klöckl, and Peter F. Stadler. Local algorithms for the prime factorization of strong product graphs. *Math. Comp. Sci.*, 2:653–682, 2009.
- [289] Fenix W. D. Huang, Jing Qin, Christian M. Reidys, and Peter F. Stadler. Target prediction and a statistical sampling algorithm for RNA-RNA interaction. *Bioinformatics*, 26:175–181, 2010.
- [290] David Langenberger, Clara Bermudez-Santana, Peter F. Stadler, and Steve Hoffmann. Identification and classification of small RNAs in transcriptome sequence data. *Pac. Symp. Biocomput.*, 15:80–87, 2010.
- [291] Andreas R. Gruber, Sven Findeiß, Stefan Washietl, Ivo L. Hofacker, and Peter F. Stadler. RNAz 2.0: improved noncoding RNA detection. *Pac. Symp. Biocomput.*, 15:69–79, 2010.
- [292] Manja Marz, Nathalie Vanzo, and Peter F. Stadler. Temperature-dependent structural variability of RNAs: spliced leader RNAs and their evolutionary history. *J. Bioinf. Comp. Biol.*, 8:1–17, 2010.
- [293] Chris T. Amemiya, Thomas P. Powers, Sonja J. Prohaska, Jane Grimwood, Jeremy Schmutz, Mark Dickson, Tsutomu Miyake, Michael A. Schoenborn, Richard M. Myers, Francis H. Ruddle, and Peter F. Stadler. Complete HOX cluster characterization of the coelacanth provides further evidence for slow evolution of its genome. *Proc. Natl. Acad. Sci.*, 107:3622–3627, 2010.
- [294] Hakim Tafer, Stephanie Kehr, Jana Hertel, and Peter F. Stadler. RNAsnoop: Efficient target prediction for box H/ACA snoRNAs. *Bioinformatics*, 26:610–616, 2010.
- [295] Cynthia M. Sharma, Steve Hoffmann, Fabien Darfeuille, Jérémy Reignier, Sven Findeiß, Alexandra Sittka, Sandrine Chabas, Kristin Reiche, Jörg Hackermüller, Richard Reinhardt Reinhardt, Peter F. Stadler, and Jörg Vogel. The primary transcriptome of the major human pathogen *Helicobacter pylori*. *Nature*, 464:250–255, 2010.
- [296] Sonja J Prohaska, Peter F. Stadler, and David C. Krakauer. Innovation in gene regulation: The case of chromatin computation. *J. Theor. Biol.*, 265:27–44, 2010.
- [297] Alexander Donath, Sven Findeiß, Jana Hertel, Manja Marz, Wolfgang Otto, Christine Schulz, Peter F. Stadler, and Stefan Wirth. Non-coding RNAs. In Gustavo Caetano-Anolles, editor, *Evolutionary Genomics and Systems Biology*, pages 251–293. Wiley-Blackwell, Hoboken, NJ, 2010.

- [298] Andrea Tanzer, Markus Riester, Jana Hertel, Clara Isabel Bermudez-Santana, Jan Gorodkin, Ivo L. Hofacker, and Peter F. Stadler. Evolutionary genomics of microRNAs and their relatives. In Gustavo Caetano-Anolles, editor, *Evolutionary Genomics and Systems Biology*, pages 295–327. Wiley-Blackwell, Hoboken, NJ, 2010.
- [299] Ilenia Boria, Andreas R. Gruber, Andrea Tanzer, Stephan Bernhart, Ronny Lorenze, Michael M. Mueller, Ivo L. Hofacker, and Peter F. Stadler. Nematode sbRNAs: homologs of vertebrate Y RNAs. *J. Mol. Evol.*, 70:346–358, 2010.
- [300] Sven Findeiß, Cornelius Schubert, Peter F. Stadler, and Ulla Bonas. A novel family of plasmid-transferred anti-sense ncRNAs. *RNA Biology*, 7:120–124, 2010.
- [301] Marleen Perseke, Detlef Bernhard, Guido Fritzsche, Franz Brümmer, Peter F. Stadler, and Martin Schlegel. Mitochondrial genome evolution in Ophiuroidea, Echinoidea, and Holothuroidea: Insights in phylogenetic relationships of Echinodermata. *Mol. Phylog. Evol.*, 56:201–211, 2010. doi: 10.1016/j.ympev.2010.01.035.
- [302] Ivo L. Hofacker, Christoph Flamm, Christian Heine, Michael T. Wolfinger, Gerik Scheuermann, and Peter F. Stadler. **BarMap**: RNA folding on dynamics energy landscapes. *RNA*, 16:1308–1316, 2010.
- [303] Mario Fasold, Peter F. Stadler, and Hans Binder. G-stack modulated probe intensities on expression arrays — sequence corrections and signal calibration. *BMC Bioinformatics*, 11:207, 2010.
- [304] Clara Bermudez-Santana, Camille Stephan-Otto Attolini, Toralf Kirsten, Jan Engelhardt, Sonja J. Prohaska, Stephan Steigele, and Peter F. Stadler. Genomic organization of eukaryotic tRNAs. *BMC Genomics*, 11:270, 2010.
- [305] Jörg Lehmann, Carina Eisenhardt, Peter F. Stadler, and Veiko Krauss. Some novel intron positions in conserved drosophila genes are caused by intron sliding or tandem duplications. *BMC Evol. Biol.*, 10:156, 2010.
- [306] Dilmurat Yusuf, Manja Marz, Peter F. Stadler, and Ivo L. Hofacker. **Bcheck**: a wrapper tool for detecting RNase P RNA genes. *BMC Bioinformatics*, 11:432, 2010.
- [307] Markus Riester, Peter F. Stadler, and Konstantin Klemm. Reconstruction of pedigrees in clonal plant populations. *Theor. Pop. Biol.*, 78:109–117, 2010.
- [308] Christian Arnold and Peter F. Stadler. Polynomial algorithms for the maximal pairing problem: efficient phylogenetic targeting on arbitrary trees. *Alg. Mol. Biol.*, 5:25, 2010.
- [309] Christoph Flamm, Alexander Ullrich, Heinz Ekker, Martin Mann, Daniel Högerl, Markus Rohrschneider, Sebastian Sauer, Gerik Scheuermann, Konstantin Klemm, Ivo L. Hofacker, and Peter F. Stadler. Evolution of metabolic networks: A computational framework. *J. Syst. Chem.*, 1:4, 2010.
- [310] P. F. Stadler. Evolution of the long non-coding RNAs MALAT1 and MEN β/ϵ . In Carlos Eduardo Ferreira, Satoru Miyano, and Peter F. Stadler, editors, *Advances in Bioinformatics and Computational Biology, 5th Brazilian Symposium on Bioinformatics*, volume 6268 of *Lecture Notes in Computer Science*, pages 1–12, Heidelberg, 2010. Springer Verlag.

- [311] Rami A. Dalloul, Julie A. Long, Aleksey V. Zimin, Luqman Aslam, Kathryn Beal, Le Ann Blomberg, Pascal Bouffard, David W. Burt, Oswald Crasta, Richard P. M. A. Crooijmans Crooijmans, Kristal Cooper, Roger A. Coulombe, Supriyo De, Mary E. Delany, Jerry B. Dodgson, Jennifer J. Dong, Clive Evans, Karin M. Frederickson, Paul Flicek, Liliana Florea, Otto Folkerts, Martien A. M. Groenen, Tim T. Harkins, Javier Herrero, Steve Hoffmann, Hendrik-Jan Megens, Andrew Jiang, Pieter de Jong, Pete Kaiser, Heebal Kim, Kyu-Won Kim, Sungwon Kim, David Langenberger, Mi-Kyung Lee, Taeheon Lee, Shrinivasrao Mane, Guillaume Marcais, Manja Marz, Audrey P. McElroy, Thero Modise, Mikhail Nefedov, Cédric Notredame, Ian R. Paton, William S. Payne, Geo Pertea, Dennis Prickett, Daniela Puiu, Dan Qioa, Emanuele Raineri, Magali Ruffier, Steven L. Salzberg, Michael C. Schatz, Chantel Scheuring, Carl J. Schmidt, Steven Schroeder, Stephen M. Searle, Edward J. Smith, Jacqueline Smith, Tad S. Sonstegard, Peter F. Stadler, Hakim Tafer, Zhijian (Jake) Tu, Curtis P. Van Tassel, Albert J. Vilella, Kelly P. Williams, James A. Yorke, Liqing Zhang, Hong-Bin Zhang, Xiaojun Zhang, Yang Zhang, and Kent M. Reed. Multi-platform next-generation sequencing of the domestic turkey (*Meleagris gallopavo*): Genome assembly and analysis. *PLoS Biology*, 8:e1000475, 2010.
- [312] Arli A. Parikesit, Peter F. Stadler, and Sonja J. Prohaska. Quantitative comparison of genomic-wide protein domain distributions. In D. Schomburg and A. Grote, editors, *German Conference on Bioinformatics 2010*, volume P-173 of *Lecture Notes in Informatics*, pages 93–102, Bonn, 2010. Gesellschaft für Informatik. Extended Abstract: *Detection of Protein Domains in Eukaryotic Genome Sequences in Advances in Bioinformatics and Computational Biology, 5th Brazilian Symposium on Bioinformatics*, Ferreira, C. E., Miyano, S, and Stadler, P. F. (eds.), Springer, Heidelberg (2010), Lect. Notes Comp. Sci. **6268**, pp. 71-74.
- [313] Alexander Ullrich, Peter F. Stadler, Markus Rohrschneider, and Peter F. Stadler. *In silico* evolution of early metabolism. In Harold Fellermann, Mark Dörr, Martin M. Hanczyc, Lone Ladegaard Laursen, Sarah Maurer, Daniel Merkle, Pierre-Alain Monnard, Kasper Stoy, and Steen Rasmussen, editors, *Artificial Life XII: Proceedings of the Twelfth International Conference on the Synthesis and Simulation of Living Systems*, pages 57–64, Cambridge, MA, 2010. MIT Press.
- [314] Bärbel M. R. Stadler and Peter F. Stadler. Combinatorial vector fields and the valley structure of fitness landscapes. *J. Math. Biol.*, 61:877–898, 2010.
- [315] Stefan Jänicke, Christian Heine, Marc Hellmuth, Peter F. Stadler, and Gerik Scheuermann. Visualization of graph products. *IEEE Trans. Vis. Comput. Graph.*, 16:1082–1089, 2010.
- [316] Markus Rohrschneider, Alexander Ullrich, Andreas Kerren, Peter F. Stadler, and Gerik Scheuermann. Visual network analysis of dynamic metabolic pathways. In George Bebis, Richard Boyle, Bahram Parvin, Darko Koracin, Ronald Chung, Riad Hammoud, Muhammad Hussain, Tan Kar-Han, Roger Crawfis, Daniel Thalmann, David Kao, and Lisa Avila, editors, *Advances in Visual Computing (ISVC 2010)*, volume 6453 of *Lect. Notes Comp. Sci.*, pages 316–327, Berlin, 2010. Springer.
- [317] Stephan A. Müller, Tibor Kohajda, Sven Findeiß, Peter F. Stadler, Stefan Washietl, Manolis Kellis, Martin von Bergen, and Stefan Kalkhof. Optimization of parameters for coverage of low molecular weight proteins. *Anal. Bioanal. Chem.*, 398:2867–2881, 2010.
- [318] Stephanie Kehr, Sebastian Bartschat, Peter F. Stadler, and Hakim Tafer. PLEXY: Efficient target prediction for box C/D snoRNAs. *Bioinformatics*, 27:279–280, 2011.

- [319] Peter Menzel, Peter F. Stadler, and Jan Gorodkin. maxAlike: Maximum-likelihood based sequence reconstruction with application to improved primer design for unknown sequences. *Bioinformatics*, 27:317–325, 2011.
- [320] Sven Findeiß, David Langenberger, Peter F. Stadler, and Steve Hoffmann. Traces of post-transcriptional RNA modifications in deep sequencing data. *Biol. Chem.*, 392:305–313, 2011.
- [321] Stefan Washietl, Sven Findeiß, Stephan Müller, Stefan Kalkhof, Martin von Bergen, Ivo L. Hofacker, Peter F. Stadler, and Nick Goldman. RNAcode: robust prediction of protein coding regions in comparative genomics data. *RNA*, 17:578–594, 2011.
- [322] Axel Mosig and Peter F. Stadler. Evolution of vault RNAs. In N.N., editor, *Encyclopedia of Life Sciences*, page doi: 10.1002/9780470015902.a0022883. Wiley-Blackwell, Hoboken, NJ, 2011.
- [323] Andrea Tramontano, Alexander Donath, Stephan H. Bernhart, Kristin Reiche, Gudrun Böhmendorfer, Peter F. Stadler, and Andreas Bachmair. Deletion analysis of the 3' long terminal repeat sequence of plant retrotransposon Tto1 identifies 125 base pairs redundancy as sufficient for first strand transfer. *Virology*, 75-82:412, 2011.
- [324] David C Krakauer, James P Collins, Douglas Erwin, Jessica C Flack, Walter Fontana, Manfred D Laubichler, Sonja J Prohaska, Geoffrey B West, and Peter F Stadler. The challenges and scope of theoretical biology. *J. Theor. Biol.*, 276:269–276, 2011.
- [325] Sonja J. Prohaska and Peter F. Stadler. The use and abuse of -omes. In Bernd Mayer, editor, *Bioinformatics for Omics Data: Methods and Protocols*, volume 719, pages 173–196. Humana Press, New York, NY, 2011. DOI: 10.1007/978-1-61779-027-0_8.
- [326] Christian Otto, Steve Hoffmann, Jan Gorodkin, and Peter F. Stadler. Fast local fragment chaining using sum-of-pair gap costs. *Alg. Mol. Biol.*, 6:4, 2011.
- [327] Christian M. Reidys, Fenix W. D. Huang, Jørgen E. Andersen, Robert C. Penner, Peter F. Stadler, and Markus E. Nebel. Topology and prediction of RNA pseudoknots. *Bioinformatics*, 27:1076–1085, 2011. Addendum in: *Bioinformatics* 28:300 (2012).
- [328] Marcus Lechner, Sven Findeiß, Lydia Steiner, Manja Marz, Peter F. Stadler, and Sonja J. Prohaska. **Proteinortho**: detection of (co-)orthologs in large-scale analysis. *BMC Bioinformatics*, 12:124, 2011.
- [329] Alexander Ullrich, Markus Rohrschneider, Gerik Scheuermann, Peter F. Stadler, and Christoph Flamm. *In silico* evolution of early metabolism. *ALife*, 17:87–108, 2011.
- [330] Christian Höner zu Siederdisen, Stephan H. Bernhart, Peter F. Stadler, and Ivo L. Hofacker. A folding algorithm for extended RNA secondary structures. *Bioinformatics*, 27:i129–i137, 2011. ISMB.
- [331] Marleen Perseke, Joerg Hetmank, Matthias Bernt, Peter F. Stadler, Martin Schlegel, and Detlef Bernhard. The enigmatic mitochondrial genome of *Rhabdopleura compacta* (PPterobranchia) reveals insights into selection of an efficient tRNA system and supports monophyly of Ambulacraria. *BMC Evol. Biol.*, 11:134, 2011.
- [332] Lydia Steiner, Peter F. Stadler, and Michael Cysouw. A pipeline for computational historical linguistics. *Language Dynamics & Change*, 1:89–127, 2011.

- [333] Dominic Rose, Michael Hiller, Katharina Schutt, Jörg Hackermüller, Rolf Backofen, and Peter F. Stadler. Computational discovery of human coding and non-coding transcripts with conserved splice sites. *Bioinformatics*, 27:1894–1900, 2011.
- [334] Hakim Tafer, Fabian Ammann, Florian Eggenhoffer, Peter F. Stadler, and Ivo L. Hofacker. Fast accessibility-based prediction of RNA-RNA interactions. *Bioinformatics*, 27:1934–1940, 2011.
- [335] Wolfgang Otto, Peter F. Stadler, and Sonja J. Prohaska. Phylogenetic footprinting and consistent sets of local alignments. In R. Giancarlo and G. Manzini, editors, *CPM 2011*, volume 6661 of *Lecture Notes in Computer Science*, pages 118–131, Heidelberg, Germany, 2011. Springer-Verlag.
- [336] Jeremy D. Raincrow, Ken Dewar, Claudia Stocsits, Sonja J. Prohaska, Chris T. Amemiya, Peter F. Stadler, and Chi-hua Chiu. Hox clusters of the bichir (Actinopterygii, *Polypterus senegalus*) highlight unique patterns of sequence evolution in gnathostome phylogeny. *J. Exp. Zool.*, 316:451–464, 2011.
- [337] David Langenberger, Sebastian Bartschat, Jana Hertel, Steve Hoffmann, Hakim Tafer, and Peter F. Stadler. Microrna or not microrna? In Osmar Norberto de Souza, Guilherme P. Telles, and Mathew J. Palakal, editors, *Advances in Bioinformatics and Computational Biology, 6th Brazilian Symposium on Bioinformatics, BSB 2011*, volume 6832 of *Lecture Notes in Computer Science*, pages 1–9, Berlin, Heidelberg, 2011. Springer.
- [338] Michael B. Clark, Paulo P. Amaral, Felix J. Schlesinger, Marcel E. Dinger, Ryan J. Taft, John L. Rinn, Chris P. Ponting, Peter F. Stadler, Kevin J. Morris, Antonin Morillon, Joel S. Rozowsky, Mark Gerstein, Claes Wahlestedt, Yoshihide Hayashizaki, Piero Carninci, Thomas R. Gingeras, and John S. Mattick. The reality of pervasive transcription. *PLoS Biology*, 9:e1000625, 2011.
- [339] Mario Fasold, David Langenberger, Hans Binder, Peter F. Stadler, and Steve Hoffmann. DARIO: A ncRNA detection and analysis tool for next-generation sequencing experiments. *Nucleic Acids Res.*, 39:W112–W117, 2011.
- [340] Florian Eggenhofer, Hakim Tafer, Peter F. Stadler, and Ivo L. Hofacker. RNApredator: Fast accessibility-based prediction of sRNA targets. *Nucleic Acids Res.*, 39:W149–W154, 2011.
- [341] Manja Marz and Peter F. Stadler. RNA interactions. In Lesley J. Collins, editor, *RNA Infrastructure and Networks*, volume 722 of *Advances in Experimental Medicine and Biology*, pages 20–38. Landes Biosciences, Springer-Verlag, Berlin, 2011. <http://www.landesbioscience.com/curie/chapter/4913/>.
- [342] Sven Findeiß, Jan Engelhardt, Sonja P. Prohaska, and Peter F. Stadler. Protein-coding structured RNAs: A computational survey of conserved RNA secondary structures overlapping coding regions in drosophilids. *Biochimie*, 93:2019–2023, 2011.
- [343] Dominic Rose and Peter F. Stadler. Molecular evolution of the non-coding eosinophil granule ontogeny transcript EGOT. *Front. Gene.*, 2:69, 2011.
- [344] A Bateman, S Agrawal, E Birney, E A Bruford, J M Bujnicki, G Cochrane, J R Cole, M E Dinger, A J Enright, P P Gardner, D Gautheret, S Griffiths-Jones, J Harrow, J Herrero, I H Holmes, H D Huang, K A Kelly, P Kersey, A Kozomara, T M Lowe, M Marz, S Moxon,

- K D Pruitt, T Samuelsson, P F Stadler, A J Vilella, J H Vogel, K P Williams, M W Wright, and C Zwieb. RNAcentral: A vision for an international database of RNA sequences. *RNA*, 17:1941–1946, 2011.
- [345] Arli A. Parikesit, Peter F. Stadler, and J. Prohaska, Sonja. Evolution and quantitative comparison of genome-wide protein domain distributions. *Genes*, 2:912–924, 2011.
- [346] Manja Marz, Andreas R. Gruber, Christian Höner zu Siederdisen, Fabian Amman, Stefan Badelt, Sebastian Bartschat, Stephan H. Bernhart, Stephanie Beyer, Kehr, Ronny Lorenz, Andrea Tanzer, Dilmurat Yusuf, Hakim Tafer, Ivo L. Hofacker, and Peter F. Stadler. Animal snoRNAs and scaRNAs with exceptional structures. *RNA Biology*, 8:938–946, 2011.
- [347] Ronny Lorenz, Stephan H Bernhart, Christian Höner zu Siederdisen, Hakim Tafer, Christoph Flamm, Peter F. Stadler, and Ivo L. Hofacker. ViennaRNA Package 2.0. *Alg. Mol. Biol.*, 6:26, 2011.
- [348] Irma Lozada-Chávez, Peter F. Stadler, and Sonja J. Prohaska. “hypothesis for the modern RNA world”: a pervasive non-coding RNA-based genetic regulation is a prerequisite for the emergence of multicellular complexity. *Orig. Life Evol. Biosph.*, 41:587–607, 2011.
- [349] Ivo L. Hofacker, Christian M. Reidys, and Peter F. Stadler. Symmetric circular matchings and RNA folding. *Discr. Math.*, 312:100–112, 2012.
- [350] Marc Hellmuth, Lydia Ostermeier, and Peter F. Stadler. Diagonalized cartesian products of S-prime graphs are S-prime. *Discr. Math.*, 312:74–80, 2012.
- [351] Catherine Florentz, Frank Jühling, Joern Pütz, Claude Sauter, Peter F. Stadler, and Richard Giegé. Structure of transfer RNAs: a function-driven refined view. *Wiley Interdiscip Rev RNA*, 3:37–61, 2012.
- [352] David Langenberger, Sachin Pundhir, Claus T. Ekstrøm, Peter F. Stadler, Steve Hoffmann, and Jan Gorodkin. deepBlockAlign: A tool for aligning RNA-seq profiles of read block patterns. *Bioinformatics*, 28:17–24, 2012.
- [353] Marc Hellmuth, Philipp-Jens Ostermeier, and Peter F. Stadler. Minimum cycles bases of lexicographic products. *Ars Math. Comptemp.*, 5:219–230, 2012.
- [354] Cornelius Schmidtke, Sven Findeiß, Cynthia M. Sharma, Juliane Kuhfuß, Steve Hoffmann, Jörg Vogel, Peter F. Stadler, and Ulla Bonas. Genome-wide transcriptome analysis of the plant pathogen *Xanthomonas* identifies sRNAs with putative virulence functions. *Nucleic Acids Res.*, 40:2020–2031, 2012.
- [355] Marc Hellmuth, Lydia Ostermeier, and Peter F. Stadler. A survey on hypergraph products. *Math. Comp. Sci.*, 6:132, 2012.
- [356] Konstantin Klemm, Anita Mehta, and Peter F. Stadler. Landscape encodings enhance optimization. *PLoS ONE*, 7:e34780, 2012.
- [357] Lydia Ostermeier, Marc Hellmuth, and Peter F. Stadler. The cartesian product of hypergraphs. *J. Graph Th.*, 70:180–196, 2012.
- [358] Jan Engelhardt and Peter F. Stadler. Hidden treasures in unspliced EST data. *Th. Biosci.*, 131:49–57, 2012. Preliminary version in *Proceedings of HIBIT 2011*, Izmir TR.

- [359] Frank Jühling, Joern Pütz, Matthias Bernt, Alexander Donath, Martin Middendorf, Catherine Florentz, and Peter F. Stadler. Improved systematic tRNA gene annotation allows new insights into the evolution of mitochondrial tRNA structures and into the mechanisms of mitochondrial genome rearrangements. *Nucleic Acids Res.*, 40:2833–2845, 2012.
- [360] Sebastian Will, Tejal Joshi, Ivo L. Hofacker, Peter F. Stadler, and Rolf Backofen. LocARNAP: Accurate boundary prediction and improved detection of structured RNAs for genome-wide screens. *RNA*, 18:900–914, 2012.
- [361] Jana Hertel, Sebastian Bartschat, Axel Wintsche, Christian Otto, The Students of the Bioinformatics Computer Lab 2011, and Peter F. Stadler. Evolution of the let-7 microRNA family. *RNA Biology*, 9:231–241, 2012.
- [362] Stefan Washietl, Ivo L. Hofacker, Peter F. Stadler, and Manolis Kellis. RNA folding with soft constraints: Reconciliation of probing data and thermodynamic secondary structure prediction. *Nucleic Acids Res.*, 2012. doi:10.1093/nar/gks009.
- [363] Marc Hellmuth, Maribel Hernandez-Rosales, Katharina T. Huber, Vincent Moulton, Peter F. Stadler, and Nicolas Wieseke. Orthology relations, symbolic ultrametrics, and cographs. *J. Math. Biol.*, 2012. doi: 10.1007/s00285-012-0525-x.
- [364] Konstantin Klemm and Peter F. Stadler. Elementary landscapes. In Yossi Borenstein and Alberto Moraglio, editors, *Theory and Principled Methods for Designing Metaheuristics*. Springer, 2012. accepted.
- [365] Oliver Niehuis, Gerrit Hartig Hartig, Sonja Garth, Hans Pohl, Jörg Lehmann, Hakim Tafer, Alexander Donath, Veiko Krauss, Carina Eisenhardt, Jana Hertel, Malte Petersen, Christoph Mayer, Karin Meusemann, Ralph S. Peters, Peter F. Stadler, Rolf G. Beutel, Erich Bornberg-Bauer, Duane D. McKenna, and Bernhard Misof. Genomic and morphological evidence converge to resolve the enigma of Strepsiptera. *Current Biol.*, 2012.
- [366] Ronny Lorenz, Stephan H. Bernhart, Fabian Externbrink, Jing Qin, Christian Höner zu Siederdisen, Fabian Amman, Ivo L. Hofacker, and Peter F. Stadler. RNA folding algorithms with G-quadruplexes. In *BSB 2012*, page 2012. accepted.
- [367] Manja Marz and Peter F. Stadler. Homology search for small structured ncRNAs. In Roland Hartmann, Albrecht Bindereif, Astrid Schön, and Eric Westhof, editors, *Handbook of RNA Biochemistry*. Wiley VCH, Weinheim, D, 2010. submitted.
- [368] Jan Engelhardt, Toralf Kirsten, Peter F. Stadler, and Sonja J. Prohaska. Genome annotation without genes. In *GI 2010*, 2010. submitted.
- [369] Markus Lechner, Manja Marz, Peter F. Stadler, and Veiko Krauss. Genome size, methylation rate, and CpG depletion in metazoans. 2010.
- [370] Anke Busch and Peter F. Stadler. Intra-genic exon duplications in the human transcriptome. 2010. submitted.
- [371] Jörg Lehmann, Peter F. Stadler, and Veiko Krauss. Near intron pairs and the metazoan tree. 2011. submitted.
- [372] Alexander Donath and Peter F. Stadler. Split-inducing indels in phylogenomic analysis. 2011. submitted.

- [373] Peter F. Stadler. Class-specific prediction of ncRNAs. In Jan Gorodkin and Larry Ruzzo, editors, *An introduction to RNA Bioinformatics*. 2011. submitted.
- [374] Jana Hertel, David Langenberger, and Peter F. Stadler. Computational prediction of microRNA genes. In Jan Gorodkin and Larry Ruzzo, editors, *An introduction to RNA Bioinformatics*. 2011. submitted.
- [375] Yangjing Long, Ling Yang, Peter F. Stadler, and Jürgen Jost. Relations between graphs. *Discr. Math.*, 2011. submitted.
- [376] Hakim Tafer, Jan Torleif Pedersen, Peter F. Stadler, and Jan Gorodkin. Accessibility is a significant feature for design of siRNAs targeting structured RNA. 2012. submitted.
- [377] Jakob L Andersen, Christoph Flamm, Daniel Merkle, and Peter F. Stadler. Inferring chemical reaction patterns using graph grammar rule composition. In *ECCB 2012*, 2012. submitted.
- [378] Matthias Bernt, Anke Braband, Bernd Schierwater, and Peter F. Stadler. Genetic aspects of mitochondrial genome evolution. *Mol. Phylog. Evol.*, 2012. submitted.
- [379] Matthias Bernt, Alexander Donath, Frank Jühling, Fabian Externbrink, Catherine Florentz, Guido Fritsch, Jörn Pütz, Martin Middendorf, and Peter F. Stadler. MitoS: Improved *de novo* metazoan mitochondrial genome annotation. *Mol. Phylog. Evol.*, 2012. submitted.
- [380] Matthias Bernt, Anke Braband, Martin Middendorf, Bernhard Misof, Omar Rota-Stabelli, and Peter F. Stadler. Bioinformatics methods for the comparative analysis of metazoan mitochondrial genome sequences. *Mol. Phylog. Evol.*, 2012. submitted.
- [381] Martin A. Smith, Tanja Gesell, Peter F. Stadler, and Mattick John S. Widespread purifying selection on RNA structure in mammals. 2012. submitted.
- [382] Felipe A. Lessa, Tainá Raiol, Marcelo M. Brígido, Daniele S. B. Martins Neto, Maria Emília M. T. Walter, and Peter F. Stadler. Clustering Rfam 10.1: Clans, families, and classes. *Genes*, 2012. submitted.
- [383] Yang Li, Manja Marz, Xiaodong Qi, Joshua D. Podlevsky, Steve Hoffmann, Peter F. Stadler, and Julian J.-L. Chen. Identification of the first invertebrate telomerase RNA by a next-generation sequencing based approach. 2012. submitted.
- [384]
- [385] Lesca M. Holdt, Steve Hoffmann, Kristina Sass, David Langenberger, Markus Scholz, Knut Krohn, Knut Finstermeier, Anika Stahringer, Wolfgang Wilfert, Frank Beutner, Stephan Gielen, Gerhard Schueler, Gabor Gäbel, Hendrick Bergert, Peter F. Stadler, Joachim Thiery, and Daniel Teupser. ANRIL regulates genes in trans and affects mechanisms of atherosclerosis at Chr9p21. 2012. submitted.

Peter F. Stadler: List of Publications

Books

- [1] Türker Bıyıkoğlu, Josef Leydold, and Peter F. Stadler. *Laplacian Eigenvectors of Graphs: Perron-Frobenius and Faber-Krahn Type Theorems*, volume 1915 of *Lecture Notes in Mathematics*. Springer Verlag, Heidelberg, 2007.
- [2] C. R. Stephens, M. Toussaint, D. Whitley, and P. F. Stadler, editors. *Foundations of Genetic Algorithms IX*, volume 4436 of *Lecture Notes Comp. Sci.* Springer, Berlin, Heidelberg, 2007. 9th International Workshop, FOGA 2007, Mexico City, Mexico, January 8-11, 2007.
- [3] Steen Rasmussen, Mark A. Bedau, Liaohai Chen, David Deamer, David C. Krakauer, Norman H. Packard, and Peter F. Stadler, editors. *Protocells*. MIT Press, Cambridge, MA, 2008.
- [4] Ivo Grosse, Steffen Neumann, Stefan Posch, Falk Schreiber, and Peter F. Stadler, editors. *German Conference on Bioinformatics 2009*, volume 157 of *Lecture Notes in Informatics*. Gesellschaft für Informatik, Bonn, 2009.
- [5] Carlos Eduardo Ferreira, Satoru Miyano, and Peter F. Stadler, editors. *Advances in Bioinformatics and Computational Biology*, volume 6268 of *Lecture Notes Comp. Sci.* Springer, Berlin, Heidelberg, 2010. 5th Brazilian Symposium on Bioinformatics, BSB 2010, Rio de Janeiro, Brazil, August 31-September 3, 2010.

Peter F. Stadler: List of Publications

Editorials

- [1] Rolf Backofen, Hamidreza Chitsaz, Ivo L. Hofacker, S. C Sahinalp, and Peter F. Stadler. Computational studies of non-coding RNAs — session introduction. *Pac Symp Biocomput.*, 15:54–56, 2010.
- [2] Andreas W. M. Dress, Bülent Karasözen, Peter F. Stadler, and Gerhard-Wilhelm Weber. Preface. *Discr. Appl. Math.*, 157:2217–2220, 2009. Networks in Computational Biology.
- [3] Olaf Breidbach, Jürgen Jost, and Peter F. Stadler. Towards theoretical formalisms. *Th. Biosci.*, 126:1–2, 2007.
- [4] Burkhard Morgenstern and Peter F. Stadler. New journal: Algorithms for molecular biology. *Alg. Mol. Biol.*, 1:1, 2006.
- [5] Ante Graovac and Peter F. Stadler. MATH/CHEM/COMP 2004 contributions. *Th. Biosci.*, 123:263–264, 2005.
- [6] Olaf Breidbach, Jürgen Jost, Peter F. Stadler, and M. Weingarten. Editorial. *Th. Biosci.*, 123:1–2, 2004.

Peter F. Stadler: List of Publication

Technical Reports

- [1] Peter F. Stadler and Robert Happel. Canonical approximation of landscapes. Technical Report 94-09-051, Santa Fe Institute, 1399 Hyde Park Rd, Santa Fe, NM 87501, 1994.
- [2] Ivo L. Hofacker, Martijn A. Huynen, Peter F. Stadler, and Paul E. Stolorz. RNA folding and parallel computers: The minimum free energy structures of complete HIV genomes. Technical Report 95-10-089, Santa Fe Institute, 1399 Hyde Park Rd, Santa Fe, NM 87501, 1995.
- [3] Petra M. Gleiss and Peter F. Stadler. Relevant cycles in biopolymers and random graphs. Technical Report 99-07-042, Santa Fe Institute, 1399 Hyde Park Rd, Santa Fe, NM 87501, 1999. Presented at the 4th Slovene conference in graph theory, Bled, SLO; Santa Fe Institute preprint.
- [4] Petra M. Gleiss, Peter F. Stadler, Andreas Wagner, and David A. Fell. Small cycles in small worlds. Technical Report 00-10-058, Santa Fe Institute, 1399 Hyde Park Rd, Santa Fe, NM 87501, 2000. Also: cond-mat/0009124.
- [5] Oliver Bastert, Dan Rockmore, Peter F. Stadler, and Gottfried Tinhofer. Some properties of robinson graphs. Technical Report TUM M0101, Techn. Univ. München, Fak. f. Math., München, Germany, 2001. (Blauer Bericht).
- [6] Sonja J. Prohaska, Claudia Fried, Christoph Flamm, and Peter F. Stadler. Analysis of phylogenetic footprint patterns in large gene clusters. In H.-W. Mewes, V. Heun, D. Frishman, and S. Kramer, editors, *Proceedings of the German Conference on Bioinformatics. GCB 2003*, volume 2, pages 108–110, München, D, 2003. belleville Verlag Michael Farin. BIOINF 03-017.
- [7] Claudia Fried, Peter Ahnert, and Peter F. Stadler. Correlation of SNPs with phylogenetic footprints. In H.-W. Mewes, V. Heun, D. Frishman, and S. Kramer, editors, *Proceedings of the German Conference on Bioinformatics. GCB 2003*, volume 2, pages 105–107, München, D, 2003. belleville Verlag Michael Farin. BIOINF 03-019.
- [8] Martin Schlegel, Guido Fritzsich, and Peter F. Stadler. Metazoan deep phylogenies: can the cambrian explosion be resolved with molecular markers? In H.-W. Mewes, V. Heun, D. Frishman, and S. Kramer, editors, *Proceedings of the German Conference on Bioinformatics. GCB 2003*, volume 2, pages 205–207, München, D, 2003. belleville Verlag Michael Farin.
- [9] Hans Binder, Toralf Kirsten, Markus Löffler, P. Richter, and Peter F. Stadler. Sequence specific sensitivity of oligonucleotide probes. In H.-W. Mewes, V. Heun, D. Frishman, and S. Kramer, editors, *Proceedings of the German Conference on Bioinformatics. GCB 2003*, volume 2, pages 145–147, München, D, 2003. belleville Verlag Michael Farin.
- [10] Gil Benkő, Christoph. Flamm, and Peter F. Stadler. The ToyChem package: A computational toolkit implementing a realistic artificial chemistry model. Technical Report 05-002, Bioinformatics Group, Univ. Leipzig, 2005. <http://www.bioinf.uni-leipzig.de/Publications/PREPRINTS/05-002.pdf>.

- [11] Peter F. Stadler and Stephan Steigele. Rna gene prediction. Technical report, U. Tübingen, 2008. EMBO Practical Course on Computational RNA Biology.