

## 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/](http://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/](http://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 Fritzsche, 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, Srecko 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.
- [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 Fritsch, 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 Lnych, 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-6 dependent 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.



- [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 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. Bompfünowerer, 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. Erratum: *Amer. J. Hum. Genet.* 83: 541 (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.
- [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] Thomas 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 Schmidtke, 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.
- [302] Ivo L. Hofacker, Christoph Flamm, Christian Heine, Michael T. Wolfinger, Gerek 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, Gerek 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 $\beta/\epsilon$ . 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, Wolfgang 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.*, 6:1–32, 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.*, 40:4261–4272, 2012.
- [363] 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 M. C. P. de Souto and M. G. Kann, editors, *BSB 2012*, volume 7409 of *Lect. Notes Bioinf.*, pages 49–60, Heidelberg, 2012. Springer.
- [364] Jakob Lykke Andersen, Christoph Flamm, Daniel Merkle, and Peter F. Stadler. Maximizing output and recognizing autocatalysis in chemical reaction networks is NP-complete. *J. Syst. Chem.*, 3:1, 2012.
- [365] Christian Otto, Peter F. Stadler, and Steve Hoffmann. Fast and sensitive mapping of bisulfite-treated sequencing data. *Bioinformatics*, 28:1698–1704, 2012.
- [366] 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*, 3:378–390, 2012.
- [367] Oliver Niehuis, Gerrit 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.*, 22:1309–1313, 2012.
- [368] Sylvia C Tippmann, Robert Ivanek, Dimos Gaidatzis, Anne Schöler, Leslie Hoerner, Erik van Nimwegen, Peter F. Stadler, Michael B. Stadler, and Dirk Schübeler. Chromatin measurements reveal contributions of synthesis and decay to steady-state mRNA levels. *Mol. Systems Biol.*, 8:593, 2012.
- [369] Martin Mann, Heinz Ekker, Peter F. Stadler, and Christoph Flamm. Atom mapping with constraint programming. In R. Backofen and S. Will, editors, *Proceedings of the Workshop on Constraint Based Methods for Bioinformatics WCB12*, pages 23–29, Freiburg, 2012. Uni Freiburg. <http://www.bioinf.uni-freiburg.de/Events/WCB12/proceedings.pdf>.
- [370] Frank Jühling, Joern Pütz, Catherine Florentz, and Peter F. Stadler. Armless mitochondrial tRNAs in Enoplea (Nematoda). *RNA Biology*, 9:1161–1166, 2012.

- [371] Markus Rohrschneider, Peter F. Stadler, and Gerik Scheuermann. A visual cross-database comparison of metabolic networks. In George Bebis, Richard Boyle, Bahram Parvin, Darko Koracin, Charless Fowlkes, Sen Wang, Min-Hyung Choi, Stephan Mantler, Jürgen Schulze, Daniel Acevedo, Klaus Mueller, and Michael Papka, editors, *Advances in Visual Computing, ISVC 2012. Part II*, volume 7432 of *Lect. Notes Comp. Sci.*, pages 678–687, Berlin, 2012. Springer.
- [372] Martien A. M. Groenen, Alan L. Archibald, Hirohide Uenishi, Christopher K. Tuggle, Yasuhiro Takeuchi, Max F. Rothschild, Claire Rogel-Gaillard, Chankyu Park, Denis Milan, Shengting Megens, Hendrik-Jan and Li, Denis M. Larkin, Heebal Kim, Laurent A. F. Frantz, Mario Caccamo, Hyeonju Ahn, Bronwen L. Alken, Anna Anselmo, Christian Anthon, Loretta Auvil, Bouabid Badaoui, Craig W. Beattie, Christian Bendixen, Daniel Berman, Frank Blecha, Jonas Blomberg, Lars Bolund, Mirte Bosse, Sara Botti, Zhan Bujie, Megan Bystrom, Boris Capitanu, Denise Carvalho-Silva, Patrick Chardon, Celine Chen, Ryan Cheng, Sang-Haeng Choi, William Chow, Richard C. Clark, Christopher Clee, Richard P. M. A. Crooijmans, Harry D. Dawson, Patrice Dehais, Fioravante De Sapio, Bert Dibbitts, Nizar Drou, Zhi-Qiang Du, Kellye Eversole, João Fadista, Susan Fairley, Thomas Faraut, Geoffrey J. Faulkner, Katie E Fowler, Merete Fredholm, Eric Fritz, James G. R. Gilbert, Elisabetta Giuffra, Jan Gorodkin, Darren Griffin, Jennifer L. Harrow, Alexander Hayward, Kerstin Howe, Zhi-Liang Hu, Sean J. Humphray, Toby Hunt, Henrik H. Jensen, Jin-Tae Jeon, Patric Jern, Matthew Jones, Jerzy Jurka, Hiroyuki Kanamori, Ronan Kapetanovic, Jaebum Kim, Jae-Hwan Kim, Kyu-Won Kim, Tae-Hun Kim, Greger Larson, Kyooyeol Lee, Kyung-Tai Lee, Richard Leggett, Harris A. Lewin, Yingrui Li, Wansheng Liu, Jane E. Loveland, Yao Lu, Joan K. Lunney, Jian Ma, Ole Madsen, Katherine Mann, Lucy Matthews, Stuart McLaren, Takeya Morozumi, Michael P. Murtaugh, Jitendra Narayan, Dinh Truong Nguyen, Peixiang Ni, Song-Jung Oh, Suneel Onteru, Frank Panitz, Eung-Woo Park, Hong-Seog Park, Geraldine Pascal, Yogesh Paudel, Miguel Perez-Enciso, Ricardo Ramirez-Gonzalez, James M. Reecy, Sandra Rodriguez-Zas, Gary A. Rohrer, Lauretta Rund, Yongming Sang, Kyle Schachtschneider, Joshua G. Schraiber, John Schwartz, Linda Scobie, Carol Scott, Stephen Searle, Bertrand Servin, Bruce R. Southey, Goran Sperber, Peter F. Stadler, Jonathan V. Sweedler, Hakim Tafer, Bo Thomsen, Rashmi Wali, Jian Wang Wang, Jun Wang, Simon White, Xun Xu, Martine Yerle, Guojie Zhang, Jianguo Zhang, Jie Zhang, Shuhong Zhao, Jane Rogers, Carol Churcher, and Lawrence B. Schook. Analyses of pig genomes provide insight into porcine demography and evolution. *Nature*, 491:393–398, 2012.
- [373] Julia Richter, Matthias Schlesner, Steve Hoffmann, Markus Kreuz, Ellen Leich, Birgit Burkhardt, Maciej Rosolowski, Ole Ammerpohl, Rabea Wagener, Stephan H. Bernhart, Dido Lenze, Monika Szczepanowski, Maren Paulsen, Simone Lipinski, Robert B. Russell, Sabine Adam-Klages, Gordana Apic, Alexander Claviez, Dirk Hasenclever, Volker Hovestadt, Nadine Hornig, Jan Korbelt, Dieter Kube, David Langenberger, Chris Lawerenz, Jasmin Lisfeld, Katharina Meyer, Simone Picelli, Jordan Pischmarov, Bernhard Radlwimmer, Tobias Rausch, Marius Rohde, Markus Schilhabel, René Scholtysik, Rainer Spang, Heiko Trautmann, Thorsten Zenz, Arndt Borkhardt, Hans G. Drexler, Peter Möller, Roderick A. F. MacLeod, Christiane Pott Pott, Stephan Schreiber, Lorenz Trümper, Markus Löffler, Peter F. Stadler, Peter Lichter, Roland Eils, Ralf Küppers, Michael Hummel, Wolfram Klapper, Philip Rosentiel, Andreas Rosenwald, Benedikt Brors, and Reiner Siebert. Recurrent mutation of the ID3 gene in Burkitt Lymphoma identified by integrated genome, exome and transcriptome sequencing. *Nature Gen.*, 44:1316–1320, 2012.

- [374] Maribel Hernandez-Rosales, Marc Hellmuth, Nick Wieseke, Katharina T. Huber, Vincent Moulton, and Peter F. Stadler. From event-labeled gene trees to species trees. *BMC Bioinformatics*, 13(Suppl. 19):S6, 2012.
- [375] Christoph Dieterich and P. F. Stadler. Computational biology of RNA interactions. *Wiley Interdiscip. Rev. RNA*, 4:107–120, 2013.
- [376] David Langenberger, M. Volkan Çakir, Steve Hoffmann, and Peter F. Stadler. Dicer-processed small RNAs: Rules and exceptions. *J. Exp. Zool: Mol. Dev. Evol.*, 320:35–46, 2012.
- [377] Xiaodong Qi, Yang Li, Shinji Honda, Steve Hoffmann, Manja Marz, Axel Mosig, Joshua D. Podlevskya, Peter F. Stadler, Eric U. Selker, and Julian J. L. Chen. The common ancestral core of vertebrate and fungal telomerase RNAs. *Nucleic Acids Res.*, 41:450–462, 2013.
- [378] 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.*, 66:399–420, 2013.
- [379] Jan Hubička, Jürgen Jost, Yangjing Long, Peter F. Stadler, and Ling Yang. Relations between graphs. *Ars Math. Contemp.*, 6:323–350, 2013.
- [380] Jörg Lehmann, Peter F. Stadler, and Veiko Krauss. Near intron pairs and the metazoan tree. *Mol. Phylog. Evol.*, 66:811–823, 2012.
- [381] Markus Lechner, Manja Marz, Christian Ihling, Peter F. Sinz, Andrea Stadler, and Veiko Krauss. The correlation of genome size and DNA methylation rate in metazoans. *Th. Biosci.*, 132:47–60, 2013.
- [382] Manja Wachsmuth, Sven Findeiß, Nadine Weissheimer, Peter F. Stadler, and Mario Mörl. *De novo* design of a synthetic riboswitch that regulates transcription termination. *Nucleic Acids Res.*, 41:2541–2551, 2013.
- [383] Radhakrishnan Sabarinathan, Hakim Tafer, Stefan E. Seemann, Ivo L. Hofacker, Peter F. Stadler, and Jan Gorodkin. **RNA<sub>snp</sub>**: Efficient detection of local RNA secondary structure changes induced by SNPs. *Hum. Mut.*, 34:546–556, 2013.
- [384] Chris T. Amemiya, Jessica Alföldi, Alison P. Lee, Shaohua Fan, Hervé Philippe, Iain MacCallum, Ingo Braasch, Tereza Manousaki, Igor Schneider, Nicolas Rohner, Chris Organ, Domitille Chalopin, Jeramiah J. Smith, Mark Robinson, Rosemary A. Dorrington, Marco Gerdo, Bronwen Aken, Maria Assunta Biscotti, Marco Barucca, Denis Baurain, Aaron M. Berlin, Gregory L. Blatch, Francesco Buonocore, Thorsten Burmester, Michael S. Campbell, Adriana Canapa, John P. Cannon, Alan Christoffels, Gianluca De Moro, Adrienne L. Edkins, Lin Fan, Anna Maria Fausto, Nathalie Feiner, Mariko Forconi, Junaid Gamiieldien, Sante Gnerre, Andy Gnirke, Jared V. Goldstone, Wilfried Haerty, Mark E. Hahn, Uljana Hesse, Steve Hoffmann, Jeremy Johnson, Sibel I. Karchner, Shigehiru Kuraku, Marcia Lara, Joshua Z. Levin, Gary W. Litman, Evan 3 Mauceli, Tsutomu Miyake, M. Gail Mueller Mueller, David R. Nelson, Anne Nitsche, Ettore Olmo, Tatsuya Ota, Alberto Pallavicini, Sumir Panji, Barbara Picone, Chris P. Ponting, Sonja J. Prohaska, Dariusz Przybylski, Nil Ratan Saha, Vydianathan Ravi, Filipe J. Ribeiro, Tatjana Sauka-Spengler Sauka-Spengler, Giuseppe Scapigliati, Stephen M. J. Searle, Ted Sharpe, Oleg Simakov, Peter F. Stadler, John J. Stegeman, Kenta Sumiyama, Hakim Tafer Tafer, Jason Turner-Maier, Peter van Heusden,

- Simon White, Louise Williams, Mark Yandell, Henner Brinkmann, Jean-Nicolas Volff, Clifford J. Tabin, Neil Shubin, Manfred Schartl, David Jaffe, John H. Postlethwait, Byrappa Venkatesh, Federica Di Palma, Eric S. Lander, Axel Meyer, and Kerstin Lindblad-Toh. The african coelacanth genome provides insights into tetrapod evolution. *Nature*, 496:311–316, 2013.
- [385] Gero Doose, Maria Alexis, Rebecca Kirsch, Sven Findeiß, David Langenberger, Rainer Machné, Mario Mörl, Steve Hoffmann, and Peter F. Stadler. Mapping the RNA-seq trash bin: Unusual transcripts in prokaryotic transcriptome sequencing data. *RNA Biology*, 10:1204–1210, 2013.
- [386] Stephan A. Müller, Sven Findeiß, Sandy R. Pernitzsch, Peter F. Stadler, Ivo L. Hofacker, Cynthia M. Sharma, Martin von Bergen, and Stefan Kalkhof. Identification of new protein coding sequences and signal peptidase cleavage sites of *Helicobacter pylori* strain 26695 by proteogenomics. *J. Proteomics*, 86:27–42, 2013.
- [387] Yang Li, Manja Marz, Xiaodong Qi, Joshua D. Podlevsky, Steve Hoffmann, Peter F. Stadler, and Julian J.-L. Chen. Identification of purple sea urchin telomerase RNA using a next-generation sequencing based approach. *RNA*, 19:852–860, 2013.
- [388] Radhakrishnan Sabarinathan, Hakim Tafer, Stefan Seemann, Ivo L. Hofacker, Peter F. Stadler, and Jan Gorodkin. The RNAsnp Web Server: Predicting SNP effects on local RNA secondary structure. *Nucleic Acids Res.*, 41:W475–W479, 2013.
- [389] Yinhua Huang, Yingrui Li, David W Burt, Hualan Chen, Yong Zhang, Wubin Qian, Hee-bal Kim, Shangquan Gan, Yiqiang Zhao, Jianwen Li, Kang Yi, Huapeng Feng, Pengyang Zhu, Bo Li, Qiuyue Liu, Suan Fairley, Katharine E Magor, Zhenlin Du, Xiaoxiang Hu, Laurie Goodman, Hakim Tafer, Alain Vignat, Taeheon Lee, Kyu-Won Kim, Zheyang Sheng, Yang An, Steve Searle, Javier Herrero, Martien A M Groenen, Richard P M A Crooijmans, Thomas Faraut, Qingle Cai, Robert G Webster, Jerry R Aldridge, Wesley C Warren, Sebastian Bartschat, Stephanie Kehr, Manja Marz, Peter F Stadler, Jacqueline Smith, Robert H S Kraus, Yaofeng Zhao, Liming Ren, Jing Feil, Mireille Morisson, Pete Kaiser, Darren K Griffin, Man Rao, Frederique Pitel, Jun Wang, and Ning Li. The duck genome and transcriptome provide insight into an avian influenza virus reservoir species. *Nature Genetics*, 45:776–783, 2013.
- [390] Lesca M. Holdt, Steve Hoffmann, Kristina Sass, David Langenberger, Markus Scholz, Knut Krohn, Knut Finstermeier, Anika Stahringer, Wolfgang Wilfert, Frank Beutner, Stephan Gielen, Gerhard Schuler, Gabor Gäbel, Hendrick Bergert, Ingo Bachmann, Peter F. Stadler, Joachim Thiery, and Daniel Teupser. Alu elements in ANRIL non-coding RNA at chromosome 9p21 modulate atherogenic cell functions through trans-regulation of gene networks. *PLoS Genet.*, 9:e1003588, 2013.
- [391] Christian Arnold, Peter F. Stadler, and Sonja J. Prohaska. Chromatin computation: Epigenetic inheritance as a pattern reconstruction problem. *J. Theor. Biol.*, 336:61–74, 2013.
- [392] Rolf Backofen, Markus Fricke, Manja Marz, Jing Qin, and Peter F. Stadler. Distribution of graph-distances in Boltzmann ensembles of RNA secondary structures. In Aaron Darlin and Jens Stoye, editors, *Algorithms in Bioinformatics: WABI 2013*, volume 8126 of *Lect. Notes Comp. Sci.*, pages 112–125, Heidelberg, 2013. Springer.

- [393] Sebastian Will, Michael F. Siebauer, Steffen Heyne, Jan Engelhardt, Peter F. Stadler, Kristin Reiche, and Rolf Backofen. LocARNAscan: Incorporating thermodynamic stability in sequence and structure-based RNA homology search. *Alg. Mol. Biol.*, 8:14, 2013.
- [394] Jakob L Andersen, Christoph Flamm, Daniel Merkle, and Peter F. Stadler. Inferring chemical reaction patterns using graph grammar rule composition. *J. Syst. Chem.*, 4:4, 2013.
- [395] Martin Mann, Feras Nahar, Heinz Ekker, Rolf Backofen, Peter F. Stadler, and Christoph Flamm. Atom mapping with constraint programming. In Christian Schulte, editor, *Principles and Practice of Constraint Programming*, volume 8124 of *Lect. Notes Comp. Sci.*, pages 805–822, Berlin, Heidelberg, 2013. Springer-Verlag.
- [396] Matthias Bernt, Alexander Donath, Frank Jühling, Fabian Externbrink, Catherine Florentz, Guido Fritzs, Jörn Pütz, Martin Middendorf, and Peter F. Stadler. MITOS: Improved *de novo* metazoan mitochondrial genome annotation. *Mol. Phylog. Evol.*, 69:313–319, 2013.
- [397] 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.*, 69:320–327, 2013.
- [398] Matthias Bernt, Anke Braband, Bernd Schierwater, and Peter F. Stadler. Genetic aspects of mitochondrial genome evolution. *Mol. Phylog. Evol.*, 69:328–338, 2013.
- [399] Matthias Bernt, Christoph Bleidorn, Anke Braband, Johannes Dambach, Alexander Donath, Guido Fritzs, Anja Golombek, Heike Hadrys, Frank Jühling, Karen Meusemann, Martin Middendorf, Bernhard Misof, Marleen Perseke, Lars Podsiadlowski, Björn von Reumont, Bernd Schierwater, Martin Schlegel, Michael Schrödl, Sabrina Simon, Peter F. Stadler, Isabella Stöger, and Torsten H. Struck. A comprehensive analysis of metazoan mitochondrial genomes and animal phylogeny. *Mol. Phylog. Evol.*, 69:352–364, 2013.
- [400] Catherine Florentz, Joern Pütz, Frank Jühling, H. Schwenzer, Peter F. Stadler, Bernard Lorber, Claude Sauter, and Marie Sissler. Translation in mammalian mitochondria: Order and disorder linked to tRNAs and aminoacyl-tRNA synthetases. In Anne-Marie Duchêne, editor, *Translation in Mitochondria and Other Organelles*, pages 55–85. Springer, Heidelberg, 2013.
- [401] Jakob L. Andersen, Tommy Andersen, Christoph Flamm, Martin Hanczyc, Daniel Merkle, and Peter F. Stadler. Navigating the chemical space of HCN polymerization and hydrolysis: Guiding graph grammars by mass spectrometry data. *Entropy*, 15:4066–4083, 2013.
- [402] Martin A. Smith, Tanja Gesell, Peter F. Stadler, and John S. Mattick. Widespread purifying selection on RNA structure in mammals. *Nucleic Acids Res.*, 41:8220–8236, 2013.
- [403] Christian Höner zu Siederdisen, Stefan Hammer, Ingrid Abfalter, Ivo L. Hofacker, Christoph Flamm, and Peter F. Stadler. Computational design of RNAs with complex energy landscapes. *Biopolymers*, 99:1124–1136, 2013.
- [404] Matthias Bernt, Rainer Machné, Abdullah H. Sahyoun, Martin Middendorf, and Peter F. Stadler. Mitochondrial genome evolution. In N.N., editor, *eLS*, page doi:10.1002/9780470015902.a0025142. Wiley-Blackwell, Hoboken, NJ, 2013. Article ID: A25142.



- [405] Fabian Amman, Stephan H. Bernhart, Gero Doose, Ivo L. Hofacker, Jing Qin, Peter F. Stadler, The Students of the Bioinformatics II Lab Class 2013, and Sebastian Will. The trouble with long-range base pairs in RNA folding. In João C. Setubal and Nalvo F. Almeida, editors, *Advances in Bioinformatics and Computational Biology, 8th BSB*, volume 8213 of *Lect. Notes Comp. Sci.*, pages 1–11, 2013.
- [406] Christian Höner zu Siederdisen, Ivo L. Hofacker, and Peter F. Stadler. How to multiply dynamic programming algorithms. In João C. Setubal and Nalvo F. Almeida, editors, *Advances in Bioinformatics and Computational Biology, 8th BSB*, volume 8213 of *Lect. Notes Comp. Sci.*, pages 82–93, 2013.
- [407] Wosley Arruda, Célia G. Ralha, Tainá Raiol, Marcelo M. Brígido, Maria Emília M. T. Walter, and Peter F. Stadler. ncRNA-Agents: A multiagent system for non-coding RNA annotation. In João C. Setubal and Nalvo F. Almeida, editors, *Advances in Bioinformatics and Computational Biology, 8th BSB*, volume 8213 of *Lect. Notes Comp. Sci.*, pages 136–147, 2013.
- [408] Rolf Fagerberg, Christoph Flamm, Daniel Merkle, Philipp Peters, and Peter F. Stadler. On the complexity of reconstructing chemical reaction networks. *Math. Comp. Sci.*, 7:275–292, 2013.
- [409] Ronny Lorenz, Stephan H. Bernhart, Jing Qin, Christian Höner zu Siederdisen, Andrea Tanzer, Fabian Amman, Ivo L. Hofacker, and Peter F. Stadler. 2D meets 4G: G-quadruplexes in RNA secondary structure prediction. *IEEE Trans. Comp. Biol. Bioinf.*, 10:832–844, 2013.
- [410] Marc Hellmuth, Josef Leydold, and Peter F. Stadler. Convex cycle bases. *Acta Math. Contemp.*, 7:123–140, 2014. Bled’11 contribution.
- [411] Arli A. Parikesit, Lydia Steiner, Peter F. Stadler, and Sonja J. Prohaska. Pitfalls of ascertainment biases in genome annotations — computing comparable protein domain distributions in eukarya. *Malaysian J. Fund. Appl. Sci.*, 10:65–75, 2014.
- [412] Sebastian Bartschat, Stephanie Kehr, Hakim Tafer, Peter F. Stadler, and Jana Hertel. snoStrip: A snoRNA annotation pipeline. *Bioinformatics*, 30:115–116, 2014.
- [413] Stephanie Kehr, Sebastian Bartschat, Hakim Tafer, Peter F. Stadler, and Jana Hertel. Matching of soulmates: Coevolution of snoRNAs and their targets. *Mol. Biol. Evol.*, 31:455–467, 2014.
- [414] Marc Hellmuth, Lydia Ostermeier, and Peter F. Stadler. Unique square property, equitable partitions, and product-like graphs. *Discrete Math.*, 320:92–103, 2014.
- [415] Juliane C. Dohm, André E. Minoche, Daniela Holtgräwe, Salvador Capella-Gutiérrez, Falk Zakrzewski, Hakim Tafer, Oliver Rupp, Thomas Rosleff Sørensen, Ralf Stracke, Richard Reinhardt, Alexander Goesmann, Thomas Kraft, Britta Schulz, Peter F. Stadler, Thomas Schmidt, Toni Gabaldón, Hans Lehrach, Bernd Weisshaar, and Heinz Himmelbauer. The genome of the recently domesticated crop plant sugar beet (*Beta vulgaris*). *Nature*, 505:546–549, 2014.
- [416] Maribel Hernandez-Rosales, Nicolas Wieseke, Marc Hellmuth, and Peter F. Stadler. Simulation of gene family histories. *BMC Bioinformatics*, 15:S3–A8, 2014.

- [417] Steve Hoffmann, Christian Otto, Gero Doose, Andrea Tanzer, David Langenberger, Sabina Christ, Manfred Kunz, Lesca M. Holdt, Daniel Teupser, Jörg Hackermüller, and Peter F. Stadler. A multi-split mapping algorithm for circular RNA, splicing, trans-splicing, and fusion detection. *Genome Biology*, 15:R34, 2014.
- [418] Konstantin Klemm and Peter F. Stadler. Rugged and elementary landscapes. In Yossi Borenstein and Alberto Moraglio, editors, *Theory and Principled Methods for Designing Metaheuristics*, Natural Computing Series, pages 41–61. Springer, Berlin, 2014.
- [419] Konstantin Klemm, Jing Qin, and Peter F. Stadler. Geometry and coarse-grained representations of landscapes. In Andries Engelbrecht and Hendrik Richter, editors, *Recent advances in the theory and application of fitness landscapes*, volume 6 of *Emergence, Complexity, and Computation*, pages 153–176. Springer-Verlag, Berlin, 2014.
- [420] Peter F. Stadler. Class-specific prediction of ncRNAs. In Jan Gorodkin and Larry Ruzzo, editors, *RNA Sequence, Structure, and Function: Computational and Bioinformatic Methods*, volume 1097 of *Meth. Mol. Biol.*, pages 199–214. Humana Press, New York, 2014.
- [421] Jana Hertel, David Langenberger, and Peter F. Stadler. Computational prediction of microRNA genes. In Jan Gorodkin and Larry Ruzzo, editors, *RNA Sequence, Structure, and Function: Computational and Bioinformatic Methods*, volume 1097 of *Meth. Mol. Biol.*, pages 437–456. Humana Press, New York, 2014.
- [422] Sandra Wende, Edward G. Platzer, Frank Jühling, Joern Pütz, Catherine Florentz, Peter F. Stadler, and Mario Mörl. Biological evidence for the worlds smallest tRNAs. *Biochimie*, 100:151–158, 2014.
- [423] Fabian Amman, Michael T Wolfinger, Ronny Lorenz, Ivo L Hofacker, Peter F Stadler, and S. Findeiß. TSSAR: TSS annotation regime for dRNA-seq data. *BMC Bioinformatics*, 15:89, 2014.
- [424] Lorena Rivarola-Duarte, Christian Otto, Daria Bedulina, Frank Jühling, Stephan Schreiber, Lena Jakob, Anton Gurkov, Denis Axenov-Gribanov, Abdullah H. Sahyoun, Magnus Lucassen, Jörg Hackermüller, Steve Hoffmann, Franz Sartoris, Hans-Otto Pörtner, Maxim Timofeyev, Till Luckenbach, and Peter F. Stadler. A first glimpse at the genome of the baikalian amphipod *Eulimnogammarus verrucosus*. *J. Exp. Zool. B: Mol. Dev. Evol.*, 322:177–189, 2014.
- [425] Manja Marz, Stefanie Wehner, 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*, pages 619–632. Wiley VCH, Weinheim, D, 2nd edition, 2013.
- [426] Jakob Lykke Andersen, Christoph Flamm, Daniel Merkle, and Peter F. Stadler. Generic strategies for chemical space exploration. *Int. J. Comp. Biol. Drug Design*, 7:225–258, 2014. ICIBM 2013 contribution.
- [427] Martin Schlegel, Michael Weidhase, and Peter F. Stadler. Deuterostome phylogeny – a molecular perspective. In J. Wolfgang Wägele and Thomas Bartolomaeus, editors, *Deep Metazoan Phylogeny: The Backbone of the Tree of Life. New insights from analyses of molecules, morphology, and theory of data analysis*, chapter 17, pages 414–424. de Gruyter, Berlin, 2014.

- [428] Matthias Bernt, Daniel Merkle, Martin Middendorf, Bernd Schierwater, Martin Schlegel, and Peter F Stadler. Computational methods for the analysis of mitochondrial genome rearrangements. In J. Wolfgang Wägele and Thomas Bartolomaeus, editors, *Deep Metazoan Phylogeny: The Backbone of the Tree of Life. New insights from analyses of molecules, morphology, and theory of data analysis*, chapter 22, pages 515–530. de Gruyter, Berlin, 2014.
- [429] Roman R. Stocsits, Harald Letsch, Karen Meusemann, Björn M. von Reumont, Bernhard Misof, Jana Hertel, Hakim Tafer, and Peter F. Stadler. RNA in phylogenetic reconstruction. In J. Wolfgang Wägele and Thomas Bartolomaeus, editors, *Deep Metazoan Phylogeny: The Backbone of the Tree of Life. New insights from analyses of molecules, morphology, and theory of data analysis*, chapter 23, pages 531–538. de Gruyter, Berlin, 2014.
- [430] Jörg Lehmann, Carina Eisenhardt, Veiko Krauss, and Peter F. Stadler. Intron positions and near intron pairs. In J. Wolfgang Wägele and Thomas Bartolomaeus, editors, *Deep Metazoan Phylogeny: The Backbone of the Tree of Life. New insights from analyses of molecules, morphology, and theory of data analysis*, chapter 24, pages 539–548. de Gruyter, Berlin, 2014.
- [431] Alexander Donath and Peter F. Stadler. Molecular morphology: Higher order characters derivable from sequence information. In J. Wolfgang Wägele and Thomas Bartolomaeus, editors, *Deep Metazoan Phylogeny: The Backbone of the Tree of Life. New insights from analyses of molecules, morphology, and theory of data analysis*, chapter 25, pages 549–562. de Gruyter, Berlin, 2014.
- [432] Marcel Kucharik, Ivo L. Hofacker, Peter F. Stadler, and Jing Qin. Basin hopping graph: A computational framework to characterize RNA folding landscapes. *Bioinformatics*, 30:2009–2017, 2014.
- [433] Abdullah H. Sahyoun, Matthias Bernt, Peter F. Stadler, and Kifah Tout. GC skew and mitochondrial origins of replication. *Mitochondrion*, 17:56–66, 2014.
- [434] Jörg Hackermüller, Kristin Reiche, Christian Otto, Nadine Hösler, Conny Blumert, Katja Brocke-Heidrich, Levin Böhlig, Anne Nitsche, Katharina Kasack, Peter Ahnert, Wolfgang Krupp, Kurt Engeland, Peter F Stadler, and Friedemann Horn. Cell cycle, oncogenic and tumor suppressor pathways regulate numerous long and macro non-protein coding RNAs. *Genome Biol.*, 15:R48, 2014.
- [435] Manja Marz, Niko Beerenwinkel, Christian Drost, Markus Fricke, Dmitriy Frishman, Ivo L. Hofacker, Dieter Hoffmann, Martin Middendorf, Thomas Rattei, Peter F. Stadler, and Armin Töpfer. Challenges in RNA virus bioinformatics. *Bioinformatics*, 1793-1799:30, 2014.
- [436] Christian Otto, Peter F. Stadler, and Steve Hoffmann. Lacking alignments? The versatile and accurate next generation sequencing mapper *segemehl* revisited. *Bioinformatics*, 30:1837–1843, 2014.
- [437] Anne Nitsche, Gero Doose, Hakim Tafer, Mark Robinson, Nil Ratan Saha, Marco Gerdol, Adriana Canapa, Steve Hoffmann, Chris T. Amemiya, and Peter F. Stadler. Atypical RNAs in the coelacanth transcriptome. *J. Exp. Zool. B: Mol. Dev. Evol.*, 322:342–351, 2014.
- [438] Christian Anthon, Hakim Tafer, Jakob H Havgaard, Bo Thomsen, Jakob Hedegaard, Stefan E Seemann, Sachin Pundhir, Stephanie Kehr, Sebastian Bartschat, Mathilde Nielsen, Rasmus O Nielsen, Merete Fredholm, Peter F Stadler, and Jan Gorodkin. Structured RNAs and syntenic regions in the pig genome. *BMC Genomics*, 15:459, 2014.

- [439] Marcus Lechner, Maribel Hernandez-Rosales, Daniel Doerr, Nicolas Wieseke, Annelise Thévenin, Jens Stoye, Roland K. Hartmann, Sonja J. Prohaska, and Peter F. Stadler. Orthology detection combining clustering and synteny for very large datasets. *PLoS ONE*, 9:e105015, 2014.
- [440] Rolf Backofen, Fabian Amman, Fabrizio Costa, Sven Findeiß, Andreas S. Richter, and Peter F. Stadler. Bioinformatics of prokaryotic RNAs. *RNA Biology*, 11:470–483, 2014.
- [441] Jakob Lykke Andersen, Christoph Flamm, Daniel Merkle, and Peter F. Stadler. 50 shades of rule composition: From chemical reactions to higher levels of abstraction. In François Fages and Carla Piazza, editors, *Formal Methods in Macro-Biology*, volume 8738 of *Lect. Notes Comp. Sci.*, pages 117–135, 2014.
- [442] Sebastian Will and Peter F. Stadler. A common framework for linear and cyclic multiple sequence alignment problems. In D. Brown and B. Morgenstern, editors, *WABI 2014*, volume 8701 of *Lect. Notes Comp. Sci.*, pages 135–147, 2014.
- [443] Gerd A. Müller, Axel Wintsche, Konstanze Stangner, Sonja J. Prohaska, Peter F. Stadler, and Kurt Engeland. The CHR site: definition and genome-wide identification of a cell cycle transcriptional element. *Nucleic Acids Res.*, 42:10331–10350, 2014.
- [444] Jing Qin, Markus Fricke, Manja Marz, Peter F. Stadler, and Rolf Backofen. Graph-distance distribution of the Boltzmann ensemble of RNA secondary structures. *Alg. Mol. Biol.*, 9:19, 2014.
- [445] Bernhard Misof, Karen Meusemann, Björn M. von Reumont, Patrick Kück, Sonja J. Prohaska, and Peter F. Stadler. *A priori* assessment of data quality in molecular phylogenetics. *Alg. Mol. Biol.*, 9:22, 2014.
- [446] Christian Höner zu Siederdisen, Sonja J. Prohaska, and Peter F. Stadler. Dynamic programming for set data types. In Sérgio Campos, editor, *Advances in Bioinformatics and Computational Biology: BSB 2014*, volume 8826 of *Lect. Notes Comp. Sci.*, pages 57–64, 2014.
- [447] Hugo W. Schneider, Sebastian Bartschat, Gero Doose, Lucas Maciel, Erick Pizani, Marcelo Bassani, Fernando Araripe Torres, Sebastian Will, Tainá Raiol, Marcelo M. Brigido, Maria Emilia Telles Walter, and Peter F. Stadler. Genome-wide identification of non-coding RNAs in *Komagatella pastoris* str. gs115. In Sérgio Campos, editor, *Advances in Bioinformatics and Computational Biology: BSB 2014*, volume 8826 of *Lect. Notes Comp. Sci.*, pages 115–122, 2014.
- [448] Tainá Raiol, João Victor A. Oliveira, Helena Schubert da Incarnação Lima Silva, Juliana Capella de Orem, Danilo Andrade Cavalcante, Nalvo F. Almeida jr., Guilherme P. Telles, João Carlos Setubal, Marcelo M. Brígido, Fernando A. Torres, Peter F. Stadler, Maria Emília M. T. Walter, Marlene Teixeira De-Souza, and Lídia M. P. Moreas. Draft genome sequence of FT9, a novel *Bacillus cereus* strain isolated from a Brazilian thermal spring. *Genome Announc.*, 2:e01027–14, 2014.
- [449] Martin Machyna, Stephanie Kehr, Korinna Straube, Dennis Kappei, Falk Butter, Jernej Ule, Jana Hertel, Peter F. Stadler, and Karla Neugebauer. The coilin interactome identifies hundreds of small noncoding RNAs that traffic through Cajal bodies. *Mol. Cell*, 56:389–399, 2014.

- [450] Martin Mann, Feras Nahar, Norah Schnorr, Rolf Backofen, Peter F. Stadler, and Christoph Flamm. Atom mapping with constraint programming. *Alg. Mol. Biol.*, 9:23, 2014.
- [451] Deblina Patra, Mario Fasold, David Langenberger, Gerhard Steger, Ivo Grosse, and Peter F. Stadler. `plantDARIO`: Web-based quantitative and qualitative analysis of small RNA-seq data in plants. *Frontiers Plant Sci.*, 5:708, 2014.
- [452] Guojie Zhang, Cai Li, Qiye Li, Bo Li, Denis M. Larkin, Chu Lee, Jay F. Storz, Agostinho Antunes, Matthew J. Greenwold, Robert W. Meredith, Anders Ödeen, Jie Cui, Qi Zhou, Luohai Xu, Hailin Pan, Zongji Wang, Lijun Jin, Pei Zhang, Haofu Hu, Wei Yang, Jiang Hu, Jin Xiao, Zhikai Yang, Yang Liu, Qiaolin Xie, Hao Yu, Jinmin Lian, Ping Wen, Fang Zhang, Hui Li, Yongli Zeng, Shiping Liu, Long Zhou, Zhiyong Huang, Na An, Jie Wang, Qiumei Zheng, Yingqi Xiong, Guangbiao Wang, Bo Wang, Jingjing Wang, Yu Fu, Rute R. da Fonseca, Alonzo Alfaro-Núñez, Mikkel Schubert, Ludovic Orlando, Tobias Mourier, Jason T. Howard, Ganeshkumar Ganapathy, Andreas Pfenning, Osceola Whitney, Miriam V. Rivas, Erina Hara, Julia Smith, Marta Farré, Jitendra Narayan, Gancho Slavov, Michael N Romanov, Rui Borges, João Paulo Machado, Imran Khan, Mark S. Springer, John Gatesby, Federico G. Hoffmann, Juan C. Opazo, Olle Håstad, Roger H. Sawyer, Heebal Kim, Kyu-Won Kim, Hyeon Jeong Kim, Seoae Cho, Ning Li, Yinhua Huang, Michael W. Bruford, Xiangjiang Zhan, Andrew Dixon, Mads F. Bertelsen, Elizabeth Derryberry, Wesley Warren, Richard K Wilson, Shengbin Li, David A. Ray, Richard E. Green, Stephen J. O'Brien, Darren Griffin, Warren E. Johnson, David Haussler, Oliver A. Ryder, Eske Willerslev, Gary R. Graves, Per Alström, Jon Fjeldså, David P. Mindell, Scott V. Edwards, Edward L. Braun, Carsten Rahbek, David W. Burt, Peter Houde, Yong Zhang, Huanming Yang, Jian Wang, Avian Genome Consortium, Erich D. Jarvis, M. Thomas P. Gilbert, and Jun Wang. Comparative genomics reveals insights into avian genome evolution and adaptation. *Science*, 346:1311–1320, 2014.
- [453] Christian Höner zu Siederdisen, Sarah Berkemer, Fabian Amman, Axel Wintsche, Sebastian Will, Sonja J. Prohaska, and Peter F. Stadler. Comparative detection of processed small RNAs in Archaea. In *IWBBIO 2014*, pages 286–297. Univ. Granada, 2014. [http://iwbbio.ugr.es/2014/papers/IWBBIO\\_2014\\_paper\\_33.pdf](http://iwbbio.ugr.es/2014/papers/IWBBIO_2014_paper_33.pdf).
- [454] Xiaodong Qi, Dustin P Rand, Joshua D Podlevsky, Yang Li, Axel Mosig, Peter F Stadler, and Julian J.-L. Chen. Prevalent and distinct spliceosomal 3'-end processing mechanisms for fungal telomerase RNA. *Nat Commun.*, 6:6105, 2015.
- [455] Sven Findeiß, Manja Wachsmuth, Mario Mörl, and Peter F. Stadler. Design of transcription regulating riboswitches. *Methods Enzymol.*, 550:1–22, 2014.
- [456] Marc Hellmuth, Nicolas Wieseke, Marcus Lechner, Hans-Peter Lenhof, Martin Middendorf, and Peter F. Stadler. Phylogenetics from paralogs. *Proc. Natl. Acad. Sci. USA*, 112:2058–2063, 2015.
- [457] Lydia Ostermeier and Peter F. Stadler. The grid-property and product-like hypergraphs. *Graphs Combinatorics*, 31:757–770, 2015. presented at IndoSlov 2013.
- [458] Jana Hertel and Peter F. Stadler. The expansion of animal microRNA families revisited. *Life*, 5:905–920, 2015.
- [459] Christoph Flamm, Bärbel M. R. Stadler, and Peter F. Stadler. Generalized topologies: hypergraphs, chemical reactions, and biological evolution. In Subhash C. Basak, Guillermo

- Restrepo, and Jose Luis Villaveces, editors, *Advances in Mathematical Chemistry: With applications to chemoinformatics, bioinformatics, drug discovery, and Predictive toxicology*, volume 2, pages 300–327. Bentham, Sharjah, UAE, 2013.
- [460] Anne Nitsche, Dominic Rose, Mario Fasold, Kristin Reiche, and Peter F. Stadler. Comparison of splice sites reveals that long non-coding RNAs are evolutionarily well conserved. *RNA*, 21:801–812, 2015.
- [461] Manja Wachsmuth, Gesine Domin Domin, Ronny Lorenz, Robert Serfling, Sven Findeiß, Peter F Stadler, and Mario Mörl. Design criteria for synthetic riboswitches acting on transcription. *RNA Biology*, 12:221–231, 2015.
- [462] Xuanshi Liu, Markus Scholz, Anke Tönjes, Michael Stumvoll, Peter F. Stadler, and Yvonne Böttcher. Indications for potential parent of origin effects within the FTO gene. *PLoS ONE*, 10:e0119206, 2015.
- [463] Steve Hoffmann, Peter F. Stadler, and Korbinian Strimmer. A simple data-adaptive probabilistic variant calling model. *Alg. Mol. Biol.*, 10:10, 2015.
- [464] Paul P. Gardner, Mario Fasold, Sarah W. Burge, Maria Ninova, Jana Hertel, Stephanie Kehr, Tammy E. Steeves, Sam Griffiths-Jones, and Peter F. Stadler. Conservation and losses of non-coding RNAs in avian genomes. *PLoS One*, 10:e0121797, 2015.
- [465] Alberto Angrisani, Hakim Tafer, Peter F Stadler, and Maria Furia. Developmentally regulated expression and expression strategies of Drosophila snoRNAs. *Insect Biochem Mol Biol*, 61:69–78, 2015.
- [466] Marc Hellmuth, Tilen Marc, Lydia Ostermeier, and Peter F. Stadler. The relaxed square property. *Australasian J. Comb.*, 62:240–270, 2015.
- [467] Diana Le Duc, Gabriel Renaud, Arunkumar Krishnan, Markus Sällman Almén, Leon Huynen, Sonja J. Prohaska, Matthias Ongyerth, Bárbara D. Bitarello, Helgi B. Schiöth, Michael Hofreiter, Peter F. Stadler, Kay Prüfer, David Lambert, Janet Kelso, and Torsten Schöneberg. Kiwi genome provides insights into nocturnal adaptation. *Genome Biology*, 16:147, 2015.
- [468] Alberto Angrisani, Hakim Tafer, Peter F. Stadler, and Maria Furia. Unusual novel snorna-like rnas in *Drosophila melanogaster*. *ncRNA*, 1:139–150, 2015.
- [469] Christian Höner zu Siederdissen, Ivo L. Hofacker, and Peter F. Stadler. Product grammars for alignment and folding. *IEEE/ACM Trans. Comp. Biol. Bioinf.*, 12:507–519, 2015.
- [470] Jakob L. Andersen, Christoph Flamm, Daniel Merkle, and Peter F. Stadler. *In silico* support for Eschenmoser’s glyoxylate scenario. *Israel J. Chem.*, 55:919–933, 2015.
- [471] Heike Betat, Tobias Mede, Sandy Tretbar, Lydia Müller, Peter F. Stadler, Mario Mörl, and Sonja J. Prohaska. The ancestor of modern Holozoa acquired the CCA-adding enzyme from Alphaproteobacteria by horizontal gene transfer. *Nucleic Acids Res.*, 43:6739–6746, 2015.
- [472] M Schmid, J Smith, D W Burt, B L Aken, P B Antin, AL Archibald, C Ashwell, P J Blackshear, C Boschiero, CT Brown, S C Burgess, H H Cheng, W Chow, D J Coble, A Cooksey, R P Crooijmans, J Damas, R V Davis, D J de Koning, M E Delany, T Derrien, T T Desta, I C Dunn, M Dunn, H Ellegren, L Eöry, I Erb, M Farré, M Fasold, D Fleming, P Flicek, K E

- Fowler, L Frésard, D P Froman, V Garceau, P P Gardner, A A Gheyas, D K Griffin, M A Groenen, T Haaf, O Hanotte, A Hart, J Häsler, S B Hedges, J Hertel, K Howe, A Hubbard, D A Hume, P Kaiser, D Kedra, S J Kemp, C Klopp, K E Kniel, R Kuo, S Lagarrigue, S J Lamont, D M Larkin, R A Lawal, S M Markland, F McCarthy, H A McCormack, M C McPherson, A Motegi, S A Muljo, A Münsterberg, R Nag, I Nanda, M Neuberger, A Nitsche, C Notredame, H Noyes, R O'Connor, EA O'Hare, A J Oler, S C Ommeh, H Pais, M Persia, F Pitel, L Preeyanon, P Prieto, Barja, E M Pritchett, D D Rhoads, C M Robinson, M N Romanov, M Rothschild, P F Roux, C J Schmidt, A S Schneider, M G Schwartz, S M Searle, M A Skinner, C A Smith, P F Stadler, T E Steeves, C Steinlein, L Sun, M Takata, I Ulitsky, Q Wang, Y Wang, W C Warren, J M Wood, D Wragg, and H Zhou. Third report on chicken genes and chromosomes 2015. *Cytogenet Genome Res*, 145:78–179, 2015.
- [473] Jan Engelhardt and Peter F. Stadler. Evolution of the unspliced transcriptome. *BMC Evol Biol*, 15:166, 2015.
- [474] Helene Kretzmer, Stephan H. Bernhart, Wei Wang, Andrea Haake, Marc A. Weniger, Anke K. Bergmann, Matthew J. Betts Betts, Enrique Carrillo-de Santa-Pau, Gero Doose, Jana Gutwein, Julia Richter, Volker Hovestadt, Bingding Huang, Daniel Rico, Frank Jühling, Julia Kolarova, Qianhao Lu, Christian Otto, Rabea Wagner, Judith Arnolds, Birgit Burkhardt, Alexander Claviez, Hans G. Drexler, Sonja Eberth, Roland Eils, Paul Flicek, Siegfried Haas, Michael Hummel, Dennis Karsch, Hinrik H. D. Kerstens, Wolfram Klapper, Markus Kreuz, Chris Lawerenz, Dido Lenze, Markus Löffler, Cristina López, Roderick A. F. MacLeod, Joost H. A. Martens Martens, José Ignacio Martín-Subero, Peter Möller, Inga Nagel, Simone Picelli, Inga Vater, Marius Rohde, Philip Rosenstiel, Maciej Rosolowski, Robert B. Russell, Markus Schilhabel, Matthias Schlesner, Peter F. Stadler, Monika Szczepanowski, Lorenz Trümper, Hendrik G. Stunnenberg, Ralf Küppers, Ole Ammerpohl, Peter Lichter, Reiner Siebert, Steve Hoffmann, and Bernhard Radlwimmer. Linking differential DNA methylation in gene regions with the mutational landscape of Burkitt lymphoma. *Nature Gen.*, 47:1316–1325, 2015.
- [475] Abdullah H. Sahyoun, Martin Hölzer, Frank Jühling, Christian Höner zu Siederdisen, Marwa Al-Arab, Kifah Tout, Manja Marz, Martin Middendorf, Peter F. Stadler, and Matthias Bernt. Towards a comprehensive picture of alloacceptor tRNA remolding in metazoan mitochondrial genomes. *Nucleic Acids Res.*, 43:8044–8056, 2015.
- [476] Nikolai Hecker, Mikkel Christensen-Dalsgaard, Stefan E. Seemann, Jakob Hull Havgaard, Peter F. Stadler, Ivo L. Hofacker, Henrik Nielsen, and Jan Gorodkin. Improvement of RNA structure probabilities by sequence extensions using RNAcop. *Nucleic Acids Res.*, 43:8135–8145, 2015.
- [477] Sarah J. Berkemer, Christian Höner zu Siederdisen, Fabian Amman, Axel Wintsche, Sebastian Will, Ivo L. Hofacker, Sonja J. Prohaska, and Peter F. Stadler. Processed small RNAs in Archaea and BHB elements. *Genomics Comp. Biol.*, 1:e18, 2015.
- [478] Bärbel M. R. Stadler and Peter F. Stadler. Connectivity spaces. *Math. Comp. Sci*, 9:409–436, 2015.
- [479] Sarah Berkemer, Ricardo Chaves, Adrian Fritz, Marc Hellmuth, Maribel Hernandez-Rosales, and Peter F. Stadler. Spiders can be recognized by counting their legs. *Math. Comp. Sci.*, 9:437–441, 2015.

- [480] Christian Höner zu Siederdisen, Sonja J. Prohaska, and Peter F. Stadler. Algebraic dynamic programming over general data structures. *BMC Bioinformatics*, 16:19:S2, 2015.
- [481] Manfred D. Laubichler, Peter F. Stadler, Sonja J. Prohaska, and Katja Nowick. The relativity of biological function. *Th. Biosci.*, 143:143–147, 2015.
- [482] Wosley C Arruda, Daniel S. Souza, Célia G Ralha, Maria Emila M. T. Walter, Tainá Raiol, Marcelo M. Brigido, and Peter F. Stadler. Knowledge-based reasoning to annotate noncoding RNA using multi-agent system. *J. Bioinf. Comp. Biol.*, 13:1550021, 2015.
- [483] Jiao Gu, Jürgen Jost, Shiping Liu, and Peter F. Stadler. Spectral classes of regular, random, and empirical graphs. *Linear Alg. Appl.*, 489:30–49, 2016.
- [484] Ronny Lorenz, Dominik Luntzer, Ivo L. Hofacker, Peter F. Stadler, and Michael T. Wolfinger. SHAPE directed RNA folding. *Bioinformatics*, 32:145–147, 2016.
- [485] Marcel Kucharík, Ivo L. Hofacker, Peter F. Stadler, and Jing Qin. Pseudoknots in RNA folding landscapes. *Bioinformatics*, 32:187–194, 2016.
- [486] Alexander J. Westermann, Konrad U. Förstner, Fabian Amman, Lars Barquist, Yanjie Chao, Leon Schulte, Lydia Müller, Richard Reinardt, Peter F. Stadler, and Jörg Vogel. Dual RNA-seq unveils noncoding RNA functions in host-pathogen interactions. *Nature*, 529:496–501, 2016.
- [487] Bernd Schierwater, Peter W H Holland, David John Miller, Peter F Stadler, Brian M. Wiegmann, Gert Wörheide, Gregory Wray, and Rob DeSalle. Never ending analysis of a century old evolutionary debate: “unringing” the urmetazoon bell. *Front. Ecol. Evol.*, 4:5, 2016.
- [488] Henrike Indrischek, Nicolas Wieseke, Peter F. Stadler, and Sonja J. Prohaska. The paralog-to-contig assignment problem: High quality gene models from fragmented assemblies. *Alg. Mol. Biol.*, 11:1, 2016.
- [489] Sebastian Canzler, Peter F. Stadler, and Jana Hertel. U6 snRNA intron insertion occurred multiple times during fungi evolution. *RNA Biol.*, 13:119–127, 2016.
- [490] Frank Jühling, Helene Kretzmer, Stephan H. Bernhart, Christian Otto, Peter F. Stadler, and Steve Hoffmann. **metilene**: Fast and sensitive calling of differentially methylated regions from bisulfite sequencing data. *Genome Res.*, 26:256–262, 2016.
- [491] Peter F. Stadler. Evolution of RNA-based networks. In Esteban Domingo and Peter Schuster, editors, *Quasispecies: From Theory to Experimental Systems*, volume 392 of *Curr. Topics Microbiol. Immun.*, pages 43–59. Springer, Berlin, Heidelberg D, 2016.
- [492] Ingo Braasch, Andrew R. Gehrke, Jeramiah J. Smith, Kazuhiko Kawasaki, Tereza Manousaki, Jeremy Pasquier, Angel Amores, Thomas Desvignes, Peter Batzel, Julian Catchen, Aaron Berlin, Michael Campbell, Daniel Barrell, Kyle J. Martin, John Mulley, Vydianathan Ravi, Alison Lee, Tetsuya Nakamura, Domitille Chalopin, Shaohua Fan, Dustin Weisel, Cristian Cañestro, Jason Sydes, Felix Beaudry, Yi Sun, Jana Hertel, Michael J. Beam, Federica Di Palma, Mario Fasold, Mikio Ishiyama, Jeremy Johnson, Stephanie Kehr, Marcia Lara, John Letaw, Gary Litman, Ronda Litman, Masato Mikami, Tatsuya Ota, Nil Ratan Saha, Louise Williams, Peter F. Stadler, Han Wang, John S. Taylor, Quentin Fontenot, Allyse Ferrara, Stephen M. J. Searle, Bronwen Aken, Mark Yandell, Igor Schneider,



- Jeffrey Yoder, Jean-Nicolas Volff, Chris T. Meyer, Axel and Amemiya, Byrappa Venkatesh, Peter W. H. Holland, Yann Guiguen, Julien Bobe, Neil H. Shubin, Jessica Alföldi, Kerstin Lindblad-Toh, and John H. Postlethwait. The spotted gar genome illuminates vertebrate evolution and facilitates human-to-teleost comparisons. *Nature Gen.*, 48:427–437, 2016. Corrigendum: *Nature Gen.* **48**: 700 (2016); doi:10.1038/ng0616-700c.
- [493] Guillermo Restrepo and Peter F. Stadler. Assessing greenness of chemical reactions and synthesis plans through posetic landscapes. *ACS Sustainable Chem. Eng.*, 4:21912199, 2016.
- [494] Ronny Lorenz, Ivo L. Hofacker, and Peter F. Stadler. RNA folding with hard and soft constraints. *Alg. Mol. Biol.*, 11:8, 2016.
- [495] Jakob Lykke Andersen, Christoph Flamm, Daniel Merkle, and Peter F. Stadler. A software package for chemically inspired graph transformation. In Rachid Echahed and Mark Minas, editors, *Graph Transformation, ICGT 2016*, volume 9761 of *Lecture Notes Comp. Sci.*, pages 73–88, Berlin, Heidelberg, D, 2016. Springer Verlag.
- [496] Christoph Flamm, Daniel Merkle, Peter F. Stadler, and Uffe Thorsen. Automatic inference of graph rewriting rules using the cyclic nature of chemical reactions. In Rachid Echahed and Mark Minas, editors, *Graph Transformation, ICGT 2016*, volume 9761 of *Lecture Notes Comp. Sci.*, pages 208–222, Berlin, Heidelberg, D, 2016. Springer Verlag.
- [497] Hadi Jorjani, Stephanie Kehr, Dominik J. Jedlinski, Rafal Gumienny, Jana Hertel, Peter F. Stadler, Mihaela Zavolan, and Andreas R. Gruber. An updated human snoRNAome. *Nucleic Acids Res.*, 44:5068–5082, 2016.
- [498] Maik Riechert, Christian Höner zu Siederdisen, and Peter F. Stadler. Algebraic dynamic programming for multiple context-free grammars. *Theor. Comp. Sci.*, 639:91–109, 2016.
- [499] Francesco Righetti, Aaron Mischa Nuss, Christian Twittenhoff, Sascha Beele, Kristina Urban, Sebastian Will, Stephan H. Bernhart, Peter F. Stadler, Petra Dersch, and Franz Narberhaus. The temperature-responsive RNA structurome of *Yersinia pseudotuberculosis*. *Proc. Natl. Acad. Sci. USA*, 113:7237–7242, 2016.
- [500] Cristian A Velandia-Huerto, Adriaan Gittenberger, Federico D Brown, Peter F. Stadler, and Clara I Bermúdez-Santana. Automated detection of ncRNAs in the draft genome sequence of a basal chordate: The carpet sea squirt *Didemnum vexillum*. *BMC Genomics*, 17:591, 2016.
- [501] Cristian A Velandia-Huerto, Sarah J Berkemer, Anne Hoffmann, Nancy Retzlaff, Liliana C Romero Marroquín, Maribel Hernández Rosales, Peter F. Stadler, and Clara I Bermúdez-Santana. Orthologs, turn-over, and remolding of tRNAs in primates and fruit flies. *BMC Genomics*, 17:617, 2016.
- [502] Damián Blasi, Morten H. Christiansen, Harald Hammarström, Peter F. Stadler, and Soeren Wichmann. Sound-meaning association biases evidenced across thousands of languages. *Proc. Natl. Acad. Sci. USA*, 113:10818–10823, 2016.
- [503] Martin Hölzer, Verena Krähling, Fabian Amman, Emanuel Barth, Stephan H Bernhart, Victor A O Carmelo, Maximilian Collatz, Gero Doose, Florian Eggenhofer, Jan Ewald, Jörg Fallmann, Lasse M Feldhahn, Markus Fricke, Juliane Gebauer, Andreas J Gruber, Franziska Hufsky, Henrike Indrischek, Sabina Kanton, Jörg Linde, Nelly Mostajo, Roman Ochsenreiter, Konstantin Riege1, Lorena Rivarola-Duarte, Abdullah Sahyoun, Sita J Saunders, Stefan

- E Seemann Seemann, Andrea Tanzer, Bertram Vogel, Stefanie Wehner, Michael T Wolfinger, Rolf Backofen, Jan Gorodkin, Ivo Grosse, Ivo Hofacker, Steve Hoffmann, Cristoph Kaleta, Peter F Stadler, Stephan Becker, and Manja Marz. Differential transcriptional responses to Ebola and Marburg virus infection in bat and human cells. *Sci. Rep.*, 6:34589, 2016. Corrigendum *Sci. Rep.* 7:39421 (2017) doi: 10.1038/srep39421.
- [504] Marwa Al Arab, Christian Höner zu Siderdissen, Kifah Tout, Abdullah H. Sahyoun, Peter F. Stadler, and Matthias Bernt. Accurate annotation of protein-coding genes in mitochondrial genomes. *Mol. Phylog. Evol.*, 106:209–216, 2016.
- [505] Richard H. Hammack, Marc Hellmuth, Lydia Ostermeier, and Peter F. Stadler. Associativity and non-associativity of some hypergraph products. *Math. Comp.Sci.*, 10:403–408, 2016. arXiv 1511.07162.
- [506] Stephan H Bernhart, Helene Kretzmer, Lesca M Holdt, Frank Jühling, Ole Ammerpol, Anke K. Bergmann, Bernd Northoff, Gero Doose, Rainer Siebert, Peter F. Stadler, and Steve Hoffmann. Hypermethylation of bivalent chromatin coincides with increased expression of developmental genes in cancer. *Sci. Rep.*, 6:37393, 2016.
- [507] Deblina Patra Bhattacharya, Sebastian Canzler, Stephanie Kehr, Jana Hertel, Ivo Grosse, and Peter F Stadler. Phylogenetic distribution of plant snoRNA families. *BMC Genomics*, 17:969, 2016.
- [508] K Hezaveh, A Kloetgen, S H Bernhart, K D Mahapatra, D Lenze, J Richter, A Haake, A K Bergmann, B Brors, B Burkhardt, A Claviez, H G Drexler, R Eils, S Haas, S Hoffmann, D Karsch, W Klapper, K Kleinheinz, J Korbel, H Kretzmer, M Kreuz, R Kppers, C Lawrenz, E Leich, M Loeffler, L Mantovani-Loeffler, C López, A C McHardy, P Möller, M Rohde, P Rosenstiel, A Rosenwald, M Schilhabel, M Schlesner, I Scholz, P F Stadler, S Stilgenbauer, S Sungalee, M Szczepanowski, L Trümper, M A Weniger, R Siebert, A Borkhardt, M Hummel, and J I Hoell. Alterations of miRNAs and miRNA-regulated mRNA expression in GC B cell lymphomas determined by integrative sequencing analysis. *Haematologica*, 1380-1389:101, 2016.
- [509] David C. Krakauer, Lydia Müller, Sonja J. Prohaska, and Peter F. Stadler. Design specifications for cellular regulation. *Th. Biosci.*, 135:231–240, 2016.
- [510] Anne Nitsche and Peter F. Stadler. Evolutionary clues in lncRNAs. *Wiley Interdiscip Rev RNA*, 8:1, 2017.
- [511] João Victor de Araujo Oliveira, Fabrizio Costa, Rolf Backofen, Peter F. Stadler, Maria Emília Machado Telles Walter, and Jana Hertel. SnoReport 2.0: new features and a refined Support Vector Machine to improve snoRNA identification. *BMC Bioinformatics*, 17 Suppl. 18:464, 2016.
- [512] Sebastian Canzler, Peter F. Stadler Stadler, and Jana Hertel. Evolution of fungal U3 snoRNAs: Structural variation and introns. *Non-Coding RNA*, 3:3, 2017.
- [513] Sree Rohit Kolora, Rui Faria, Anne Weigert, Stefan Schaffer, Annegret Grimm, Klaus Henle, Abdullah H. Sahyoun, Peter F. Stadler, Katja Nowick Nowick, Christoph Bleidorn, and Martin Schlegel. The complete mitochondrial genome of *Lacerta bilineata* and comparison with its closely related congener *L. Viridis*. *Mitochondrial DNA, A DNA Mapp Seq Anal*, 2017:116–118, 2017.

- [514] Gesine Domin, Sven Findeiß, Manja Wachsmuth, Sebastian Will, Peter F Stadler, and Mario Mörl. Applicability of a computational design approach for synthetic riboswitches. *Nucleic Acids Res.*, 45:4108–4119, 2017.
- [515] Ferhat Alkan, Anne Wenzel, Oana Palasca, Peter Kerpedjiev, Anders F. Rudebeck, Peter F. Stadler, Ivo L. Hofacker, and Jan Gorodkin. RIssearch2: suffix array-based large-scale prediction of RNA–RNA interactions and siRNA off-targets. *Nucleic Acids Res.*, 45:e60, 2017.
- [516] Rituparno Sen, Gero Doose, and Peter F. Stadler. Rare splice variants in long non-coding RNAs. *Non-coding RNA*, 3:23, 2017.
- [517] Henrike Indrischek, Sonja J. Prohaska, Vsevolod Gurevich, Eugenia Gurevich, and Peter F. Stadler. Uncovering missing pieces: Duplication and deletion history of arrestins in Deuterostomes. *BMC Evol. Biol.*, 17:163, 2017.
- [518] Marc Hellmuth, Peter F. Stadler, and Nicolas Wieseke. The mathematics of xenology: Dico-graphs, symbolic ultrametrics, 2-structures and tree-representable systems of binary relations. *J. Math. Biol.*, 75:299–237, 2017.
- [519] Jakob Lykke Andersen, Christoph Flamm, Daniel Merkle, and Peter F. Stadler. Chemical graph transformation with stereo-information. In Juan de Lara and Detlef Plump, editors, *10th International Conference on Graph Transformation (ICGT 2017)*, volume 10373 of *Lect. Notes Comp. Sci.*, pages 54–69, Heidelberg, 2017. Springer.
- [520] Sven Findeiß, Maja Etzel, Sebastian Will, Mario Mörl, and Peter F. Stadler. Design of artificial riboswitches as biosensors. *Sensors*, 17:1990, 2017.
- [521] Rolf Backofen, Jan Engelhardt, Anika Erxleben, Jörg Fallmann, Björn Grüning, Uwe Ohler, Nikolaus Rajewsky, and Peter F. Stadler. RNA-bioinformatics: Tools, services and databases for the analysis of RNA-based regulation. *J. Biotechnology*, 261:76–84, 2017.
- [522] Jörg Fallmann, Sebastian Will, Jan Engelhardt, Björn Grüning, Rolf Backofen, and Peter F. Stadler. Recent advances in RNA folding. *J. Biotech.*, 261:97–104, 2017.
- [523] Stefanie Binder, Nadine Hösler, Diana Riedel, Ivonne Zipfel, Tilo Buschmann, Christoph Kämpf, Kristin Reiche, Renate Burger, Martin Gramatzki, Jörg Hackermüller, Peter F. Stadler, and Friedemann Horn. STAT3-induced long noncoding RNAs in multiple myeloma cells display different properties in cancer. *Sci. Rep.*, 7:7976, 2017.
- [524] Bärbel M. R. Stadler and Peter F. Stadler. Oriented components and their separations. *Appl. Gen. Topology*, 18:255–275, 2017. SFI preprint 2016.04.007.
- [525] Marwa Al Arab, Matthias Bernt, Christian Höner zu Siederdisen, Kifah Tout, and Peter F. Stadler. Partially local three-way alignments and the sequence signatures of mitochondrial genome rearrangements. *Alg. Mol. Biol.*, 12:22, 2017. 10.1186/s13015-017-0113-0.
- [526] Ali M. Yazbeck, Kifah R. Tout, Peter F. Stadler, and Jana Hertel. Towards a consistent, quantitative evaluation of microRNA evolution. *J. Integrative Bioinf.*, 14:20160013, 2017.
- [527] Rainer Machné, Douglas B. Murray, and Peter F. Stadler. Similarity-based segmentation of multi-dimensional signals. *Sci. Rep.*, 7:12355, 2017.

- [528] Björn A. Grüning, Jörg Fallmann, Dilmurat Yusuf, Sebastian Will, Anika Erxleben, Torsten Houwaart, Bérénice Batut, Pavankumar Videm, Andrea Bagnacani, Markus Wolfien, Florian Eggenhofer, Steffen Lott, Youri Hoogstrate, Wolfgang Hess, Olaf Wolkenhauer, Altuna Akalin, Steve Hoffmann, Uwe Ohler, Peter F. Stadler, and Rolf Backofen. The RNA workbench: Best practices for RNA and high-throughput sequencing bioinformatics in Galaxy. *Nucleic Acids Res.*, 45:W650–W566, 2017.
- [529] Nikolai Nøjgaard, Manuela Geiß, Daniel Merkle, Peter F. Stadler, Nicolas Wieseke, and Marc Hellmuth. Forbidden time travel: Characterization of time-consistent tree reconciliation maps. In Russell Schwartz and Knut Reinert, editors, *17th International Workshop on Algorithms in Bioinformatics (WABI 2017)*, volume 88 of *Leibniz International Proceedings in Informatics (LIPIcs)*, pages 17:1–17:12, Dagstuhl, Germany, 2017. Schloss Dagstuhl–Leibniz-Zentrum fuer Informatik.
- [530] Felix Kühnl, Peter F. Stadler, and Sebastian Will. Tractable analysis of RNA–ligand interaction kinetics. *BMC Bioinformatics*, 18(Suppl 12):424, 2017.
- [531] Hugo W. Schneider, Taina Raiol, Marcelo M. Brigido, Maria Emilia M. T. Walter, and Peter F. Stadler. A support vector machine based method to distinguish long non-coding RNAs from protein coding transcripts. *BMC Genomics*, 18:804, 2017.
- [532] Matus Valach, Sandrine Moreira, Steve Hoffmann, Peter F. Stadler, and Gertraud Burger. Keeping it complicated: Mitochondrial genome plasticity in diplomonids. *Sci. Rep.*, 7:14166, 2017.
- [533] Sarah J. Berkemer, Anne Hoffmann, Cameron R. Murray, and Peter F. Stadler. SMORE: Snyeny MOdulator of repetitive elements. *LIFE*, 7:42, 2017.
- [534] Christina L. Richards, Conchita Alonso, Claude Becker, Oliver Bossdorf, Etienne Bucher, Maria Colomé-Tatché, Walter Durka, Jan Engelhardt, Bence Gaspar, Andreas Gogol-Döring, Ivo Grosse, Thomas P. van Gulp, Katrin Heer, Ilkka Kronholm, Latzel Lampei, Christian Vít, Marie Mirouze, Lars Opgenoorth, Ovidiu Paun, Sonja J. Prohaska, Stefan A. Rensing, Peter F. Stadler, Emiliano Trucchi, Kristian Ullrich, and Koen J. F. Verhoeven. Ecological plant epigenetics: Evidence from model and non-model species, and the way forward. *Ecology Letters*, 20:15761590, 2017.
- [535] Jakob Lykke Andersen, Christoph Flamm, Daniel Merkle, and Peter F. Stadler. An intermediate level of abstraction for computational systems chemistry. *Phil. Trans. R. Soc. A*, 375:20160354, 2017.
- [536] Halima Saker, Peter F. Stadler, and Ahmad M. Shahin. Multidimensional segmentation of heterogeneous data. In Mohamad Khalil, editor, *Fourth International Conference on Advances in Biomedical Engineering (ICABME)*, pages 33–36, Piscataway, NJ, 2017. IEEE.
- [537] Sarah J. Berkemer, Christian Höner zu Siederdisen, and Peter F. Stadler. Algebraic dynamic programming on trees. *Algorithms*, 10:135, 2017.
- [538] Manoj Changat, Ferdoos Hossein Nezhad, and Peter F. Stadler. Axiomatic characterization of transit functions of hierarchies. *Ars Math. Contemp.*, 14:117–128, 2018.
- [539] João C. Setubal and Peter F. Stadler. Gene phylogenies and orthologous groups. In João C. Setubal, Peter F. Stadler, and Jens Stoye, editors, *Comparative Genomics*, volume 1704, pages 1–28. Springer, Heidelberg, 2018.

- [540] Rolf Backofen, Jan Gorodkin, Ivo L. Hofacker, and Peter F. Stadler. Comparative RNA genomics. In João C. Setubal, Peter F. Stadler, and Jens Stoye, editors, *Comparative Genomics*, volume 1704, pages 363–400. Springer, Heidelberg, 2018.
- [541] Maria Beatriz Walter Costa, Christian Höner zu Siederdisen, Dan Tulpan, Peter F. Stadler, and Katja Nowick. Temporal ordering of substitutions in RNA evolution: Uncovering the structural evolution of the human accelerated region 1. *J. Theor. Biol.*, 438:143–150, 2018.
- [542] Ali Yazbeck, Kifah R. Tout, and Peter F. Stadler. Detailed secondary structure models of invertebrate 7SK RNAs. *RNA Biology*, 15:158–164, 2018.
- [543] Nikolai Nøjgaard, Manuela Geiß, Daniel Merkle, Peter F. Stadler, Nicolas Wieseke, and Marc Hellmuth. Time-consistent reconciliation maps and forbidden time travel. *Alg. Mol. Biol.*, 13:2, 2018.
- [544] Sebastian Canzler, Peter F. Stadler, and Jana Schoor. The fungal snoRNAome. *RNA*, 24:342–360, 2018.
- [545] Marc Hellmuth, Yangjing Long, Manuela Geiß, and Peter F. Stadler. A short note on undirected fitch graphs. *Art Discr. Appl. Math.*, 1:P1.08, 2018. 10.26493/2590-9770.1.1.08.
- [546] Manfred Laubichler, Sonja J. Prohaska, and Peter F. Stadler. Towards a mechanistic explanation of phenotypic evolution: The need for a theory of theory integration. *J. Exp. Zool.: Mol. Dev. Evol.*, 330:5–14, 2018.
- [547] Rolf Fagerberg, Christoph Flamm, Rojin Kianian, Daniel Merkle, and Peter F. Stadler. Finding the  $k$  best synthesis plans. *J. Cheminformatics*, 10:19, 2018.
- [548] Alyssa D. Lokits, Henrike Indrischek, Jens Meiler, Heidi E. Hamm, and Peter F. Stadler. Tracing the evolution of the heterotrimeric G protein  $\alpha$  subunit in Metazoa. *BMC Evolutionary Biology*, 18:51, 2018.
- [549] F X Reymond Sutandy, Stefanie Ebersberger, Lu Huang, Anke Busch, Maximilian Bach, Hyun Seo Kang, Jörg Fallmann, Daniel Maticzka, Rolf Backofen, Peter F. Stadler, Kathi Zarnack, Michael Sattler, Stefan Legewie, and Julian König. iCLIP-based modeling uncovers 3' splice site definition: how U2AF65 specificity relies on regulation by co-factors. *Genome Res.*, 28:699–713, 2018.
- [550] Nancy Retzlaff and Peter F. Stadler. Partially local multi-way alignments. *Math. Comp. Sci.*, 12:207–234, 2018.
- [551] Marc Hellmuth, Maribel Hernandez-Rosales, Yangjing Long, and Peter F. Stadler. Inferring phylogenetic trees from the knowledge of rare evolutionary events. *J. Math. Biol.*, 76:1623–1653, 2018.
- [552] Anne Hoffmann, Jörg Fallmann, Elisa Vilardo, Mario Mörl, Peter F. Stadler, and Fabian Amman. Accurate mapping of tRNA reads. *Bioinformatics*, 34:1116–1124, 2018.
- [553] Bärbel M. R. Stadler and Peter F. Stadler. Reachability, connectivity, and proximity in chemical spaces. *MATCH Commun. Math. Comput. Chem.*, 80:639–659, 2018.
- [554] Jakob Lykke Andersen, Christoph Flamm, Daniel Merkle, and Peter F. Stadler. Rule composition in graph transformation models of chemical reactions. *MATCH Commun. Math. Comput. Chem.*, 80:661–704, 2018.

- [555] Jakob Lykke Andersen, Rolf Fagerberg, Christoph Flamm, Rojin Kianian, Daniel Merkle, and Peter F. Stadler. Towards mechanistic prediction of mass spectra using graph transformation. *MATCH Commun. Math. Comput. Chem.*, 80:705–731, 2018.
- [556] Tanmoy Bhattacharya, Damian Blasi, William Croft, Michael Cysouw, Daniel Hruschka, Ian Maddieson, Lydia Müller, Nancy Retzlaff, Eric Smith, Peter F. Stadler, George Starostin, and Hyejin Youn. Studying language evolution in the age of big data. *J. Language Evol.*, 2018.
- [557] Alexandre Rossi Paschoal, Irma Lozada-Chávez, Douglas Silva Domingues, and Peter F. Stadler. ceRNAs in plants: computational approaches and associated challenges for Target Mimics research. *Brief. Bioinf.*, 2017.
- [558] Jakob Lykke Andersen, Christoph Flamm, Daniel Merkle, and Peter F. Stadler. Chemical transformation motifs — modelling pathways as integer hyperflows. *IEEE/ACM Trans. Comp. Biol.*, 2017.
- [559] Sonja J. Prohaska, Sarah J. Berkemer, Fabian Gärtner, Thomas Gatter, Nancy Retzlaff, The Students of the Graphs and Biological Networks Lab 2017, Christian Höner zu Siederdisen, and Peter F. Stadler. Expansion of gene clusters, circular orders, and the shortest Hamiltonian path problem. *J. Math. Biol.*, 2017.
- [560] Konstantin Klemm, Anita Mehta, and Peter F. Stadler. Cover-encodings of fitness landscapes. *Bull. Math. Biol.*, 2018.
- [561] Aniela Skrzypczyk, Stephanie Kehr, Ilona Krystel, Stephan H. Bernhart, Shibashish Giri, Augustinus Bader, and Peter F. Stadler. Non-coding RNA transcripts during differentiation of human induced pluripotent stem cells into hepatocytes. 2018. Stem Cells International.
- [562] Alexander Donath and Peter F. Stadler. Split-inducing indels in phylogenomic analysis. *Alg. Mol. Biol.*, 2018. accepted.
- [563] Melanie von Brandenstein, Stephan H. Bernhart, Andreas Pansky, Claudia Richter, Tobias Kohl, Martina Deckert, Axel Heidenreich, Peter F. Stadler, Manuel Montesinos-Rongen, and Jochen W. U. Fries. Beyond 3’UTR binding – microRNA-induced protein truncation via DNA-binding. 2014. submitted.
- [564] Marc Hellmuth, Adrian Fritz, Nicolas Wieseke, and Peter F. Stadler. Techniques for the cograph editing problem: Module merge is equivalent to edit  $p_4$ ’s. 2015. submitted; arXiv 1509.06983v2.
- [565] Daniel Gerighausen, Lydia Müller, Jens Steuck, Dirk Zeckzer, and Peter F. Stadler. The Sierra Platinum Service for generating peak-calls for replicated ChIP-seq experiments. 2017.
- [566] Haleh Ebadi, Michael Perry, Keith Short, Konstantin Klemm, Claude Desplan, Peter F. Stadler, and Anita Mehta. Patterning the insect eye: from stochastic to deterministic mechanisms. 2016. arXiv:1704.02379.
- [567] Anne Nitsche, Kristin Reiche, Uwe Ueberham, Christian Arnold, Jörg Hackermüller, Friedemann Horn, Peter F. Stadler, and Thomas Arendt. Alzheimer related genes show accelerated evolution. 2017. bioRxiv doi: 10.1101/114108.

- [568] Maria Beatriz Walter Costa, Christian Höner zu Siederdisen, Peter F. Stadler, and Katja Nowick. SSS-test: A novel test for detecting selection on the secondary structures of non-coding RNAs. 2017. submitted.
- [569] Fabian Gärtner, Christian Höner zu Siederdisen, Lydia Müller, and Peter F. Stadler. Coordinate systems for supergenomes. 2017. submitted.
- [570] Nancy Retzlaff, Andreas Niekler, Gerhard Heyer, Christoph Kleine, and Peter F. Stadler. Does a phylogeny of topics recapitulate the history of ideas and institutions? 2017. submitted.
- [571] Manuela Geiß, John Anders, Peter F. Stadler, Nicolas Wieseke, and Marc Hellmuth. Reconstructing gene trees from Fitch’s xenology relation. *J. Math. Biol.*, 2018. in revision; arxiv 1711.02152.
- [572] Manoj Changat, Prasanth G. Narasimha-Shenoi, Matjaž Kovše, Ferdoos Hosseinnzhad, Shilpa Mohandas, Abisha Ramachandran, and Peter F. Stadler. Topological representation of the transit sets of  $k$ -point crossover operators. 2017. submitted; arXiv 1712.09022.
- [573] Lisa K. Kutsche, Deisy M. Gysi, Kerstin Lenk, Jörg Fallmann, Rebecca Petri, Simon D. Klapper, Karolina Piracs, Peter F. Stadler, Johan Jakobsson, Katja Nowick, and Volker Busskamp. A systems-level analysis reveals multiple concurrent layers of miR-124 regulation during human neurogenesis. 2018. submitted.
- [574] Rebecca Kirsch, Stefan Ernst Seemann, Walter Larry Ruzzo, Stephen Michael Cohen, Peter F. Stadler, and Jan Gorodkin. Identification and characterization of novel conserved RNA structures in *Drosophila*. 2018. submitted.
- [575] Joachim Ludwig, Christian Höner zu Siederdisen, Zishu Liu, Peter F. Stadler, and Susann Müller. flowEMMi: An automated model-based clustering tool for microbial cytometric data. 2018. submitted.
- [576] Alexander Donath, Frank Jühling, Marwa Al-Arab, Peter F. Stadler, Martin Middendorf, and Matthias Bernt. Precise annotation of protein coding genes boundaries in metazoan mitochondrial genomes. 2018. submitted.

# Peter F. Stadler: List of Publication

## Publications as Member of Consortium

- [1] L B Alexandrov, S Nik-Zainal, D C Wedge, S A Aparicio, S Behjati, A V Biankin, G R Bignell, N Bolli, A Borg, A L Børresen-Dale, S Boyault, B Burkhardt, A P Butler, C Caldas, H R Davies, C Desmedt, R Eils, J E Eyfjörd, J A Foekens, M Greaves, F Hosoda, B Hutter, T Ilicic, S Imbeaud, M Imielinski, N Jäger, D T Jones, D Jones, S Knappskog, M Kool, S R Lakhani, C López-Otin, S Martin, NC Munshi, H Nakamura, P A Northcott, M Pajic, E Papaemmanuil, A Paradiso, J V Pearson, X S Puente, K Raine, M Ramakrishna, A L Richardson, J Richter, P Rosenstiel, M Schlesner, T N Schumacher, P N Span, J W Teague, Y Totoki, A N Tutt, R Valdés-Mas, M M van Buuren, L van 't Veer, A Vincent-Salomon, N Waddell, L R Yates, Australian Pancreatic Cancer Genome Initiative, ICGC Breast Cancer Consortium, ICGC MMML-Seq Consortium, ICGC PedBrain, J Zucman-Rossi, P A Futreal, U McDermott, P Lichter, M Meyerson, S M Grimmond, R Siebert, E Campo, T Shibata, S M Pfister, P J Campbell, and M R Stratton. Signatures of mutational processes in human cancer. *Nature*, 500:415–421, 2013. as member of *ICGC MMML-Seq Consortium*.
- [2] Gero Doose, A Haake, Stephan H Bernhart, C López, S Duggimpudi, F Wojciech, A K Bergmann, A Borkhardt, B Burkhardt, A Claviez, L Dimitrova, S Haas, J I Hoell, M Hummel, D Karsch, W Klapper, K Kleo, Helene Kretzmer, M Kreuz, R Küppers, C Lawrenz, D Lenze, M Loeffler, L Mantovani-Löffler, P Müller, G Ott, J Richter, M Rohde, P Rosenstiel, A Rosenwald, M Schilhabel, M Schneider, I Scholz, S Stilgenbauer, H G Stunnenberg, M Szczepanowski, L Trümper, M A Weniger, ICGC MMML-Seq Consortium, S Hoffmann, R Siebert, and I Iaccharino. MINCR is a MYC-induced lncRNA able to modulate MYC's transcriptional network in Burkitt lymphoma cells. *Proc Natl Acad Sci USA*, 112:E5261–E5270, 2015. as member of the *ICGC MMML-Seq Consortium*.
- [3] R Wagener, S M Aukema, M Schlesner, A Haake, B Burkhardt, H G Claviez, A andDrexler, M Hummel, M Kreuz, M Loeffler, M Rosolowski, C López, P Möller, J Richter, M Rohde, M J Betts, R B Russell, Stephan H Bernhart, Steve Hoffmann, P Rosenstiel, M Schilhabel, M Szczepanowski, L Trümper, W Klapper, R Siebert, ICGC MMML-Seq-Project, and Molecular Mechanisms in Malignant Lymphomas Network Project of the Deutsch Krebshilfe. The PCBP1 gene encoding poly(rC) binding protein I is recurrently mutated in Burkitt lymphoma. *Genes Chromosomes Cancer*, 54:555–564, 2015. as member of *ICGC MMML-Seq-Project*.
- [4] A Shostak, B Ruppert, N Ha, P Bruns, U H Toprak, ICGC MMML-Seq Project, R Eils, M Schlesner, A Diernfellner, and M Brunner. MYC/MIZ1-dependent gene repression inversely coordinates the circadian clock with cell cycle and proliferation. *Nat Commun.*, 7:11807, 2016. as member of *ICGC MMML-Seq-Project*.
- [5] M Rohde, BR Bonn, M Zimmermann, J Lange, A Möricke, W Klapper, I Oschlies, M Szczepanowski, I Nagel, M Schrappe, M Loeffler, R Siebert, A Reiter, B Burkhardt, ICGC-MMML-Seq, and MMML-MYC-SYS. Relevance of ID3-TCF3-CCND3 pathway mutations in pediatric aggressive B-cell lymphoma treated according to the NHL-BFM protocols. *Haematologica*, 102:1091–1098, 2017. as member of *ICGC MMML-Seq*.



- [6] S N Gröbner, BC Worst, J Weischenfeldt, I Buchhalter, K Kleinheinz, V A Rudneva, P D Johann, G P Balasubramanian, M Segura-Wang, S Brabetz, S Bender, B Hutter, D Sturm, E Pfaff, D Hübschmann, G Zipprich, M Heinold, J Eils, C Lawerenz, S Erkek, S Lambo, S Waszak, C Blattmann, A Borkhardt, M Kuhlen, A Eggert, S Fulda, M Gessler, J Wegert, R Kappler, D Baumhoer, S Burdach, R Kirschner-Schwabe, U Kontny, A E Kulozik, D Lohmann, S Hettmer, C Eckert, S Bielack, M Nathrath, C Niemeyer, G H Richter, J Schulte, R Siebert, F Westermann, J J Molenaar, G Vassal, H Witt, ICGC PedBrain-Seq Project, ICGC MMML-Seq Project, B Burkhardt, C P Kratz, O Witt, C M van Tilburg, C M Kramm, G Fleischhack, U Dirksen, S Rutkowski, M Frühwald, K von Hoff, S Wolf, T Klingebiel, E Koscielniak, P Landgraf, J Koster, A C Resnick, J Zhang, Y Liu, X Zhou, A J Waanders, D A Zwijnenburg, P Raman, B Brors, U D Weber, P A Northcott, K W Pajtler, M Kool, R M Piro, J O Korbel, M Schlesner, R Eils, D T W Jones, P Lichter, L Chavez, M Zapatka, and S M Pfister. The landscape of genomic alterations across childhood cancers. *Nature*, 555:321–327, 2018. Author Correction. *Nature* doi: 10.1038/s41586-018-0167-2.

# 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] Eric Bonabeau and Stadler Peter F. Call for proposals. *Adv. Complex Syst.*, 2:195, 1999.
- [2] Olaf Breidbach, Jürgen Jost, Peter F. Stadler, and M. Weingarten. Editorial. *Th. Biosci.*, 123:1–2, 2004.
- [3] Ante Graovac and Peter F. Stadler. MATH/CHEM/COMP 2004 contributions. *Th. Biosci.*, 123:263–264, 2005.
- [4] Burkhard Morgenstern and Peter F. Stadler. New journal: Algorithms for molecular biology. *Alg. Mol. Biol.*, 1:1, 2006.
- [5] Olaf Breidbach, Jürgen Jost, and Peter F. Stadler. Towards theoretical formalisms. *Th. Biosci.*, 126:1–2, 2007.
- [6] 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.
- [7] 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.
- [8] Bernd Schierwater, Peter F. Stadler, Robert De Salle, and Lars Podsiadlowski. Mitogenomics and metazoan evolution. *Mol. Phylog. Evol.*, 69:311–312, 2013.
- [9] Vassily Lyubetsky, William Piel, and Peter F. Stadler. Molecular phylogenetics 2014. *BioMed Res. Intl.*, 2015:919251, 2015. doi: 10.1155/2015/919251.

# Peter F. Stadler: List of Publications

## Published Abstracts

## References

- [1] Erich G. Bornberg-Bauer and Peter F. Stadler. Random structures and evolution of biopolymers. *Ber. Bunsenges. Phys. Chem.*, 98:1128, 1994.
- [2] S. Cepok, S. Hoffmann, V. Grummel, K. Lehmann-Horn, Jörg Hackermüller, Peter F. Stadler, H.-P. Hartung, A. Berhele, F. Deisenhammer, R. Wassmuth, and B. Hemmer. HLA-DRB1 0401 and HLA-DRB1 0408 are strongly associated with the development of antibodies against interferon-beta therapy in multiple sclerosis. *J. Neuroimmunology*, 203:194, 2008. International Congress of Neuroimmunology (26-30 Oct 2008, Dallas-Ft.Worth).
- [3] Levin Böhling, Jörg Hackermüller, Dominic Rose, Kristin Reiche, Antje Kretzschmar, Peter F. Stadler, Friedemann Horn, and Kurt Engeland. Transcriptome profiling reveals many novel p53-regulated human non-coding RNAs. *J. Neurochem.*, 110:98–99, 2009. 4th European Society for Neurochemistry Conference on Advances in Molecular Mechanisms of Neurological Disorders (11-14 July 2009, Leipzig, Germany); Abstr. 263.
- [4] Jörg Hackermüller, Katja Brocke-Heidrich, Kristin Reiche, Antje Kretzschmar, K. Schutt, Peter Ahnert, Levin Böhling, Peter F. Stadler, Kurt Engeland, and Friedemann Horn. Long non-protein coding RNAs in oncogenic pathways. *J. Neurochem.*, 110:99–100, 2009. 4th European Society for Neurochemistry Conference on Advances in Molecular Mechanisms of Neurological Disorders (11-14 July 2009, Leipzig, Germany); Abstr. 266.
- [5] Friedemann Horn, Katja Brocke-Heidrich, Jörg Hackermüller, and Peter F. Stadler. Regulation of non-protein-coding RNA genes by the Stat3 pathway. *J. Neurochem.*, 110:98, 2009. 4th European Society for Neurochemistry Conference on Advances in Molecular Mechanisms of Neurological Disorders (11-14 July 2009, Leipzig, Germany); Abstr. 261.
- [6] D. Buck, S. Cepok, S. Hoffmann, V. Grummel, K. Lehmann-Horn, Jörg Hackermüller, Peter F. Stadler, H.-P. Hartung, A. Berhele, F. Deisenhammer, R. Wassmuth, and B. Hemmer. HLA-alleles determine the risk to develop antibodies against interferon-beta therapy in multiple sclerosis. *Multiple sclerosis*, 15:S183, 2009. 25th Congress of the European Committee for Treatment and Research in Multiple Sclerosis (9-12 Sep. 2009, Düsseldorf, Germany).
- [7] A. A. Parikesit, S. J. Prohaska, and Peter F. Stadler. Protein domain co-occurrences reveal functional changes of regulatory mechanisms during evolution. *New Biotechnology*, 27:S44–S45, 2010. Abstracts of the 4th ESF Conference on Functional Genomics & Disease (14-17 April 2010, Dresden, Germany); Poster P1.61.
- [8] A. J. Westermann, L. N. Schulte, K. U. Förstner, S. Hoffmann, P. F. Stadler, and J. Vogel. Transcriptomic analysis of host-pathogen interplay. *Int. J. Med. Microbiol.*, 302:S1.42, 2012. 64. Jahrestagung der Deutschen Gesellschaft für Hygiene und Mikrobiologie (DGHM); II.P37 poster abstract.

- [9] Damián E Blasi, Morten H. Christiansen, Søren Wichman, and Harald Hammarström. Sound symbolism and the origins of language. In Erica A Cartmill, Seán Roberts, Heidi Lyn, and Hannah Cornish, editors, *The Evolution of Language – Proceedings of the 10th International Conference*, pages 391–392, Singapore, 2014. World Scientific.
- [10] X Liu, M Scholz, A Tönjes, M Stumvoll, P F Stadler, and Y Böttcher. Analysis of parent of origin effects in Sorbs using long range phasing algorithms. *Diabetologie und Stoffwechsel*, 9:P176, 2014.
- [11] Jan Engelhardt and Peter F Stadler. Evolution of 3’UTR-associated RNAs. *BMC Bioinformatics*, 16:A7, 2016.
- [12] Felix Kühnl, Peter F. Stadler, and Sebastian Will. Tractable kinetics of RNA–ligand interaction. In Anu Bourgeois, Pavel Skums, Xiang Wan, and Alex Zelikovsky, editors, *Bioinformatics Research and Applications, 12th International Symposium, ISBRA 2016*, volume 9683, pages 337–338, Berlin, 2016. Springer Verlag.
- [13] Vassily Lyubetsky, William H. Piel, and Peter F. Stadler. Molecular phylogenetics 2016. *Biomed Res Int*, 2016:9029306, 2016.
- [14] Guillermo Restrepo, Peter F. Stadler, and Jürgen Jost. Proceedings of the “mathematics in chemistry meeting”, leipzig, germany, october 26-28 2016. *MATCH Commun. Math. Comput. Chem.*, 80:541–545, 2018.

# 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.
- [12] Anke Busch and Peter F. Stadler. Intra-genic exon duplications in the human transcriptome. Technical Report BIOINF 10-037, U. Leipzig, Bioinformatics, 2010.
- [13] Jan Engelhardt, Toralf Kirsten, Peter F. Stadler, and Sonja J. Prohaska. Genome annotation without genes. Technical Report BIOINF 10-013, U. Leipzig, Bioinformatics, 2010.
- [14] Arli A. Parikesit, Peter F. Stadler, and Sonja J. Prohaska. Large-scale evolutionary patterns of protein domain distributions in eukaryotes. Technical Report BIOINF 12-007, U. Leipzig, Bioinformatics, 2012.
- [15] Jakob L. Andersen, Christoph Flamm, Daniel Merkle, and Peter F Stadler. Algorithmic Cheminformatics (Dagstuhl Seminar 17452). *Dagstuhl Reports*, 7:11, 2018.