

Erich G Bornberg-Bauer

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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	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
146	Functional and evolutionary insights from the genomes of three parasitoid <i>Nasonia</i> species. <i>Science</i> , 2010 , 327, 343-8	33.3	682
145	The genome of <i>Eucalyptus grandis</i> . <i>Nature</i> , 2014 , 510, 356-62	50.4	497
144	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
143	Molecular traces of alternative social organization in a termite genome. <i>Nature Communications</i> , 2014 , 5, 3636	17.4	250
142	The genomes of two key bumblebee species with primitive eusocial organization. <i>Genome Biology</i> , 2015 , 16, 76	18.3	229
141	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
140	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
139	RNA folding and combinatorial landscapes. <i>Physical Review E</i> , 1993 , 47, 2083-2099	2.4	175
138	Metabolism of halophilic archaea. <i>Extremophiles</i> , 2008 , 12, 177-96	3	174
137	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
136	Arrangements in the modular evolution of proteins. <i>Trends in Biochemical Sciences</i> , 2008 , 33, 444-51	10.3	165
135	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
134	Switching from simple to complex oscillations in calcium signaling. <i>Biophysical Journal</i> , 2000 , 79, 1188-95	5.9	146
133	The interface of protein structure, protein biophysics, and molecular evolution. <i>Protein Science</i> , 2012 , 21, 769-85	6.3	136
132	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
131	How are model protein structures distributed in sequence space?. <i>Biophysical Journal</i> , 1997 , 73, 2393-403	3.9	124

130	Hemimetabolous genomes reveal molecular basis of termite eusociality. <i>Nature Ecology and Evolution</i> , 2018 , 2, 557-566	12.3	120
129	Genomic and morphological evidence converge to resolve the enigma of Strepsiptera. <i>Current Biology</i> , 2012 , 22, 1309-13	6.3	117
128	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
127	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
126	The evolution of domain arrangements in proteins and interaction networks. <i>Cellular and Molecular Life Sciences</i> , 2005 , 62, 435-45	10.3	100
125	Genomics of divergence along a continuum of parapatric population differentiation. <i>PLoS Genetics</i> , 2015 , 11, e1004966	6	97
124	Mechanisms and dynamics of orphan gene emergence in insect genomes. <i>Genome Biology and Evolution</i> , 2013 , 5, 439-55	3.9	97
123	Computational approaches to identify leucine zippers. <i>Nucleic Acids Research</i> , 1998 , 26, 2740-6	20.1	96
122	Domain deletions and substitutions in the modular protein evolution. <i>FEBS Journal</i> , 2006 , 273, 2037-47	5.7	93
121	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
120	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
119	Convergent evolution of gene networks by single-gene duplications in higher eukaryotes. <i>EMBO Reports</i> , 2004 , 5, 274-9	6.5	75
118	Proteome of Hydra nematocyst. <i>Journal of Biological Chemistry</i> , 2012 , 287, 9672-9681	5.4	73
117	Algorithm independent properties of RNA secondary structure predictions. <i>European Biophysics Journal</i> , 1996 , 25, 115-130	1.9	71
116	Dynamics and adaptive benefits of modular protein evolution. <i>Current Opinion in Structural Biology</i> , 2013 , 23, 459-66	8.1	69
115	Evaluating characteristics of de novo assembly software on 454 transcriptome data: a simulation approach. <i>PLoS ONE</i> , 2012 , 7, e31410	3.7	68
114	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
113	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

112	Gene content evolution in the arthropods. <i>Genome Biology</i> , 2020 , 21, 15	18.3	63
111	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
110	Evolution of circular permutations in multidomain proteins. <i>Molecular Biology and Evolution</i> , 2006 , 23, 734-43	8.3	58
109	The dynamics and evolutionary potential of domain loss and emergence. <i>Molecular Biology and Evolution</i> , 2012 , 29, 787-96	8.3	57
108	Extensive copy-number variation of young genes across stickleback populations. <i>PLoS Genetics</i> , 2014 , 10, e1004830	6	56
107	A structural model of latent evolutionary potentials underlying neutral networks in proteins. <i>HFSP Journal</i> , 2007 , 1, 79-87		55
106	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
105	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
104	How do new proteins arise?. <i>Current Opinion in Structural Biology</i> , 2010 , 20, 390-6	8.1	53
103	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
102	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
101	The look-ahead effect of phenotypic mutations. <i>Biology Direct</i> , 2008 , 3, 18	7.2	49
100	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
99	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
98	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
97	Just how versatile are domains?. <i>BMC Evolutionary Biology</i> , 2008 , 8, 285	3	41
96	Perspectives on protein evolution from simple exact models. <i>Applied Bioinformatics</i> , 2002 , 1, 121-44		40
95	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

94	Rapid motif-based prediction of circular permutations in multi-domain proteins. <i>Bioinformatics</i> , 2005 , 21, 932-7	7.2	37
93	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
92	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
91	Higher-order epistasis shapes the fitness landscape of a xenobiotic-degrading enzyme. <i>Nature Chemical Biology</i> , 2019 , 15, 1120-1128	11.7	35
90	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
89	DoMosaics: software for domain arrangement visualization and domain-centric analysis of proteins. <i>Bioinformatics</i> , 2014 , 30, 282-3	7.2	34
88	Conceptual data modelling for bioinformatics. <i>Briefings in Bioinformatics</i> , 2002 , 3, 166-80	13.4	34
87	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
86	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
85	Genomic divergence between nine- and three-spined sticklebacks. <i>BMC Genomics</i> , 2013 , 14, 756	4.5	33
84	Mechanisms of transcription factor evolution in Metazoa. <i>Nucleic Acids Research</i> , 2016 , 44, 6287-97	20.1	32
83	Application of constraint programming techniques for structure prediction of lattice proteins with extended alphabets. <i>Bioinformatics</i> , 1999 , 15, 234-42	7.2	32
82	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
81	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
80	Rapid similarity search of proteins using alignments of domain arrangements. <i>Bioinformatics</i> , 2014 , 30, 274-81	7.2	31
79	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
78	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
77	DOGMA: domain-based transcriptome and proteome quality assessment. <i>Bioinformatics</i> , 2016 , 32, 2577-81	8.1	28

76	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
75	Emergence of de novo proteins from Rlark genomic matterRby Rgrow slow and moultR <i>Biochemical Society Transactions</i> , 2015 , 43, 867-73	5.1	25
74	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
73	Reduction/oxidation-phosphorylation control of DNA binding in the bZIP dimerization network. <i>BMC Genomics</i> , 2006 , 7, 107	4.5	24
72	Detection of orphan domains in Drosophila using "hydrophobic cluster analysis". <i>Biochimie</i> , 2015 , 119, 244-53	4.6	23
71	Evolution of Protein Domain Repeats in Metazoa. <i>Molecular Biology and Evolution</i> , 2016 , 33, 3170-3182	8.3	22
70	Evolutionary dynamics on protein bi-stability landscapes can potentially resolve adaptive conflicts. <i>PLoS Computational Biology</i> , 2012 , 8, e1002659	5	22
69	The Goddard and Saturn Genes Are Essential for Drosophila Male Fertility and May Have Arisen De Novo. <i>Molecular Biology and Evolution</i> , 2017 , 34, 1066-1082	8.3	22
68	Specific gene expression responses to parasite genotypes reveal redundancy of innate immunity in vertebrates. <i>PLoS ONE</i> , 2014 , 9, e108001	3.7	21
67	TreeWiz: interactive exploration of huge trees. <i>Bioinformatics</i> , 2002 , 18, 109-14	7.2	21
66	A Continuum of Evolving De Novo Genes Drives Protein-Coding Novelty in Drosophila. <i>Journal of Molecular Evolution</i> , 2020 , 88, 382-398	3.1	19
65	The sieve element occlusion gene family in dicotyledonous plants. <i>Plant Signaling and Behavior</i> , 2011 , 6, 151-3	2.5	18
64	The evolution of protein interaction networks in regulatory proteins. <i>Comparative and Functional Genomics</i> , 2004 , 5, 79-84		18
63	Comparative analysis of lincRNA in insect species. <i>BMC Evolutionary Biology</i> , 2017 , 17, 155	3	17
62	The Crohn's disease susceptibility gene DLG5 as a member of the CARD interaction network. <i>Journal of Molecular Medicine</i> , 2008 , 86, 423-32	5.5	16
61	Comparative transcriptomics of stickleback immune gene responses upon infection by two helminth parasites, Diplostomum pseudospathaceum and Schistocephalus solidus. <i>Zoology</i> , 2016 , 119, 307-13	1.7	15
60	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
59	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

58	Automated Improvement of Domain ANnotations using context analysis of domain arrangements (AIDAN). <i>Bioinformatics</i> , 2007 , 23, 1834-6	7.2	14
57	Randomness, Structural Uniqueness, Modularity and Neutral Evolution in Sequence Space of Model Proteins. <i>Zeitschrift Fur Physikalische Chemie</i> , 2002 , 216,	3.1	14
56	WWW access to the SYSTERS protein sequence cluster set. <i>Bioinformatics</i> , 1999 , 15, 262-3	7.2	14
55	High-Throughput, Lysis-Free Screening for Sulfatase Activity Using Autodisplay in Microdroplets. <i>ACS Synthetic Biology</i> , 2019 , 8, 2690-2700	5.7	14
54	Protein domain evolution is associated with reproductive diversification and adaptive radiation in the genus Eucalyptus. <i>New Phytologist</i> , 2015 , 206, 1328-36	9.8	13
53	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
52	Robustness by intrinsically disordered C-termini and translational readthrough. <i>Nucleic Acids Research</i> , 2018 , 46, 10184-10194	20.1	13
51	The modular nature of protein evolution: domain rearrangement rates across eukaryotic life. <i>BMC Evolutionary Biology</i> , 2020 , 20, 30	3	12
50	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
49	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
48	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
47	Structural and functional characterization of a putative de novo gene in <i>Drosophila</i> . <i>Nature Communications</i> , 2021 , 12, 1667	17.4	10
46	Domain similarity based orthology detection. <i>BMC Bioinformatics</i> , 2015 , 16, 154	3.6	9
45	Evolution of novel genes in three-spined stickleback populations. <i>Heredity</i> , 2020 , 125, 50-59	3.6	9
44	Structure and function of naturally evolved de novo proteins. <i>Current Opinion in Structural Biology</i> , 2021 , 68, 175-183	8.1	9
43	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
42	Evolvability and single-genotype fluctuation in phenotypic properties: a simple heteropolymer model. <i>Biophysical Journal</i> , 2010 , 98, 2487-96	2.9	8
41	Hybrid Genome Assembly of a Neotropical Mutualistic Ant. <i>Genome Biology and Evolution</i> , 2019 , 11, 2306-2317	23.1	7

40	DOGMA: a web server for proteome and transcriptome quality assessment. <i>Nucleic Acids Research</i> , 2019 , 47, W507-W510	20.1	7
39	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
38	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
37	Gene Content Evolution in the Arthropods		7
36	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
35	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
34	Robustness versus evolvability: a paradigm revisited. <i>HFSP Journal</i> , 2010 , 4, 105-8		6
33	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
32	A putative transcription factor inducing mobility in <i>Mycoplasma pneumoniae</i> . <i>Microbiology (United Kingdom)</i> , 2002 , 148, 3764-3765	2.9	6
31	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
30	Becoming a de novo gene. <i>Nature Ecology and Evolution</i> , 2019 , 3, 524-525	12.3	4
29	<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
28	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
27	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
26	Evolution After and Before Gene Duplication? 2011 , 105-131		3
25	Signals: tinkering with domains. <i>Science Signaling</i> , 2010 , 3, pe31	8.8	3
24	Convergent loss of chemoreceptors across independent origins of slave-making in ants. <i>Molecular Biology and Evolution</i> , 2021 ,	8.3	3
23	The evolution of protein interaction networks. <i>Methods in Molecular Biology</i> , 2011 , 696, 273-89	1.4	3

22	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
21	Finding Common Protein Interaction Patterns Across Organisms. <i>Evolutionary Bioinformatics</i> , 2006 , 2, 117693430600200	1.9	2
20	Simple folding model for HP lattice proteins. <i>Lecture Notes in Computer Science</i> , 1996 , 125-136	0.9	2
19	Random structures and evolution of biopolymers: A computational case study on RNA secondary structures. <i>Pharmaceutica Acta Helvetica</i> , 1996 , 71, 79-85		2
18	Experimental characterisation of de novo proteins and their unevolved random-sequence counterparts		2
17	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
16	Higher-order epistatic networks underlie the evolutionary fitness landscape of a xenobiotic-degrading enzyme		2
15	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
14	Enzyme sub-functionalization driven by regulation. <i>EMBO Reports</i> , 2017 , 18, 1043-1045	6.5	1
13	MDAT- Aligning multiple domain arrangements. <i>BMC Bioinformatics</i> , 2015 , 16, 19	3.6	1
12	New genomic signals underlying the emergence of human proto-genes		1
11	Finding common protein interaction patterns across organisms. <i>Evolutionary Bioinformatics</i> , 2007 , 2, 45-52	1.9	1
10	Hemimetabolous genomes reveal molecular basis of termite eusociality		1
9	A Roadmap to Domain Based Proteomics. <i>Methods in Molecular Biology</i> , 2019 , 1851, 287-300	1.4	1
8	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
7	Gene co-expression network reveals highly conserved, well-regulated anti-ageing mechanisms in old ant queens		1
6	Chaperones facilitate heterologous expression of naturally evolved putative de novo proteins		1
5	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

4 Protein Domains as Evolutionary Units **2010**, 213-230

3 EVOLUTION OF REGULATORY NETWORKS. *Complex Systems and Interdisciplinary Science*, **2007**, 257-289

2 Random structures and evolution of biopolymers. *Zeitschrift Fur Elektrotechnik Und Elektrochemie*, **1994**, 98, 1128-1128

1 Ancestral sequences of a large promiscuous enzyme family correspond to bridges in sequence space in a network representation. *Journal of the Royal Society Interface*, **2021**, 18, 20210389

4.1