

Xuhua Xia

List of Publications by Year in descending order

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155
papers

10,416
citations

87401

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60403

85
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168
all docs

168
docs citations

168
times ranked

11818
citing authors

#	ARTICLE	IF	CITATIONS
1	Inheritance of marsh spot disease resistance in cranberry common bean (<i>Phaseolus vulgaris</i> L.). <i>Crop Journal</i> , 2022, 10, 456-467.	2.3	2
2	Conservation of griseofulvin genes in the <i>gsf</i> gene cluster among fungal genomes. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	5
3	In Silico Molecular Dynamics of Griseofulvin and Its Derivatives Revealed Potential Therapeutic Applications for COVID-19. <i>International Journal of Molecular Sciences</i> , 2022, 23, 6889.	1.8	6
4	Quantitative Trait Locus Mapping of Marsh Spot Disease Resistance in Cranberry Common Bean (<i>Phaseolus vulgaris</i> L.). <i>International Journal of Molecular Sciences</i> , 2022, 23, 7639.	1.8	3
5	Domains and Functions of Spike Protein in SARS-Cov-2 in the Context of Vaccine Design. <i>Viruses</i> , 2021, 13, 109.	1.5	223
6	Marsh Spot Disease and Its Causal Factor, Manganese Deficiency in Plants: A Historical and Prospective Review. <i>Agricultural Sciences</i> , 2021, 12, 928-948.	0.2	1
7	Predicting mammalian species at risk of being infected by SARS-CoV-2 from an ACE2 perspective. <i>Scientific Reports</i> , 2021, 11, 1702.	1.6	22
8	Applications of Protein Secondary Structure Algorithms in SARS-CoV-2 Research. <i>Journal of Proteome Research</i> , 2021, 20, 1457-1463.	1.8	3
9	Does <i>Saccharomyces cerevisiae</i> Require Specific Post-Translational Silencing against Leaky Translation of <i>Hac1</i> up?. <i>Microorganisms</i> , 2021, 9, 620.	1.6	1
10	Detailed Dissection and Critical Evaluation of the Pfizer/BioNTech and Moderna mRNA Vaccines. <i>Vaccines</i> , 2021, 9, 734.	2.1	89
11	Dating the Common Ancestor from an NCBI Tree of 83688 High-Quality and Full-Length SARS-CoV-2 Genomes. <i>Viruses</i> , 2021, 13, 1790.	1.5	15
12	Post-Alignment Adjustment and Its Automation. <i>Genes</i> , 2021, 12, 1809.	1.0	1
13	RNA-Seq approach for accurate characterization of splicing efficiency of yeast introns. <i>Methods</i> , 2020, 176, 25-33.	1.9	12
14	Drug efficacy and toxicity prediction: an innovative application of transcriptomic data. <i>Cell Biology and Toxicology</i> , 2020, 36, 591-602.	2.4	4
15	Beyond Trees: Regulons and Regulatory Motif Characterization. <i>Genes</i> , 2020, 11, 995.	1.0	2
16	Improving Phylogenetic Signals of Mitochondrial Genes Using a New Method of Codon Degeneration. <i>Life</i> , 2020, 10, 171.	1.1	1
17	Editorial for the special issue "RNA-Seq: Methods and applications". <i>Methods</i> , 2020, 176, 1-3.	1.9	1
18	Major Revisions in Arthropod Phylogeny Through Improved Supermatrix, With Support for Two Possible Waves of Land Invasion by Chelicerates. <i>Evolutionary Bioinformatics</i> , 2020, 16, 117693432090373.	0.6	19

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19	Extreme Genomic CpG Deficiency in SARS-CoV-2 and Evasion of Host Antiviral Defense. <i>Molecular Biology and Evolution</i> , 2020, 37, 2699-2705.	3.5	136
20	Coronavirus genomes carry the signatures of their habitats. <i>PLoS ONE</i> , 2020, 15, e0244025.	1.1	25
21	Is there a mutation gradient along vertebrate mitochondrial genome mediated by genome replication?. <i>Mitochondrion</i> , 2019, 46, 30-40.	1.6	7
22	Unique Shineâ€Dalgarno Sequences in Cyanobacteria and Chloroplasts Reveal Evolutionary Differences in Their Translation Initiation. <i>Genome Biology and Evolution</i> , 2019, 11, 3194-3206.	1.1	10
23	Translation Control of HAC1 by Regulation of Splicing in <i>Saccharomyces cerevisiae</i> . <i>International Journal of Molecular Sciences</i> , 2019, 20, 2860.	1.8	14
24	PGT: Visualizing temporal and spatial biogeographic patterns. <i>Global Ecology and Biogeography</i> , 2019, 28, 1195-1199.	2.7	3
25	Bioinformatic Approaches for Repurposing and Repositioning Antibiotics, Antiprotozoals, and Antivirals. , 2019, , 679-700.		0
26	An improved estimation of tRNA expression to better elucidate the coevolution between tRNA abundance and codon usage in bacteria. <i>Scientific Reports</i> , 2019, 9, 3184.	1.6	28
27	DAMBE7: New and Improved Tools for Data Analysis in Molecular Biology and Evolution. <i>Molecular Biology and Evolution</i> , 2018, 35, 1550-1552.	3.5	528
28	RNA-Seq-Based Analysis Reveals Heterogeneity in Mature 16S rRNA 3â€Termini and Extended Anti-Shine-Dalgarno Motifs in Bacterial Species. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3973-3979.	0.8	4
29	Nucleotide Substitution Models and Evolutionary Distances. , 2018, , 269-314.		3
30	String Mathematics, BLAST, and FASTA. , 2018, , 1-31.		0
31	Bioinformatics and Translation Termination in Bacteria. , 2018, , 239-254.		1
32	Distance-Based Phylogenetic Methods. , 2018, , 343-379.		3
33	Maximum Likelihood in Molecular Phylogenetics. , 2018, , 381-395.		3
34	Bioinformatics and In Silico 2D Gel Electrophoresis. , 2018, , 413-420.		0
35	Sequence Alignment. , 2018, , 33-75.		0
36	Position weight matrix and Perceptron. , 2018, , 77-98.		0

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37	Transcriptomics and RNA-Seq Data Analysis. , 2018, , 113-128.		0
38	Self-Organizing Map and Other Clustering Methods in Transcriptomics. , 2018, , 129-144.		0
39	Hidden Markov Models and Protein Secondary Structure Prediction. , 2018, , 145-172.		1
40	Bioinformatics and Translation Initiation. , 2018, , 173-195.		0
41	Bioinformatics and Translation Elongation. , 2018, , 197-238.		1
42	Genomic Features: Content Sensors, Nucleotide Skew Plot, Strand Asymmetry, and DNA Methylation. , 2018, , 255-268.		1
43	Protein Substitution Model and Evolutionary Distance. , 2018, , 315-326.		0
44	Protein Isoelectric Point and Helicobacter pylori. , 2018, , 397-412.		0
45	Fundamentals of Proteomics. , 2018, , 421-436.		0
46	Gibbs sampler. , 2018, , 99-111.		0
47	Starless bias and parameter-estimation bias in the likelihood-based phylogenetic method. AIMS Genetics, 2018, 05, 212-223.	1.9	1
48	Imputing missing distances in molecular phylogenetics. PeerJ, 2018, 6, e5321.	0.9	5
49	DAMBE6: New Tools for Microbial Genomics, Phylogenetics, and Molecular Evolution. Journal of Heredity, 2017, 108, 431-437.	1.0	318
50	How Changes in Anti-SD Sequences Would Affect SD Sequences in <i>Escherichia coli</i> and <i>Bacillus subtilis</i> . G3: Genes, Genomes, Genetics, 2017, 7, 1607-1615.	0.8	23
51	The Role of +4U as an Extended Translation Termination Signal in Bacteria. Genetics, 2017, 205, 539-549.	1.2	22
52	Elucidating the 16S rRNA 3' boundaries and defining optimal SD/aSD pairing in <i>Escherichia coli</i> and <i>Bacillus subtilis</i> using RNA-Seq data. Scientific Reports, 2017, 7, 17639.	1.6	22
53	Self-Organizing Map for Characterizing Heterogeneous Nucleotide and Amino Acid Sequence Motifs. Computation, 2017, 5, 43.	1.0	18
54	Bioinformatics and Drug Discovery. Current Topics in Medicinal Chemistry, 2017, 17, 1709-1726.	1.0	128

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55	ARSDA: A New Approach for Storing, Transmitting and Analyzing Transcriptomic Data. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3839-3848.	0.8	16
56	The Evolution and Functional Diversification of the Deubiquitinating Enzyme Superfamily. <i>Genome Biology and Evolution</i> , 2017, 9, 558-573.	1.1	29
57	Deriving Transition Probabilities and Evolutionary Distances from Substitution Rate Matrix by Probability Reasoning. <i>Journal of Genetics and Genome Research</i> , 2017, 4, .	0.3	2
58	Selection preserves Ubiquitin Specific Protease 4 alternative exon skipping in therian mammals. <i>Scientific Reports</i> , 2016, 6, 20039.	1.6	24
59	PhyPA: Phylogenetic method with pairwise sequence alignment outperforms likelihood methods in phylogenetics involving highly diverged sequences. <i>Molecular Phylogenetics and Evolution</i> , 2016, 102, 331-343.	1.2	22
60	Coevolution between Stop Codon Usage and Release Factors in Bacterial Species. <i>Molecular Biology and Evolution</i> , 2016, 33, 2357-2367.	3.5	29
61	Dating the origin of the major lineages of Branchiopoda. <i>Palaeoworld</i> , 2016, 25, 303-317.	0.5	17
62	Evolution of the highly networked deubiquitinating enzymes USP4, USP15, and USP11. <i>BMC Evolutionary Biology</i> , 2015, 15, 230.	3.2	56
63	Escherichia coli and Staphylococcus phages: effect of translation initiation efficiency on differential codon adaptation mediated by virulent and temperate lifestyles. <i>Journal of General Virology</i> , 2015, 96, 1169-1179.	1.3	28
64	A Major Controversy in Codon-Anticodon Adaptation Resolved by a New Codon Usage Index. <i>Genetics</i> , 2015, 199, 573-579.	1.2	47
65	The evolution of genomic GC content undergoes a rapid reversal within the genus Plasmodium. <i>Genome</i> , 2014, 57, 507-511.	0.9	26
66	The Effect of Mutation and Selection on Codon Adaptation in Escherichia coli Bacteriophage. <i>Genetics</i> , 2014, 197, 301-315.	1.2	42
67	Differential Codon Adaptation between dsDNA and ssDNA Phages in Escherichia coli. <i>Molecular Biology and Evolution</i> , 2014, 31, 1606-1617.	3.5	39
68	Aeromonas phages encode tRNAs for their overused codons. <i>International Journal of Computational Biology and Drug Design</i> , 2014, 7, 168.	0.3	15
69	Phylogenetic Bias in the Likelihood Method Caused by Missing Data Coupled with Among-Site Rate Variation: An Analytical Approach. <i>Lecture Notes in Computer Science</i> , 2014, , 12-23.	1.0	23
70	Comparative Genomics. <i>SpringerBriefs in Genetics</i> , 2013, , .	0.1	13
71	DAMBE5: A Comprehensive Software Package for Data Analysis in Molecular Biology and Evolution. <i>Molecular Biology and Evolution</i> , 2013, 30, 1720-1728.	3.5	992
72	An Improved Implementation of Effective Number of Codons (Nc). <i>Molecular Biology and Evolution</i> , 2013, 30, 191-196.	3.5	71

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73	NeXML: Rich, Extensible, and Verifiable Representation of Comparative Data and Metadata. <i>Systematic Biology</i> , 2012, 61, 675-689.	2.7	90
74	A comparative study of codon adaptation in ssDNA and dsDNA phages. , 2012, , .		0
75	Position Weight Matrix, Gibbs Sampler, and the Associated Significance Tests in Motif Characterization and Prediction. <i>Scientifica</i> , 2012, 2012, 1-15.	0.6	55
76	DNA Replication and Strand Asymmetry in Prokaryotic and Mitochondrial Genomes. <i>Current Genomics</i> , 2012, 13, 16-27.	0.7	48
77	Rapid evolution of animal mitochondrial DNA. , 2012, , 73-82.		18
78	A distance-based least-square method for dating speciation events. <i>Molecular Phylogenetics and Evolution</i> , 2011, 59, 342-353.	1.2	37
79	Non-AUG initiation codon and downstream inframe AUG in <i>Pyrococcus Horikoshii</i> : Evaluating two hypotheses. , 2011, , .		0
80	Factors Affecting Splicing Strength of Yeast Genes. <i>Comparative and Functional Genomics</i> , 2011, 2011, 1-13.	2.0	27
81	Translation Initiation: A Regulatory Role for Poly(A) Tracts in Front of the AUG Codon in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2011, 189, 469-478.	1.2	41
82	HIV-1 Modulates the tRNA Pool to Improve Translation Efficiency. <i>Molecular Biology and Evolution</i> , 2011, 28, 1827-1834.	3.5	94
83	<i>Comparative Genomics</i> . , 2011, , 567-600.		3
84	Mural granulosa cell gene expression associated with oocyte developmental competence. <i>Journal of Ovarian Research</i> , 2010, 3, 6.	1.3	40
85	A General Model of Codon Bias Due to GC Mutational Bias. <i>PLoS ONE</i> , 2010, 5, e13431.	1.1	144
86	Assessing substitution saturation with DAMBE. , 2009, , 615-630.		340
87	Profiling neuroendocrine gene expression changes following fadrozole-induced estrogen decline in the female goldfish. <i>Physiological Genomics</i> , 2009, 38, 351-361.	1.0	29
88	Correlations between recombination rate and intron distributions along chromosomes of <i>C. elegans</i> . <i>Progress in Natural Science: Materials International</i> , 2009, 19, 517-522.	1.8	2
89	Monophyly of the ring-forming group in Diplopoda (Myriapoda, Arthropoda) based on SSU and LSU ribosomal RNA sequences. <i>Progress in Natural Science: Materials International</i> , 2009, 19, 1297-1303.	1.8	10
90	Information-theoretic indices and an approximate significance test for testing the molecular clock hypothesis with genetic distances. <i>Molecular Phylogenetics and Evolution</i> , 2009, 52, 665-676.	1.2	30

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91	Strong Eukaryotic IRESs Have Weak Secondary Structure. PLoS ONE, 2009, 4, e4136.	1.1	54
92	Defining Global Neuroendocrine Gene Expression Patterns Associated with Reproductive Seasonality in Fish. PLoS ONE, 2009, 4, e5816.	1.1	39
93	An Extensive Study of Mutation and Selection on the Wobble Nucleotide in tRNA Anticodons in Fungal Mitochondrial Genomes. Journal of Molecular Evolution, 2008, 66, 484-493.	0.8	31
94	GC skew in protein-coding genes between the leading and lagging strands in bacterial genomes: New substitution models incorporating strand bias. Journal of Theoretical Biology, 2008, 253, 508-513.	0.8	54
95	Using Generalized Procrustes Analysis (GPA) for normalization of cDNA microarray data. BMC Bioinformatics, 2008, 9, 25.	1.2	38
96	The cost of wobble translation in fungal mitochondrial genomes: integration of two traditional hypotheses. BMC Evolutionary Biology, 2008, 8, 211.	3.2	29
97	Functional insight into Maelstrom in the germline piRNA pathway: a unique domain homologous to the DnaQ-H 3' to 5' exonuclease, its lineage-specific expansion/loss and evolutionarily active site switch. Biology Direct, 2008, 3, 48.	1.9	49
98	Auto-regulation of estrogen receptor subtypes and gene expression profiling of 17 β -estradiol action in the neuroendocrine axis of male goldfish. Molecular and Cellular Endocrinology, 2008, 283, 38-48.	1.6	113
99	The goldfish (<i>Carassius auratus</i>) as a model for neuroendocrine signaling. Molecular and Cellular Endocrinology, 2008, 293, 43-56.	1.6	147
100	Effects of fluoxetine on the reproductive axis of female goldfish (<i>Carassius auratus</i>). Physiological Genomics, 2008, 35, 273-282.	1.0	124
101	Phylogenetic Analyses: A Toolbox Expanding towards Bayesian Methods. International Journal of Plant Genomics, 2008, 2008, 1-16.	2.2	7
102	Preservation of Genes Involved in Sterol Metabolism in Cholesterol Auxotrophs: Facts and Hypotheses. PLoS ONE, 2008, 3, e2883.	1.1	48
103	Bioinformatic Approach to Identify Penultimate Amino Acids Efficient for N-Terminal Methionine Excision. , 2007, , .		0
104	Molecular Phylogenetics: Mathematical Framework and Unsolved Problems. Biological and Medical Physics Series, 2007, , 169-189.	0.3	2
105	The +4G Site in Kozak Consensus Is Not Related to the Efficiency of Translation Initiation. PLoS ONE, 2007, 2, e188.	1.1	39
106	An Improved Implementation of Codon Adaptation Index. Evolutionary Bioinformatics, 2007, 3, 117693430700300.	0.6	48
107	Internal ribosomal entry site lacks secondary structure. Nature Precedings, 2007, , .	0.1	0
108	Conflict between Translation Initiation and Elongation in Vertebrate Mitochondrial Genomes. PLoS ONE, 2007, 2, e227.	1.1	24

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109	MBEToolbox 2.0: an enhanced version of a MATLAB toolbox for molecular biology and evolution. <i>Evolutionary Bioinformatics</i> , 2007, 2, 179-82.	0.6	4
110	Topological bias in distance-based phylogenetic methods: problems with over- and underestimated genetic distances. <i>Evolutionary Bioinformatics</i> , 2007, 2, 333-45.	0.6	3
111	An improved implementation of codon adaptation index. <i>Evolutionary Bioinformatics</i> , 2007, 3, 53-8.	0.6	38
112	MBEToolbox 2.0: An enhanced version of a MATLAB toolbox for Molecular Biology and Evolution. <i>Evolutionary Bioinformatics</i> , 2006, 2, 117693430600200.	0.6	3
113	Topological Bias in Distance-Based Phylogenetic Methods: Problems with Over- and Underestimated Genetic Distances. <i>Evolutionary Bioinformatics</i> , 2006, 2, 117693430600200.	0.6	6
114	Thermal Adaptation of the Small Subunit Ribosomal RNA Gene: A Comparative Study. <i>Journal of Molecular Evolution</i> , 2006, 63, 120-126.	0.8	53
115	Cytosine Usage Modulates the Correlation between CDS Length and CG Content in Prokaryotic Genomes. <i>Molecular Biology and Evolution</i> , 2006, 23, 1450-1454.	3.5	22
116	Gene expression profiling in the neuroendocrine brain of male goldfish (<i>Carassius auratus</i>) exposed to 17 β -ethinylestradiol. <i>Physiological Genomics</i> , 2006, 27, 328-336.	1.0	76
117	CODON-BASED DETECTION OF POSITIVE SELECTION CAN BE BIASED BY HETEROGENEOUS DISTRIBUTION OF POLAR AMINO ACIDS ALONG PROTEIN SEQUENCES. , 2006, , .		13
118	Codon-based detection of positive selection can be biased by heterogeneous distribution of polar amino acids along protein sequences. <i>Computational Systems Bioinformatics / Life Sciences Society Computational Systems Bioinformatics Conference</i> , 2006, , 335-40.	0.4	3
119	MBEToolbox: a MATLAB toolbox for sequence data analysis in molecular biology and evolution. <i>BMC Bioinformatics</i> , 2005, 6, 64.	1.2	41
120	Genetic Variation in Clones of <i>Pseudomonas pseudoalcaligenes</i> After Ten Months of Selection in Different Thermal Environments in the Laboratory. <i>Current Microbiology</i> , 2005, 50, 238-245.	1.0	3
121	Differential selection and mutation between dsDNA and ssDNA phages shape the evolution of their genomic AT percentage. , 2005, 6, 20.		30
122	Mutation and selection on the anticodon of tRNA genes in vertebrate mitochondrial genomes. <i>Gene</i> , 2005, 345, 13-20.	1.0	66
123	Genomic Adaptation to Acidic Environment: Evidence from <i>Helicobacter pylori</i> . <i>American Naturalist</i> , 2005, 166, 776-784.	1.0	18
124	An evolutionary and functional analysis of FoxL2 in rainbow trout gonad differentiation. <i>Journal of Molecular Endocrinology</i> , 2004, 33, 705-715.	1.1	178
125	Morphological Changes of <i>Pseudomonas pseudoalcaligenes</i> in Response to Temperature Selection. <i>Current Microbiology</i> , 2003, 46, 120-123.	1.0	34
126	Effects of GC Content and Mutational Pressure on the Lengths of Exons and Coding Sequences. <i>Journal of Molecular Evolution</i> , 2003, 56, 362-370.	0.8	44

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127	DNA Methylation and Mycoplasma Genomes. <i>Journal of Molecular Evolution</i> , 2003, 57, S21-S28.	0.8	24
128	Changes in growth parameters of <i>Pseudomonas pseudoalcaligenes</i> after ten months culturing at increasing temperature. <i>FEMS Microbiology Ecology</i> , 2003, 45, 127-134.	1.3	12
129	An index of substitution saturation and its application. <i>Molecular Phylogenetics and Evolution</i> , 2003, 26, 1-7.	1.2	1,315
130	18S Ribosomal RNA and Tetrapod Phylogeny. <i>Systematic Biology</i> , 2003, 52, 283-295.	2.7	85
131	Structure, evolution and expression of the FOXL2 transcription unit. <i>Cytogenetic and Genome Research</i> , 2003, 101, 206-211.	0.6	125
132	Evolution and expression of FOXL2. <i>Journal of Medical Genetics</i> , 2002, 39, 916-921.	1.5	247
133	Protein Structure, Neighbor Effect, and a New Index of Amino Acid Dissimilarities. <i>Molecular Biology and Evolution</i> , 2002, 19, 58-67.	3.5	60
134	Genomic Changes in Nucleotide and Dinucleotide Frequencies in <i>Pasteurella multocida</i> Cultured Under High Temperature. <i>Genetics</i> , 2002, 161, 1385-1394.	1.2	28
135	The genus <i>Schevoderia</i> Borchmann: Phylogeny and historical biogeography, with description of a new species (Coleoptera: Tenebrionidae: Lagriinae). <i>Oriental Insects</i> , 2001, 35, 3-27.	0.1	0
136	DAMBE: Software Package for Data Analysis in Molecular Biology and Evolution. , 2001, 92, 371-373.		1,966
137	Phylogenetic Relationship Among Horseshoe Crab Species: Effect of Substitution Models on Phylogenetic Analyses. <i>Systematic Biology</i> , 2000, 49, 87-100.	2.7	58
138	What Amino Acid Properties Affect Protein Evolution?. <i>Journal of Molecular Evolution</i> , 1998, 47, 557-564.	0.8	98
139	The rate heterogeneity of nonsynonymous substitutions in mammalian mitochondrial genes. <i>Molecular Biology and Evolution</i> , 1998, 15, 336-344.	3.5	58
140	How Optimized Is the Translational Machinery in <i>Escherichia coli</i> , <i>Salmonella typhimurium</i> and <i>Saccharomyces cerevisiae</i> ?. <i>Genetics</i> , 1998, 149, 37-44.	1.2	81
141	On transition bias in mitochondrial genes of pocket gophers. <i>Journal of Molecular Evolution</i> , 1996, 43, 32-40.	0.8	41
142	Maximizing Transcription Efficiency Causes Codon Usage Bias. <i>Genetics</i> , 1996, 144, 1309-1320.	1.2	112
143	Revisiting Hamilton's Rule. <i>American Naturalist</i> , 1995, 145, 483-492.	1.0	1
144	Mating system of the meadow vole, <i>Microtus pennsylvanicus</i> . <i>Behavioral Ecology</i> , 1993, 4, 83-89.	1.0	144

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145	A Full Sibling is not as Valuable as an Offspring: On Hamilton's Rule. <i>American Naturalist</i> , 1993, 142, 174-185.	1.0	0
146	Uncertainty of Paternity Can Select Against Paternal Care. <i>American Naturalist</i> , 1992, 139, 1126-1129.	1.0	73
147	Measuring Temporal Variability of Population Density: A Critique. <i>American Naturalist</i> , 1992, 140, 883-892.	1.0	18
148	Relationships among reproductive status, nutritional status, and food characteristics in a natural population of <i>Peromyscus maniculatus</i> . <i>Canadian Journal of Zoology</i> , 1991, 69, 555-559.	0.4	16
149	Genetic evidence of promiscuity in <i>Peromyscus leucopus</i> . <i>Behavioral Ecology and Sociobiology</i> , 1991, 28, 171.	0.6	37
150	Infestations of Wild <i>Peromyscus leucopus</i> by Bot Fly Larvae. <i>Journal of Mammalogy</i> , 1990, 71, 255-258.	0.6	8
151	Dispersion of adult male <i>Peromyscus leucopus</i> in relation to female reproductive status. <i>Canadian Journal of Zoology</i> , 1989, 67, 1047-1052.	0.4	6
152	Paternal behavior by <i>Peromyscus leucopus</i> in enclosures. <i>Canadian Journal of Zoology</i> , 1988, 66, 1184-1187.	0.4	38
153	Offspring Recognition by Male <i>Peromyscus maniculatus</i> . <i>Journal of Mammalogy</i> , 1988, 69, 811-813.	0.6	3
154	Morphological variation in deer mice in relation to sex and habitat. <i>Canadian Journal of Zoology</i> , 1987, 65, 527-533.	0.4	7
155	Sex-related dispersion of breeding deer mice in the Kananaskis Valley, Alberta. <i>Canadian Journal of Zoology</i> , 1986, 64, 933-936.	0.4	5