

Erich G Bornberg-Bauer

List of Publications by Year in descending order

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Version: 2024-02-01

142
papers

11,475
citations

36271

51
h-index

32815

100
g-index

230
all docs

230
docs citations

230
times ranked

14387
citing authors

#	ARTICLE	IF	CITATIONS
1	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, 347-363.	2.8	1,322
2	Functional and Evolutionary Insights from the Genomes of Three Parasitoid <i>Nasonia</i> Species. <i>Science</i> , 2010, 327, 343-348.	6.0	808
3	The genome of <i>Eucalyptus grandis</i> . <i>Nature</i> , 2014, 510, 356-362.	13.7	725
4	The genome of the seagrass <i>Zostera marina</i> reveals angiosperm adaptation to the sea. <i>Nature</i> , 2016, 530, 331-335.	13.7	460
5	Molecular traces of alternative social organization in a termite genome. <i>Nature Communications</i> , 2014, 5, 3636.	5.8	371
6	The genomes of two key bumblebee species with primitive eusocial organization. <i>Genome Biology</i> , 2015, 16, 76.	3.8	330
7	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.	1.5	231
8	Hemimetabolous genomes reveal molecular basis of termite eusociality. <i>Nature Ecology and Evolution</i> , 2018, 2, 557-566.	3.4	223
9	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, 10689-10694.	3.3	222
10	Metabolism of halophilic archaea. <i>Extremophiles</i> , 2008, 12, 177-196.	0.9	214
11	Social insect genomes exhibit dramatic evolution in gene composition and regulation while preserving regulatory features linked to sociality. <i>Genome Research</i> , 2013, 23, 1235-1247.	2.4	205
12	RNA folding and combinatorial landscapes. <i>Physical Review E</i> , 1993, 47, 2083-2099.	0.8	202
13	Arrangements in the modular evolution of proteins. <i>Trends in Biochemical Sciences</i> , 2008, 33, 444-451.	3.7	193
14	The interface of protein structure, protein biophysics, and molecular evolution. <i>Protein Science</i> , 2012, 21, 769-785.	3.1	188
15	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, 19276-19281.	3.3	184
16	Specificity of the innate immune system and diversity of C-type lectin domain (CTL) proteins in the nematode <i>Caenorhabditis elegans</i> . <i>Immunobiology</i> , 2008, 213, 237-250.	0.8	178
17	Switching from Simple to Complex Oscillations in Calcium Signaling. <i>Biophysical Journal</i> , 2000, 79, 1188-1195.	0.2	169
18	One Billion Years of bZIP Transcription Factor Evolution: Conservation and Change in Dimerization and DNA-Binding Site Specificity. <i>Molecular Biology and Evolution</i> , 2006, 24, 827-835.	3.5	155

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19	Gene content evolution in the arthropods. <i>Genome Biology</i> , 2020, 21, 15.	3.8	150
20	Comprehensive transcriptome analysis of the highly complex <i>Pisum sativum</i> genome using next generation sequencing. <i>BMC Genomics</i> , 2011, 12, 227.	1.2	140
21	Genomic and Morphological Evidence Converge to Resolve the Enigma of Strepsiptera. <i>Current Biology</i> , 2012, 22, 1309-1313.	1.8	140
22	Genomics of Divergence along a Continuum of Parapatric Population Differentiation. <i>PLoS Genetics</i> , 2015, 11, e1004966.	1.5	135
23	How are model protein structures distributed in sequence space?. <i>Biophysical Journal</i> , 1997, 73, 2393-2403.	0.2	132
24	Mechanisms and Dynamics of Orphan Gene Emergence in Insect Genomes. <i>Genome Biology and Evolution</i> , 2013, 5, 439-455.	1.1	128
25	Computational approaches to identify leucine zippers. <i>Nucleic Acids Research</i> , 1998, 26, 2740-2746.	6.5	120
26	The evolution of domain arrangements in proteins and interaction networks. <i>Cellular and Molecular Life Sciences</i> , 2005, 62, 435-445.	2.4	120
27	Domain deletions and substitutions in the modular protein evolution. <i>FEBS Journal</i> , 2006, 273, 2037-2047.	2.2	117
28	Proteome of Hydra Nematocyst. <i>Journal of Biological Chemistry</i> , 2012, 287, 9672-9681.	1.6	95
29	Dynamics and adaptive benefits of modular protein evolution. <i>Current Opinion in Structural Biology</i> , 2013, 23, 459-466.	2.6	90
30	Back to the sea twice: identifying candidate plant genes for molecular evolution to marine life. <i>BMC Evolutionary Biology</i> , 2011, 11, 8.	3.2	88
31	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, 809-814.	3.3	85
32	Evidence of Interaction Network Evolution by Whole-Genome Duplications: A Case Study in MADS-Box Proteins. <i>Molecular Biology and Evolution</i> , 2006, 24, 670-678.	3.5	84
33	Convergent evolution of gene networks by single gene duplications in higher eukaryotes. <i>EMBO Reports</i> , 2004, 5, 274-279.	2.0	83
34	Algorithm independent properties of RNA secondary structure predictions. <i>European Biophysics Journal</i> , 1996, 25, 115-130.	1.2	79
35	Distribution of gibberellin biosynthetic genes and gibberellin production in the <i>Gibberella fujikuroi</i> species complex. <i>Phytochemistry</i> , 2005, 66, 1296-1311.	1.4	78
36	Genome-wide patterns of standing genetic variation in a marine population of three-spined sticklebacks. <i>Molecular Ecology</i> , 2013, 22, 635-649.	2.0	78

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37	Incipient de novo genes can evolve from frozen accidents that escaped rapid transcript turnover. <i>Nature Ecology and Evolution</i> , 2018, 2, 1626-1632.	3.4	74
38	The look-ahead effect of phenotypic mutations. <i>Biology Direct</i> , 2008, 3, 18.	1.9	73
39	Evaluating Characteristics of De Novo Assembly Software on 454 Transcriptome Data: A Simulation Approach. <i>PLoS ONE</i> , 2012, 7, e31410.	1.1	72
40	Evolution of Circular Permutations in Multidomain Proteins. <i>Molecular Biology and Evolution</i> , 2006, 23, 734-743.	3.5	71
41	Higher-order epistasis shapes the fitness landscape of a xenobiotic-degrading enzyme. <i>Nature Chemical Biology</i> , 2019, 15, 1120-1128.	3.9	71
42	Extensive Copy-Number Variation of Young Genes across Stickleback Populations. <i>PLoS Genetics</i> , 2014, 10, e1004830.	1.5	70
43	Host-Pathogen Coevolution: The Selective Advantage of <i>Bacillus thuringiensis</i> Virulence and Its Cry Toxin Genes. <i>PLoS Biology</i> , 2015, 13, e1002169.	2.6	69
44	The Dynamics and Evolutionary Potential of Domain Loss and Emergence. <i>Molecular Biology and Evolution</i> , 2012, 29, 787-796.	3.5	68
45	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.	0.4	68
46	Dynamics and Adaptive Benefits of Protein Domain Emergence and Arrangements during Plant Genome Evolution. <i>Genome Biology and Evolution</i> , 2012, 4, 316-329.	1.1	66
47	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.	0.6	65
48	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.	2.0	64
49	A structural model of latent evolutionary potentials underlying neutral networks in proteins. <i>HFSP Journal</i> , 2007, 1, 79-87.	2.5	61
50	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.	1.6	61
51	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.	1.2	60
52	Mechanisms of transcription factor evolution in Metazoa. <i>Nucleic Acids Research</i> , 2016, 44, 6287-6297.	6.5	60
53	Fact or fiction: updates on how protein-coding genes might emerge de novo from previously non-coding DNA. <i>F1000Research</i> , 2017, 6, 57.	0.8	60
54	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.	0.8	60

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55	Escape from Adaptive Conflict follows from weak functional trade-offs and mutational robustness. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 14888-14893.	3.3	59
56	How do new proteins arise?. Current Opinion in Structural Biology, 2010, 20, 390-396.	2.6	57
57	Comparative Analysis of Expressed Sequence Tag (EST) Libraries in the Seagrass <i>Zostera marina</i> Subjected to Temperature Stress. Marine Biotechnology, 2008, 10, 297-309.	1.1	55
58	DoMosaics: software for domain arrangement visualization and domain-centric analysis of proteins. Bioinformatics, 2014, 30, 282-283.	1.8	52
59	Transcriptome profiling of immune tissues reveals habitat-specific gene expression between lake and river sticklebacks. Molecular Ecology, 2016, 25, 943-958.	2.0	49
60	Structure and function of naturally evolved de novo proteins. Current Opinion in Structural Biology, 2021, 68, 175-183.	2.6	49
61	Conceptual data modelling for bioinformatics. Briefings in Bioinformatics, 2002, 3, 166-180.	3.2	43
62	Just how versatile are domains?. BMC Evolutionary Biology, 2008, 8, 285.	3.2	43
63	Genomic divergence between nine- and three-spined sticklebacks. BMC Genomics, 2013, 14, 756.	1.2	42
64	Perspectives on protein evolution from simple exact models. Applied Bioinformatics, 2002, 1, 121-44.	1.7	42
65	Application of constraint programming techniques for structure prediction of lattice proteins with extended alphabets. Bioinformatics, 1999, 15, 234-242.	1.8	41
66	Evolution of Protein Domain Repeats in Metazoa. Molecular Biology and Evolution, 2016, 33, 3170-3182.	3.5	41
67	Rapid motif-based prediction of circular permutations in multi-domain proteins. Bioinformatics, 2005, 21, 932-937.	1.8	40
68	How Do Genomes Create Novel Phenotypes? Insights from the Loss of the Worker Caste in Ant Social Parasites. Molecular Biology and Evolution, 2015, 32, 2919-2931.	3.5	40
69	Structural and functional characterization of a putative de novo gene in <i>Drosophila</i> . Nature Communications, 2021, 12, 1667.	5.8	40
70	DOGMA: domain-based transcriptome and proteome quality assessment. Bioinformatics, 2016, 32, 2577-2581.	1.8	39
71	The <i>goddard</i> and <i>saturn</i> genes are essential for <i>Drosophila</i> male fertility and may have arisen <i>de novo</i> . Molecular Biology and Evolution, 2017, 34, msx057.	3.5	39
72	A protein interaction atlas for the nuclear receptors: properties and quality of a hub-based dimerisation network. BMC Systems Biology, 2007, 1, 34.	3.0	38

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73	Dr. Zompo: an online data repository for <i>Zostera marina</i> and <i>Posidonia oceanica</i> ESTs. Database: the Journal of Biological Databases and Curation, 2009, 2009, bap009-bap009.	1.4	38
74	Emergence of <i>de novo</i> proteins from "dark genomic matter"™ by "grow slow and moult"™. Biochemical Society Transactions, 2015, 43, 867-873.	1.6	38
75	Rapid similarity search of proteins using alignments of domain arrangements. Bioinformatics, 2014, 30, 274-281.	1.8	37
76	Comparing Folding Codes in Simple Heteropolymer Models of Protein Evolutionary Landscape: Robustness of the Superfunnel Paradigm. Biophysical Journal, 2005, 88, 118-131.	0.2	36
77	The Rise and Fall of TRP-N, an Ancient Family of Mechanogated Ion Channels, in Metazoa. Genome Biology and Evolution, 2015, 7, 1713-1727.	1.1	36
78	The modular nature of protein evolution: domain rearrangement rates across eukaryotic life. BMC Evolutionary Biology, 2020, 20, 30.	3.2	33
79	Evolutionary divergence and limits of conserved non-coding sequence detection in plant genomes. Nucleic Acids Research, 2011, 39, 6029-6043.	6.5	32
80	Detection of orphan domains in <i>Drosophila</i> using "hydrophobic cluster analysis". Biochimie, 2015, 119, 244-253.	1.3	31
81	Origins and structural properties of novel and <i>de novo</i> protein domains during insect evolution. FEBS Journal, 2018, 285, 2605-2625.	2.2	30
82	Quantification and functional analysis of modular protein evolution in a dense phylogenetic tree. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 898-907.	1.1	29
83	Reduction/oxidation-phosphorylation control of DNA binding in the bZIP dimerization network. BMC Genomics, 2006, 7, 107.	1.2	27
84	Lifespan prolonging mechanisms and insulin upregulation without fat accumulation in long-lived reproductives of a higher termite. Communications Biology, 2022, 5, 44.	2.0	27
85	Evolutionary Dynamics on Protein Bi-stability Landscapes can Potentially Resolve Adaptive Conflicts. PLoS Computational Biology, 2012, 8, e1002659.	1.5	26
86	Robustness by intrinsically disordered C-termini and translational readthrough. Nucleic Acids Research, 2018, 46, 10184-10194.	6.5	26
87	Reconstructed evolution of insulin receptors in insects reveals duplications in early insects and cockroaches. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2018, 330, 305-311.	0.6	26
88	Stochastic Gain and Loss of Novel Transcribed Open Reading Frames in the Human Lineage. Genome Biology and Evolution, 2020, 12, 2183-2195.	1.1	26
89	TreeWiz: interactive exploration of huge trees. Bioinformatics, 2002, 18, 109-114.	1.8	25
90	High-Throughput, Lysis-Free Screening for Sulfatase Activity Using <i>Escherichia coli</i> Autodisplay in Microdroplets. ACS Synthetic Biology, 2019, 8, 2690-2700.	1.9	25

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91	The Evolution of Protein Interaction Networks in Regulatory Proteins. <i>Comparative and Functional Genomics</i> , 2004, 5, 79-84.	2.0	24
92	Evolution of novel genes in three-spined stickleback populations. <i>Heredity</i> , 2020, 125, 50-59.	1.2	24
93	Specific Gene Expression Responses to Parasite Genotypes Reveal Redundancy of Innate Immunity in Vertebrates. <i>PLoS ONE</i> , 2014, 9, e108001.	1.1	23
94	The sieve element occlusion gene family in dicotyledonous plants. <i>Plant Signaling and Behavior</i> , 2011, 6, 151-153.	1.2	22
95	Comparative analysis of lincRNA in insect species. <i>BMC Evolutionary Biology</i> , 2017, 17, 155.	3.2	22
96	The Crohn's disease susceptibility gene <i>DLC5</i> as a member of the CARD interaction network. <i>Journal of Molecular Medicine</i> , 2008, 86, 423-432.	1.7	20
97	A putative de novo evolved gene required for spermatid chromatin condensation in <i>Drosophila melanogaster</i> . <i>PLoS Genetics</i> , 2021, 17, e1009787.	1.5	20
98	Protein domain evolution is associated with reproductive diversification and adaptive radiation in the genus <i>Eucalyptus</i> . <i>New Phytologist</i> , 2015, 206, 1328-1336.	3.5	19
99	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, 307-313.	0.6	18
100	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.	2.0	18
101	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.	0.6	17
102	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.	1.1	17
103	Randomness, Structural Uniqueness, Modularity and Neutral Evolution in Sequence Space of Model Proteins. <i>Zeitschrift Fur Physikalische Chemie</i> , 2002, 216, .	1.4	16
104	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.	1.1	16
105	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.	0.6	15
106	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.	1.8	15
107	WWW access to the SYSTERS protein sequence cluster set. <i>Bioinformatics</i> , 1999, 15, 262-263.	1.8	14
108	Automated Improvement of Domain ANnotations using context analysis of domain arrangements (AIDAN). <i>Bioinformatics</i> , 2007, 23, 1834-1836.	1.8	14

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109	DOGMA: a web server for proteome and transcriptome quality assessment. <i>Nucleic Acids Research</i> , 2019, 47, W507-W510.	6.5	13
110	Climate change facilitates a parasite's host exploitation via temperature-mediated immunometabolic processes. <i>Global Change Biology</i> , 2021, 27, 94-107.	4.2	13
111	Convergent Loss of Chemoreceptors across Independent Origins of Slave-Making in Ants. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	13
112	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, 137-144.	1.0	12
113	Domain similarity based orthology detection. <i>BMC Bioinformatics</i> , 2015, 16, 154.	1.2	11
114	Hybrid Genome Assembly of a Neotropical Mutualistic Ant. <i>Genome Biology and Evolution</i> , 2019, 11, 2306-2311.	1.1	11
115	Phylogenetic profiling of protein interaction networks in eukaryotic transcription factors reveals focal proteins being ancestral to hubs. <i>Gene</i> , 2005, 347, 247-253.	1.0	10
116	Gene Coexpression Network Reveals Highly Conserved, Well-Regulated Anti-Ageing Mechanisms in Old Ant Queens. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	10
117	New Genomic Signals Underlying the Emergence of Human Proto-Genes. <i>Genes</i> , 2022, 13, 284.	1.0	10
118	Evolvability and Single-Genotype Fluctuation in Phenotypic Properties: A Simple Heteropolymer Model. <i>Biophysical Journal</i> , 2010, 98, 2487-2496.	0.2	9
119	<i>Tribolium castaneum</i> gene expression changes after <i>Paranosema whitei</i> infection. <i>Journal of Invertebrate Pathology</i> , 2018, 153, 92-98.	1.5	9
120	Evolutionary Potential of Cis-Regulatory Mutations to Cause Rapid Changes in Transcription Factor Binding. <i>Genome Biology and Evolution</i> , 2019, 11, 406-414.	1.1	9
121	A genetic variant alters the secondary structure of the lncRNA H19 and is associated with dilated cardiomyopathy. <i>RNA Biology</i> , 2021, 18, 409-415.	1.5	9
122	Heterologous expression of naturally evolved putative <i>de novo</i> proteins with chaperones. <i>Protein Science</i> , 2022, 31, .	3.1	8
123	Robustness versus evolvability: A paradigm revisited. <i>HFSP Journal</i> , 2010, 4, 105-108.	2.5	7
124	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.	0.4	7
125	A putative transcription factor inducing mobility in <i>Mycoplasma pneumoniae</i> . <i>Microbiology (United Kingdom)</i> 110784314	0.7	7
126	Comparative analyses of caste, sex, and developmental stage-specific transcriptomes in two <i>Temnothorax</i> ants. <i>Ecology and Evolution</i> , 2020, 10, 4193-4203.	0.8	6

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127	MDAT- Aligning multiple domain arrangements. BMC Bioinformatics, 2015, 16, 19.	1.2	5
128	Becoming a de novo gene. Nature Ecology and Evolution, 2019, 3, 524-525.	3.4	5
129	The Evolution of Protein Interaction Networks. Methods in Molecular Biology, 2011, 696, 273-289.	0.4	5
130	Signals: Tinkering with Domains. Science Signaling, 2010, 3, pe31.	1.6	4
131	Simple folding model for HP lattice proteins. Lecture Notes in Computer Science, 1996, , 125-136.	1.0	3
132	Random structures and evolution of biopolymers: A computational case study on RNA secondary structures. Pharmaceutica Acta Helvetiae, 1996, 71, 79-85.	1.2	3
133	Comparative genomic approaches to investigate molecular traits specific to social insects. Current Opinion in Insect Science, 2016, 16, 87-94.	2.2	3
134	Finding Common Protein Interaction Patterns Across Organisms. Evolutionary Bioinformatics, 2006, 2, 117693430600200.	0.6	2
135	A Roadmap to Domain Based Proteomics. Methods in Molecular Biology, 2019, 1851, 287-300.	0.4	2
136	Genomic and Morphological Evidence Converge to Resolve the Enigma of Strepsiptera. Current Biology, 2013, 23, 1388.	1.8	1
137	Enzyme subfunctionalization driven by regulation. EMBO Reports, 2017, 18, 1043-1045.	2.0	1
138	Random structures and evolution of biopolymers. Zeitschrift Fur Elektrotechnik Und Elektrochemie, 1994, 98, 1128-1128.	0.9	0
139	EVOLUTION OF REGULATORY NETWORKS. Complex Systems and Interdisciplinary Science, 2007, , 257-289.	0.2	0
140	The first cockroach genome and its significance for understanding development and the evolution of insect eusociality. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2018, 330, 251-253.	0.6	0
141	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.	1.5	0
142	Finding common protein interaction patterns across organisms. Evolutionary Bioinformatics, 2007, 2, 45-52.	0.6	0