

Erich G Bornberg-Bauer

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

147
papers

8,537
citations

47
h-index

90
g-index

230
ext. papers

10,382
ext. citations

7
avg, IF

5.82
L-index

| # | Paper | IF | Citations |
|-----|--|------|-----------|
| 147 | Lifespan prolonging mechanisms and insulin upregulation without fat accumulation in long-lived reproductives of a higher termite.. <i>Communications Biology</i> , 2022 , 5, 44 | 6.7 | 2 |
| 146 | Ancestral sequences of a large promiscuous enzyme family correspond to bridges in sequence space in a network representation. <i>Journal of the Royal Society Interface</i> , 2021 , 18, 20210389 | 4.1 | |
| 145 | Convergent loss of chemoreceptors across independent origins of slave-making in ants. <i>Molecular Biology and Evolution</i> , 2021 , | 8.3 | 3 |
| 144 | Structural and functional characterization of a putative de novo gene in <i>Drosophila</i> . <i>Nature Communications</i> , 2021 , 12, 1667 | 17.4 | 10 |
| 143 | Gene Coexpression Network Reveals Highly Conserved, Well-Regulated Anti-Ageing Mechanisms in Old Ant Queens. <i>Genome Biology and Evolution</i> , 2021 , 13, | 3.9 | 2 |
| 142 | Structure and function of naturally evolved de novo proteins. <i>Current Opinion in Structural Biology</i> , 2021 , 68, 175-183 | 8.1 | 9 |
| 141 | A genetic variant alters the secondary structure of the lncRNA H19 and is associated with dilated cardiomyopathy. <i>RNA Biology</i> , 2021 , 1-7 | 4.8 | 0 |
| 140 | Climate change facilitates a parasite's host exploitation via temperature-mediated immunometabolic processes. <i>Global Change Biology</i> , 2021 , 27, 94-107 | 11.4 | 1 |
| 139 | A putative de novo evolved gene required for spermatid chromatin condensation in <i>Drosophila melanogaster</i> . <i>PLoS Genetics</i> , 2021 , 17, e1009787 | 6 | 6 |
| 138 | Comparative analyses of caste, sex, and developmental stage-specific transcriptomes in two ants. <i>Ecology and Evolution</i> , 2020 , 10, 4193-4203 | 2.8 | 3 |
| 137 | The modular nature of protein evolution: domain rearrangement rates across eukaryotic life. <i>BMC Evolutionary Biology</i> , 2020 , 20, 30 | 3 | 12 |
| 136 | Gene content evolution in the arthropods. <i>Genome Biology</i> , 2020 , 21, 15 | 18.3 | 63 |
| 135 | A Continuum of Evolving De Novo Genes Drives Protein-Coding Novelty in <i>Drosophila</i> . <i>Journal of Molecular Evolution</i> , 2020 , 88, 382-398 | 3.1 | 19 |
| 134 | Sawfly Genomes Reveal Evolutionary Acquisitions That Fostered the Mega-Radiation of Parasitoid and Eusocial Hymenoptera. <i>Genome Biology and Evolution</i> , 2020 , 12, 1099-1188 | 3.9 | 7 |
| 133 | Stochastic Gain and Loss of Novel Transcribed Open Reading Frames in the Human Lineage. <i>Genome Biology and Evolution</i> , 2020 , 12, 2183-2195 | 3.9 | 7 |
| 132 | Evolution of novel genes in three-spined stickleback populations. <i>Heredity</i> , 2020 , 125, 50-59 | 3.6 | 9 |
| 131 | Hybrid Genome Assembly of a Neotropical Mutualistic Ant. <i>Genome Biology and Evolution</i> , 2019 , 11, 2306-23117 | 3.3 | 17 |

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| 130 | DOGMA: a web server for proteome and transcriptome quality assessment. <i>Nucleic Acids Research</i> , 2019 , 47, W507-W510 | 20.1 | 7 |
| 129 | Ant behaviour and brain gene expression of defending hosts depend on the ecological success of the intruding social parasite. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019 , 374, 20180192 | 5.8 | 8 |
| 128 | Becoming a de novo gene. <i>Nature Ecology and Evolution</i> , 2019 , 3, 524-525 | 12.3 | 4 |
| 127 | Genome-Wide Genotype-Expression Relationships Reveal Both Copy Number and Single Nucleotide Differentiation Contribute to Differential Gene Expression between Stickleback Ecotypes. <i>Genome Biology and Evolution</i> , 2019 , 11, 2344-2359 | 3.9 | 6 |
| 126 | High-Throughput, Lysis-Free Screening for Sulfatase Activity Using Autodisplay in Microdroplets. <i>ACS Synthetic Biology</i> , 2019 , 8, 2690-2700 | 5.7 | 14 |
| 125 | Higher-order epistasis shapes the fitness landscape of a xenobiotic-degrading enzyme. <i>Nature Chemical Biology</i> , 2019 , 15, 1120-1128 | 11.7 | 35 |
| 124 | Evolutionary Potential of Cis-Regulatory Mutations to Cause Rapid Changes in Transcription Factor Binding. <i>Genome Biology and Evolution</i> , 2019 , 11, 406-414 | 3.9 | 4 |
| 123 | A Roadmap to Domain Based Proteomics. <i>Methods in Molecular Biology</i> , 2019 , 1851, 287-300 | 1.4 | 1 |
| 122 | Structural and Mechanistic Analysis of the Choline Sulfatase from <i>Sinorhizobium melliloti</i> : A Class I Sulfatase Specific for an Alkyl Sulfate Ester. <i>Journal of Molecular Biology</i> , 2018 , 430, 1004-1023 | 6.5 | 13 |
| 121 | <i>Tribolium castaneum</i> gene expression changes after <i>Paranosema whitei</i> infection. <i>Journal of Invertebrate Pathology</i> , 2018 , 153, 92-98 | 2.6 | 4 |
| 120 | Hemimetabolous genomes reveal molecular basis of termite eusociality. <i>Nature Ecology and Evolution</i> , 2018 , 2, 557-566 | 12.3 | 120 |
| 119 | Expansions of key protein families in the German cockroach highlight the molecular basis of its remarkable success as a global indoor pest. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2018 , 330, 254-264 | 1.8 | 11 |
| 118 | Reconstructed evolution of insulin receptors in insects reveals duplications in early insects and cockroaches. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2018 , 330, 305-311 | 1.8 | 15 |
| 117 | Robustness by intrinsically disordered C-termini and translational readthrough. <i>Nucleic Acids Research</i> , 2018 , 46, 10184-10194 | 20.1 | 13 |
| 116 | Incipient de novo genes can evolve from frozen accidents that escaped rapid transcript turnover. <i>Nature Ecology and Evolution</i> , 2018 , 2, 1626-1632 | 12.3 | 35 |
| 115 | Origins and structural properties of novel and de novo protein domains during insect evolution. <i>FEBS Journal</i> , 2018 , 285, 2605-2625 | 5.7 | 15 |
| 114 | Remodeling of the juvenile hormone pathway through caste-biased gene expression and positive selection along a gradient of termite eusociality. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2018 , 330, 296-304 | 1.8 | 12 |
| 113 | Enzyme sub-functionalization driven by regulation. <i>EMBO Reports</i> , 2017 , 18, 1043-1045 | 6.5 | 1 |

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|-----|--|------|-----|
| 112 | Comparative analysis of lincRNA in insect species. <i>BMC Evolutionary Biology</i> , 2017 , 17, 155 | 3 | 17 |
| 111 | Fact or fiction: updates on how protein-coding genes might emerge from previously non-coding DNA. <i>F1000Research</i> , 2017 , 6, 57 | 3.6 | 33 |
| 110 | The Goddard and Saturn Genes Are Essential for <i>Drosophila</i> Male Fertility and May Have Arisen De Novo. <i>Molecular Biology and Evolution</i> , 2017 , 34, 1066-1082 | 8.3 | 22 |
| 109 | Evolution of Protein Domain Repeats in Metazoa. <i>Molecular Biology and Evolution</i> , 2016 , 33, 3170-3182 | 8.3 | 22 |
| 108 | Mechanisms of transcription factor evolution in Metazoa. <i>Nucleic Acids Research</i> , 2016 , 44, 6287-97 | 20.1 | 32 |
| 107 | Comparative transcriptomics of stickleback immune gene responses upon infection by two helminth parasites, <i>Diplostomum pseudospathaceum</i> and <i>Schistocephalus solidus</i> . <i>Zoology</i> , 2016 , 119, 307-13 | 1.7 | 15 |
| 106 | The genome of the seagrass <i>Zostera marina</i> reveals angiosperm adaptation to the sea. <i>Nature</i> , 2016 , 530, 331-5 | 50.4 | 276 |
| 105 | Immunity comes first: the effect of parasite genotypes on adaptive immunity and immunization in three-spined sticklebacks. <i>Developmental and Comparative Immunology</i> , 2016 , 54, 137-44 | 3.2 | 11 |
| 104 | Chapter 6. Comparative genomic approaches to investigate molecular traits specific to social insects. <i>Current Opinion in Insect Science</i> , 2016 , 16, 87-94 | 5.1 | 3 |
| 103 | Transcriptome profiling of immune tissues reveals habitat-specific gene expression between lake and river sticklebacks. <i>Molecular Ecology</i> , 2016 , 25, 943-58 | 5.7 | 34 |
| 102 | DOGMA: domain-based transcriptome and proteome quality assessment. <i>Bioinformatics</i> , 2016 , 32, 2577-81 | 8.1 | 28 |
| 101 | Phylogeographic differentiation versus transcriptomic adaptation to warm temperatures in <i>Zostera marina</i> , a globally important seagrass. <i>Molecular Ecology</i> , 2016 , 25, 5396-5411 | 5.7 | 32 |
| 100 | Detection of orphan domains in <i>Drosophila</i> using "hydrophobic cluster analysis". <i>Biochimie</i> , 2015 , 119, 244-53 | 4.6 | 23 |
| 99 | Genomics of divergence along a continuum of parapatric population differentiation. <i>PLoS Genetics</i> , 2015 , 11, e1004966 | 6 | 97 |
| 98 | The genomes of two key bumblebee species with primitive eusocial organization. <i>Genome Biology</i> , 2015 , 16, 76 | 18.3 | 229 |
| 97 | MDAT- Aligning multiple domain arrangements. <i>BMC Bioinformatics</i> , 2015 , 16, 19 | 3.6 | 1 |
| 96 | Domain similarity based orthology detection. <i>BMC Bioinformatics</i> , 2015 , 16, 154 | 3.6 | 9 |
| 95 | Protein domain evolution is associated with reproductive diversification and adaptive radiation in the genus <i>Eucalyptus</i> . <i>New Phytologist</i> , 2015 , 206, 1328-36 | 9.8 | 13 |

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|----|--|------|-----|
| 94 | Emergence of de novo proteins from dark genomic matter by R. Grow slow and moult. <i>Biochemical Society Transactions</i> , 2015 , 43, 867-73 | 5.1 | 25 |
| 93 | The Rise and Fall of TRP-N, an Ancient Family of Mechanogated Ion Channels, in Metazoa. <i>Genome Biology and Evolution</i> , 2015 , 7, 1713-27 | 3.9 | 29 |
| 92 | How Do Genomes Create Novel Phenotypes? Insights from the Loss of the Worker Caste in Ant Social Parasites. <i>Molecular Biology and Evolution</i> , 2015 , 32, 2919-31 | 8.3 | 31 |
| 91 | Host-Pathogen Coevolution: The Selective Advantage of <i>Bacillus thuringiensis</i> Virulence and Its Cry Toxin Genes. <i>PLoS Biology</i> , 2015 , 13, e1002169 | 9.7 | 55 |
| 90 | The genome of <i>Eucalyptus grandis</i> . <i>Nature</i> , 2014 , 510, 356-62 | 50.4 | 497 |
| 89 | Infection routes matter in population-specific responses of the red flour beetle to the entomopathogen <i>Bacillus thuringiensis</i> . <i>BMC Genomics</i> , 2014 , 15, 445 | 4.5 | 45 |
| 88 | Molecular traces of alternative social organization in a termite genome. <i>Nature Communications</i> , 2014 , 5, 3636 | 17.4 | 250 |
| 87 | Specific gene expression responses to parasite genotypes reveal redundancy of innate immunity in vertebrates. <i>PLoS ONE</i> , 2014 , 9, e108001 | 3.7 | 21 |
| 86 | Extensive copy-number variation of young genes across stickleback populations. <i>PLoS Genetics</i> , 2014 , 10, e1004830 | 6 | 56 |
| 85 | Rapid similarity search of proteins using alignments of domain arrangements. <i>Bioinformatics</i> , 2014 , 30, 274-81 | 7.2 | 31 |
| 84 | DoMosaics: software for domain arrangement visualization and domain-centric analysis of proteins. <i>Bioinformatics</i> , 2014 , 30, 282-3 | 7.2 | 34 |
| 83 | Genome-wide transcriptomic responses of the seagrasses <i>Zostera marina</i> and <i>Nanozostera noltii</i> under a simulated heatwave confirm functional types. <i>Marine Genomics</i> , 2014 , 15, 65-73 | 1.9 | 52 |
| 82 | Genome-wide patterns of standing genetic variation in a marine population of three-spined sticklebacks. <i>Molecular Ecology</i> , 2013 , 22, 635-49 | 5.7 | 64 |
| 81 | Genomic divergence between nine- and three-spined sticklebacks. <i>BMC Genomics</i> , 2013 , 14, 756 | 4.5 | 33 |
| 80 | Dynamics and adaptive benefits of modular protein evolution. <i>Current Opinion in Structural Biology</i> , 2013 , 23, 459-66 | 8.1 | 69 |
| 79 | Social insect genomes exhibit dramatic evolution in gene composition and regulation while preserving regulatory features linked to sociality. <i>Genome Research</i> , 2013 , 23, 1235-47 | 9.7 | 166 |
| 78 | Quantification and functional analysis of modular protein evolution in a dense phylogenetic tree. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013 , 1834, 898-907 | 4 | 27 |
| 77 | Mechanisms and dynamics of orphan gene emergence in insect genomes. <i>Genome Biology and Evolution</i> , 2013 , 5, 439-55 | 3.9 | 97 |

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|----|---|------|-----|
| 76 | Identifying core features of adaptive metabolic mechanisms for chronic heat stress attenuation contributing to systems robustness. <i>Integrative Biology (United Kingdom)</i> , 2012 , 4, 480-93 | 3.7 | 37 |
| 75 | Genomic and morphological evidence converge to resolve the enigma of Strepsiptera. <i>Current Biology</i> , 2012 , 22, 1309-13 | 6.3 | 117 |
| 74 | Evaluating characteristics of de novo assembly software on 454 transcriptome data: a simulation approach. <i>PLoS ONE</i> , 2012 , 7, e31410 | 3.7 | 68 |
| 73 | The interface of protein structure, protein biophysics, and molecular evolution. <i>Protein Science</i> , 2012 , 21, 769-85 | 6.3 | 136 |
| 72 | Proteome of Hydra nematocyst. <i>Journal of Biological Chemistry</i> , 2012 , 287, 9672-9681 | 5.4 | 73 |
| 71 | Evolutionary dynamics on protein bi-stability landscapes can potentially resolve adaptive conflicts. <i>PLoS Computational Biology</i> , 2012 , 8, e1002659 | 5 | 22 |
| 70 | The dynamics and evolutionary potential of domain loss and emergence. <i>Molecular Biology and Evolution</i> , 2012 , 29, 787-96 | 8.3 | 57 |
| 69 | Dynamics and adaptive benefits of protein domain emergence and arrangements during plant genome evolution. <i>Genome Biology and Evolution</i> , 2012 , 4, 316-29 | 3.9 | 50 |
| 68 | Evolutionary dynamics of simple sequence repeats across long evolutionary time scale in genus <i>Drosophila</i> . <i>Trends in Evolutionary Biology</i> , 2012 , 4, 7 | | 6 |
| 67 | Escape from Adaptive Conflict follows from weak functional trade-offs and mutational robustness. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 14888-93 | 11.5 | 46 |
| 66 | Back to the sea twice: identifying candidate plant genes for molecular evolution to marine life. <i>BMC Evolutionary Biology</i> , 2011 , 11, 8 | 3 | 61 |
| 65 | Comprehensive transcriptome analysis of the highly complex <i>Pisum sativum</i> genome using next generation sequencing. <i>BMC Genomics</i> , 2011 , 12, 227 | 4.5 | 124 |
| 64 | Evolution After and Before Gene Duplication? 2011 , 105-131 | | 3 |
| 63 | The sieve element occlusion gene family in dicotyledonous plants. <i>Plant Signaling and Behavior</i> , 2011 , 6, 151-3 | 2.5 | 18 |
| 62 | Transcriptomic resilience to global warming in the seagrass <i>Zostera marina</i> , a marine foundation species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 19276-81 | 11.5 | 112 |
| 61 | The genome sequence of the leaf-cutter ant <i>Atta cephalotes</i> reveals insights into its obligate symbiotic lifestyle. <i>PLoS Genetics</i> , 2011 , 7, e1002007 | 6 | 191 |
| 60 | Evolutionary divergence and limits of conserved non-coding sequence detection in plant genomes. <i>Nucleic Acids Research</i> , 2011 , 39, 6029-43 | 20.1 | 30 |
| 59 | The evolution of protein interaction networks. <i>Methods in Molecular Biology</i> , 2011 , 696, 273-89 | 1.4 | 3 |

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|----|---|------|------|
| 58 | Signals: tinkering with domains. <i>Science Signaling</i> , 2010 , 3, pe31 | 8.8 | 3 |
| 57 | Evolvability and single-genotype fluctuation in phenotypic properties: a simple heteropolymer model. <i>Biophysical Journal</i> , 2010 , 98, 2487-96 | 2.9 | 8 |
| 56 | Robustness versus evolvability: a paradigm revisited. <i>HFSP Journal</i> , 2010 , 4, 105-8 | | 6 |
| 55 | Functional and evolutionary insights from the genomes of three parasitoid <i>Nasonia</i> species. <i>Science</i> , 2010 , 327, 343-8 | 33.3 | 682 |
| 54 | How do new proteins arise?. <i>Current Opinion in Structural Biology</i> , 2010 , 20, 390-6 | 8.1 | 53 |
| 53 | Molecular and phylogenetic characterization of the sieve element occlusion gene family in Fabaceae and non-Fabaceae plants. <i>BMC Plant Biology</i> , 2010 , 10, 219 | 5.3 | 54 |
| 52 | Protein Domains as Evolutionary Units 2010 , 213-230 | | |
| 51 | Dr. Zompo: an online data repository for <i>Zostera marina</i> and <i>Posidonia oceanica</i> ESTs. <i>Database: the Journal of Biological Databases and Curation</i> , 2009 , 2009, bap009 | 5 | 36 |
| 50 | Just how versatile are domains?. <i>BMC Evolutionary Biology</i> , 2008 , 8, 285 | 3 | 41 |
| 49 | Arrangements in the modular evolution of proteins. <i>Trends in Biochemical Sciences</i> , 2008 , 33, 444-51 | 10.3 | 165 |
| 48 | The look-ahead effect of phenotypic mutations. <i>Biology Direct</i> , 2008 , 3, 18 | 7.2 | 49 |
| 47 | Specificity of the innate immune system and diversity of C-type lectin domain (CTLD) proteins in the nematode <i>Caenorhabditis elegans</i> . <i>Immunobiology</i> , 2008 , 213, 237-50 | 3.4 | 146 |
| 46 | The Crohn's disease susceptibility gene <i>DLG5</i> as a member of the CARD interaction network. <i>Journal of Molecular Medicine</i> , 2008 , 86, 423-32 | 5.5 | 16 |
| 45 | Metabolism of halophilic archaea. <i>Extremophiles</i> , 2008 , 12, 177-96 | 3 | 174 |
| 44 | Comparative analysis of expressed sequence tag (EST) libraries in the seagrass <i>Zostera marina</i> subjected to temperature stress. <i>Marine Biotechnology</i> , 2008 , 10, 297-309 | 3.4 | 47 |
| 43 | The AtGenExpress global stress expression data set: protocols, evaluation and model data analysis of UV-B light, drought and cold stress responses. <i>Plant Journal</i> , 2007 , 50, 347-63 | 6.9 | 1071 |
| 42 | A protein interaction atlas for the nuclear receptors: properties and quality of a hub-based dimerisation network. <i>BMC Systems Biology</i> , 2007 , 1, 34 | 3.5 | 25 |
| 41 | One billion years of bZIP transcription factor evolution: conservation and change in dimerization and DNA-binding site specificity. <i>Molecular Biology and Evolution</i> , 2007 , 24, 827-35 | 8.3 | 111 |

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|----|--|------|-----|
| 40 | Evidence of interaction network evolution by whole-genome duplications: a case study in MADS-box proteins. <i>Molecular Biology and Evolution</i> , 2007 , 24, 670-8 | 8.3 | 75 |
| 39 | EVOLUTION OF REGULATORY NETWORKS. <i>Complex Systems and Interdisciplinary Science</i> , 2007 , 257-289 | | |
| 38 | A structural model of latent evolutionary potentials underlying neutral networks in proteins. <i>HFSP Journal</i> , 2007 , 1, 79-87 | | 55 |
| 37 | Automated Improvement of Domain ANnotations using context analysis of domain arrangements (AIDAN). <i>Bioinformatics</i> , 2007 , 23, 1834-6 | 7.2 | 14 |
| 36 | Finding common protein interaction patterns across organisms. <i>Evolutionary Bioinformatics</i> , 2007 , 2, 45-52 | 1.9 | 1 |
| 35 | Reduction/oxidation-phosphorylation control of DNA binding in the bZIP dimerization network. <i>BMC Genomics</i> , 2006 , 7, 107 | 4.5 | 24 |
| 34 | Evolution of circular permutations in multidomain proteins. <i>Molecular Biology and Evolution</i> , 2006 , 23, 734-43 | 8.3 | 58 |
| 33 | Finding Common Protein Interaction Patterns Across Organisms. <i>Evolutionary Bioinformatics</i> , 2006 , 2, 117693430600200 | 1.9 | 2 |
| 32 | Domain deletions and substitutions in the modular protein evolution. <i>FEBS Journal</i> , 2006 , 273, 2037-47 | 5.7 | 93 |
| 31 | Phylogenetic profiling of protein interaction networks in eukaryotic transcription factors reveals focal proteins being ancestral to hubs. <i>Gene</i> , 2005 , 347, 247-53 | 3.8 | 7 |
| 30 | Comparing folding codes in simple heteropolymer models of protein evolutionary landscape: robustness of the superfunnel paradigm. <i>Biophysical Journal</i> , 2005 , 88, 118-31 | 2.9 | 35 |
| 29 | The evolution of domain arrangements in proteins and interaction networks. <i>Cellular and Molecular Life Sciences</i> , 2005 , 62, 435-45 | 10.3 | 100 |
| 28 | Distribution of gibberellin biosynthetic genes and gibberellin production in the <i>Gibberella fujikuroi</i> species complex. <i>Phytochemistry</i> , 2005 , 66, 1296-311 | 4 | 64 |
| 27 | Rapid motif-based prediction of circular permutations in multi-domain proteins. <i>Bioinformatics</i> , 2005 , 21, 932-7 | 7.2 | 37 |
| 26 | Convergent evolution of gene networks by single-gene duplications in higher eukaryotes. <i>EMBO Reports</i> , 2004 , 5, 274-9 | 6.5 | 75 |
| 25 | The evolution of protein interaction networks in regulatory proteins. <i>Comparative and Functional Genomics</i> , 2004 , 5, 79-84 | | 18 |
| 24 | Recombinatoric exploration of novel folded structures: a heteropolymer-based model of protein evolutionary landscapes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 809-14 | 11.5 | 80 |
| 23 | Randomness, Structural Uniqueness, Modularity and Neutral Evolution in Sequence Space of Model Proteins. <i>Zeitschrift Fur Physikalische Chemie</i> , 2002 , 216, | 3.1 | 14 |

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|----|---|------|-----|
| 22 | TreeWiz: interactive exploration of huge trees. <i>Bioinformatics</i> , 2002 , 18, 109-14 | 7.2 | 21 |
| 21 | Conceptual data modelling for bioinformatics. <i>Briefings in Bioinformatics</i> , 2002 , 3, 166-80 | 13.4 | 34 |
| 20 | A putative transcription factor inducing mobility in <i>Mycoplasma pneumoniae</i> . <i>Microbiology (United Kingdom)</i> , 2002 , 148, 3764-3765 | 2.9 | 6 |
| 19 | Perspectives on protein evolution from simple exact models. <i>Applied Bioinformatics</i> , 2002 , 1, 121-44 | | 40 |
| 18 | Switching from simple to complex oscillations in calcium signaling. <i>Biophysical Journal</i> , 2000 , 79, 1188-95. | 5.9 | 146 |
| 17 | Application of constraint programming techniques for structure prediction of lattice proteins with extended alphabets. <i>Bioinformatics</i> , 1999 , 15, 234-42 | 7.2 | 32 |
| 16 | WWW access to the SYSTERS protein sequence cluster set. <i>Bioinformatics</i> , 1999 , 15, 262-3 | 7.2 | 14 |
| 15 | Modeling evolutionary landscapes: mutational stability, topology, and superfunnels in sequence space. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999 , 96, 10689-94 | 11.5 | 195 |
| 14 | Computational approaches to identify leucine zippers. <i>Nucleic Acids Research</i> , 1998 , 26, 2740-6 | 20.1 | 96 |
| 13 | How are model protein structures distributed in sequence space?. <i>Biophysical Journal</i> , 1997 , 73, 2393-403. | 3.9 | 124 |
| 12 | Simple folding model for HP lattice proteins. <i>Lecture Notes in Computer Science</i> , 1996 , 125-136 | 0.9 | 2 |
| 11 | Random structures and evolution of biopolymers: A computational case study on RNA secondary structures. <i>Pharmaceutica Acta Helveticae</i> , 1996 , 71, 79-85 | | 2 |
| 10 | Algorithm independent properties of RNA secondary structure predictions. <i>European Biophysics Journal</i> , 1996 , 25, 115-130 | 1.9 | 71 |
| 9 | Random structures and evolution of biopolymers. <i>Zeitschrift Fur Elektrotechnik Und Elektrochemie</i> , 1994 , 98, 1128-1128 | | |
| 8 | RNA folding and combinatorial landscapes. <i>Physical Review E</i> , 1993 , 47, 2083-2099 | 2.4 | 175 |
| 7 | New genomic signals underlying the emergence of human proto-genes | | 1 |
| 6 | Experimental characterisation of de novo proteins and their unevolved random-sequence counterparts | | 2 |
| 5 | Gene Content Evolution in the Arthropods | | 7 |

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| 4 | Higher-order epistatic networks underlie the evolutionary fitness landscape of a xenobiotic-degrading enzyme | 2 |
| 3 | Hemimetabolous genomes reveal molecular basis of termite eusociality | 1 |
| 2 | Gene co-expression network reveals highly conserved, well-regulated anti-ageing mechanisms in old ant queens | 1 |
| 1 | Chaperones facilitate heterologous expression of naturally evolved putative de novo proteins | 1 |