Xuhua Xia

List of Publications by Year
in descending order

155 papers	10,416 citations	76326 40 h-index	53230 85 g-index
168 all docs	168 docs citations	168 times ranked	10695 citing authors

#	Article	IF	Citations
1	DAMBE: Software Package for Data Analysis in Molecular Biology and Evolution. , 2001, 92, 371-373.		1,966
2	An index of substitution saturation and its application. Molecular Phylogenetics and Evolution, 2003, 26, 1-7.	2.7	1,315
3	DAMBE5: A Comprehensive Software Package for Data Analysis in Molecular Biology and Evolution. Molecular Biology and Evolution, 2013, 30, 1720-1728.	8.9	992
4	DAMBE7: New and Improved Tools for Data Analysis in Molecular Biology and Evolution. Molecular Biology and Evolution, 2018, 35, 1550-1552.	8.9	528
5	Assessing substitution saturation with DAMBE. , 2009, , 615-630.		340
6	DAMBE6: New Tools for Microbial Genomics, Phylogenetics, and Molecular Evolution. Journal of Heredity, 2017, 108, 431-437.	2.4	318
7	Evolution and expression of FOXL2. Journal of Medical Genetics, 2002, 39, 916-921.	3.2	247
8	Domains and Functions of Spike Protein in SARS-Cov-2 in the Context of Vaccine Design. Viruses, 2021, 13, 109.	3.3	223
9	An evolutionary and functional analysis of FoxL2 in rainbow trout gonad differentiation. Journal of Molecular Endocrinology, 2004, 33, 705-715.	2.5	178
10	The goldfish (Carassius auratus) as a model for neuroendocrine signaling. Molecular and Cellular Endocrinology, 2008, 293, 43-56.	3.2	147
11	Mating system of the meadow vole, *Microtus pennsylvanicus*. Behavioral Ecology, 1993, 4, 83-89.	2.2	144
12	A General Model of Codon Bias Due to GC Mutational Bias. PLoS ONE, 2010, 5, e13431.	2.5	144
13	Extreme Genomic CpG Deficiency in SARS-CoV-2 and Evasion of Host Antiviral Defense. Molecular Biology and Evolution, 2020, 37, 2699-2705.	8.9	136
14	Bioinformatics and Drug Discovery. Current Topics in Medicinal Chemistry, 2017, 17, 1709-1726.	2.1	128
15	Structure, evolution and expression of the FOXL2 transcription unit. Cytogenetic and Genome Research, 2003, 101, 206-211.	1.1	125
16	Effects of fluoxetine on the reproductive axis of female goldfish (*Carassius auratus*). Physiological Genomics, 2008, 35, 273-282.	2.3	124
17	Auto-regulation of estrogen receptor subtypes and gene expression profiling of 17β-estradiol action in the neuroendocrine axis of male goldfish. Molecular and Cellular Endocrinology, 2008, 283, 38-48.	3.2	113
18	Maximizing Transcription Efficiency Causes Codon Usage Bias. Genetics, 1996, 144, 1309-1320.	2.9	112

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19	What Amino Acid Properties Affect Protein Evolution?. Journal of Molecular Evolution, 1998, 47, 557-564.	1.8	98
20	HIV-1 Modulates the tRNA Pool to Improve Translation Efficiency. Molecular Biology and Evolution, 2011, 28, 1827-1834.	8.9	94
21	NeXML: Rich, Extensible, and Verifiable Representation of Comparative Data and Metadata. Systematic Biology, 2012, 61, 675-689.	5.6	90
22	Detailed Dissection and Critical Evaluation of the Pfizer/BioNTech and Moderna mRNA Vaccines. Vaccines, 2021, 9, 734.	4.4	89
23	18S Ribosomal RNA and Tetrapod Phylogeny. Systematic Biology, 2003, 52, 283-295.	5.6	85
24	How Optimized Is the Translational Machinery in Escherichia coli, Salmonella typhimurium and Saccharomyces cerevisiae?. Genetics, 1998, 149, 37-44.	2.9	81
25	Gene expression profiling in the neuroendocrine brain of male goldfish (<i>Carassius auratus</i>) exposed to 17Î±-ethinylestradiol. Physiological Genomics, 2006, 27, 328-336.	2.3	76
26	Uncertainty of Paternity Can Select Against Paternal Care. American Naturalist, 1992, 139, 1126-1129.	2.1	73
27	An Improved Implementation of Effective Number of Codons (Nc). Molecular Biology and Evolution, 2013, 30, 191-196.	8.9	71
28	Mutation and selection on the anticodon of tRNA genes in vertebrate mitochondrial genomes. Gene, 2005, 345, 13-20.	2.2	66
29	Protein Structure, Neighbor Effect, and a New Index of Amino Acid Dissimilarities. Molecular Biology and Evolution, 2002, 19, 58-67.	8.9	60
30	The rate heterogeneity of nonsynonymous substitutions in mammalian mitochondrial genes. Molecular Biology and Evolution, 1998, 15, 336-344.	8.9	58
31	Phylogenetic Relationship Among Horseshoe Crab Species: Effect of Substitution Models on Phylogenetic Analyses. Systematic Biology, 2000, 49, 87-100.	5.6	58
32	Evolution of the highly networked deubiquitinating enzymes USP4, USP15, and USP11. BMC Evolutionary Biology, 2015, 15, 230.	3.2	56
33	Position Weight Matrix, Gibbs Sampler, and the Associated Significance Tests in Motif Characterization and Prediction. Scientifica, 2012, 2012, 1-15.	1.7	55
34	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.	1.7	54
35	Strong Eukaryotic IRESs Have Weak Secondary Structure. PLoS ONE, 2009, 4, e4136.	2.5	54
36	Thermal Adaptation of the Small Subunit Ribosomal RNA Gene: A Comparative Study. Journal of Molecular Evolution, 2006, 63, 120-126.	1.8	53

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37	Functional insight into Maelstrom in the germline piRNA pathway: a unique domain homologous to the DnaQ-H 3'â€"5' exonuclease, its lineage-specific expansion/loss and evolutionarily active site switch. Biology Direct, 2008, 3, 48.	4.6	49
38	An Improved Implementation of Codon Adaptation Index. Evolutionary Bioinformatics, 2007, 3, 117693430700300.	1.2	48
39	DNA Replication and Strand Asymmetry in Prokaryotic and Mitochondrial Genomes. Current Genomics, 2012, 13, 16-27.	1.6	48
40	Preservation of Genes Involved in Sterol Metabolism in Cholesterol Auxotrophs: Facts and Hypotheses. PLoS ONE, 2008, 3, e2883.	2.5	48
41	A Major Controversy in Codon-Anticodon Adaptation Resolved by a New Codon Usage Index. Genetics, 2015, 199, 573-579.	2.9	47
42	Effects of GC Content and Mutational Pressure on the Lengths of Exons and Coding Sequences. Journal of Molecular Evolution, 2003, 56, 362-370.	1.8	44
43	The Effect of Mutation and Selection on Codon Adaptation in Escherichia coli Bacteriophage. Genetics, 2014, 197, 301-315.	2.9	42
44	On transition bias in mitochondrial genes of pocket gophers. Journal of Molecular Evolution, 1996, 43, 32-40.	1.8	41
45	MBEToolbox: a Matlab toolbox for sequence data analysis in molecular biology and evolution. BMC Bioinformatics, 2005, 6, 64.	2.6	41
46	Translation Initiation: A Regulatory Role for Poly(A) Tracts in Front of the AUG Codon in <i>Saccharomyces cerevisiae</i>. Genetics, 2011, 189, 469-478.	2.9	41
47	Mural granulosa cell gene expression associated with oocyte developmental competence. Journal of Ovarian Research, 2010, 3, 6.	3.0	40
48	The +4G Site in Kozak Consensus Is Not Related to the Efficiency of Translation Initiation. PLoS ONE, 2007, 2, e188.	2.5	39
49	Differential Codon Adaptation between dsDNA and ssDNA Phages in Escherichia coli. Molecular Biology and Evolution, 2014, 31, 1606-1617.	8.9	39
50	Defining Global Neuroendocrine Gene Expression Patterns Associated with Reproductive Seasonality in Fish. PLoS ONE, 2009, 4, e5816.	2.5	39
51	Paternal behavior by <i>Peromyscus leucopus</i> in enclosures. Canadian Journal of Zoology, 1988, 66, 1184-1187.	1.0	38
52	Using Generalized Procrustes Analysis (GPA) for normalization of cDNA microarray data. BMC Bioinformatics, 2008, 9, 25.	2.6	38
53	An improved implementation of codon adaptation index. Evolutionary Bioinformatics, 2007, 3, 53-8.	1.2	38
54	Genetic evidence of promiscuity in Peromyscus leucopus. Behavioral Ecology and Sociobiology, 1991, 28, 171.	1.4	37

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55	A distance-based least-square method for dating speciation events. Molecular Phylogenetics and Evolution, 2011, 59, 342-353.	2.7	37
56	Morphological Changes of Pseudomonas pseudoalcaligenes in Response to Temperature Selection. Current Microbiology, 2003, 46, 120-123.	2.2	34
57	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.	1.8	31
58	Differential selection and mutation between dsDNA and ssDNA phages shape the evolution of their genomic AT percentage. , 2005, 6, 20.		30
59	Information-theoretic indices and an approximate significance test for testing the molecular clock hypothesis with genetic distances. Molecular Phylogenetics and Evolution, 2009, 52, 665-676.	2.7	30
60	The cost of wobble translation in fungal mitochondrial genomes: integration of two traditional hypotheses. BMC Evolutionary Biology, 2008, 8, 211.	3.2	29
61	Profiling neuroendocrine gene expression changes following fadrozole-induced estrogen decline in the female goldfish. Physiological Genomics, 2009, 38, 351-361.	2.3	29
62	Coevolution between Stop Codon Usage and Release Factors in Bacterial Species. Molecular Biology and Evolution, 2016, 33, 2357-2367.	8.9	29
63	The Evolution and Functional Diversification of the Deubiquitinating Enzyme Superfamily. Genome Biology and Evolution, 2017, 9, 558-573.	2.5	29
64	Escherichia coli and Staphylococcus phages: effect of translation initiation efficiency on differential codon adaptation mediated by virulent and temperate lifestyles. Journal of General Virology, 2015, 96, 1169-1179.	2.9	28
65	An improved estimation of tRNA expression to better elucidate the coevolution between tRNA abundance and codon usage in bacteria. Scientific Reports, 2019, 9, 3184.	3.3	28
66	Genomic Changes in Nucleotide and Dinucleotide Frequencies in *Pasteurella multocida* Cultured Under High Temperature. Genetics, 2002, 161, 1385-1394.	2.9	28
67	Factors Affecting Splicing Strength of Yeast Genes. Comparative and Functional Genomics, 2011, 2011, 1-13.	2.0	27
68	The evolution of genomic GC content undergoes a rapid reversal within the genus Plasmodium. Genome, 2014, 57, 507-511.	2.0	26
69	Coronavirus genomes carry the signatures of their habitats. PLoS ONE, 2020, 15, e0244025.	2.5	25
70	DNA Methylation and Mycoplasma Genomes. Journal of Molecular Evolution, 2003, 57, S21-S28.	1.8	24
71	Selection preserves Ubiquitin Specific Protease 4 alternative exon skipping in therian mammals. Scientific Reports, 2016, 6, 20039.	3.3	24
72	Conflict between Translation Initiation and Elongation in Vertebrate Mitochondrial Genomes. PLoS ONE, 2007, 2, e227.	2.5	24

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73	How Changes in Anti-SD Sequences Would Affect SD Sequences in *Escherichia coli* and *Bacillus subtilis*. G3: Genes, Genomes, Genetics, 2017, 7, 1607-1615.	1.8	23
74	Phylogenetic Bias in the Likelihood Method Caused by Missing Data Coupled with Among-Site Rate Variation: An Analytical Approach. Lecture Notes in Computer Science, 2014, , 12-23.	1.3	23
75	Cytosine Usage Modulates the Correlation between CDS Length and CG Content in Prokaryotic Genomes. Molecular Biology and Evolution, 2006, 23, 1450-1454.	8.9	22
76	PhyPA: Phylogenetic method with pairwise sequence alignment outperforms likelihood methods in phylogenetics involving highly diverged sequences. Molecular Phylogenetics and Evolution, 2016, 102, 331-343.	2.7	22
77	The Role of +4U as an Extended Translation Termination Signal in Bacteria. Genetics, 2017, 205, 539-549.	2.9	22
78	Elucidating the 16S rRNA 3′ boundaries and defining optimal SD/aSD pairing in Escherichia coli and Bacillus subtilis using RNA-Seq data. Scientific Reports, 2017, 7, 17639.	3.3	22
79	Predicting mammalian species at risk of being infected by SARS-CoV-2 from an ACE2 perspective. Scientific Reports, 2021, 11, 1702.	3.3	22
80	Major Revisions in Arthropod Phylogeny Through Improved Supermatrix, With Support for Two Possible Waves of Land Invasion by Chelicerates. Evolutionary Bioinformatics, 2020, 16, 117693432090373.	1.2	19
81	Measuring Temporal Variability of Population Density: A Critique. American Naturalist, 1992, 140, 883-892.	2.1	18
82	Genomic Adaptation to Acidic Environment: Evidence fromHelicobacter pylori. American Naturalist, 2005, 166, 776-784.	2.1	18
83	Self-Organizing Map for Characterizing Heterogeneous Nucleotide and Amino Acid Sequence Motifs. Computation, 2017, 5, 43.	2.0	18
84	Rapid evolution of animal mitochondrial DNA. , 2012, , 73-82.		18
85	Dating the origin of the major lineages of Branchiopoda. Palaeoworld, 2016, 25, 303-317.	1.1	17
86	Relationships among reproductive status, nutritional status, and food characteristics in a natural population of *Peromyscus maniculatus*. Canadian Journal of Zoology, 1991, 69, 555-559.	1.0	16
87	ARSDA: A New Approach for Storing, Transmitting and Analyzing Transcriptomic Data. G3: Genes, Genomes, Genetics, 2017, 7, 3839-3848.	1.8	16
88	Aeromonas phages encode tRNAs for their overused codons. International Journal of Computational Biology and Drug Design, 2014, 7, 168.	0.3	15
89	Dating the Common Ancestor from an NCBI Tree of 83688 High-Quality and Full-Length SARS-CoV-2 Genomes. Viruses, 2021, 13, 1790.	3.3	15
90	Translation Control of HAC1 by Regulation of Splicing in Saccharomyces cerevisiae. International Journal of Molecular Sciences, 2019, 20, 2860.	4.1	14

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91	Comparative Genomics. SpringerBriefs in Genetics, 2013, , .	0.1	13
92	CODON-BASED DETECTION OF POSITIVE SELECTION CAN BE BIASED BY HETEROGENEOUS DISTRIBUTION OF POLAR AMINO ACIDS ALONG PROTEIN SEQUENCES. , 2006, , .		13
93	Changes in growth parameters of Pseudomonas pseudoalcaligenes after ten months culturing at increasing temperature. FEMS Microbiology Ecology, 2003, 45, 127-134.	2.7	12
94	RNA-Seq approach for accurate characterization of splicing efficiency of yeast introns. Methods, 2020, 176, 25-33.	3.8	12
95	Monophyly of the ring-forming group in Diplopoda (Myriapoda, Arthropoda) based on SSU and LSU ribosomal RNA sequences. Progress in Natural Science: Materials International, 2009, 19, 1297-1303.	4.4	10
96	Unique Shine–Dalgarno Sequences in Cyanobacteria and Chloroplasts Reveal Evolutionary Differences in Their Translation Initiation. Genome Biology and Evolution, 2019, 11, 3194-3206.	2.5	10
97	Infestations of Wild Peromyscus leucopus by Bot Fly Larvae. Journal of Mammalogy, 1990, 71, 255-258.	1.3	8
98	Morphological variation in deer mice in relation to sex and habitat. Canadian Journal of Zoology, 1987, 65, 527-533.	1.0	7
99	Phylogenetic Analyses: A Toolbox Expanding towards Bayesian Methods. International Journal of Plant Genomics, 2008, 2008, 1-16.	2.2	7
100	Is there a mutation gradient along vertebrate mitochondrial genome mediated by genome replication?. Mitochondrion, 2019, 46, 30-40.	3.4	7
101	Dispersion of adult male Peromyscus leucopus in relation to female reproductive status. Canadian Journal of Zoology, 1989, 67, 1047-1052.	1.0	6
102	Topological Bias in Distance-Based Phylogenetic Methods: Problems with Over- and Underestimated Genetic Distances. Evolutionary Bioinformatics, 2006, 2, 117693430600200.	1.2	6
103	In Silico Molecular Dynamics of Griseofulvin and Its Derivatives Revealed Potential Therapeutic Applications for COVID-19. International Journal of Molecular Sciences, 2022, 23, 6889.	4.1	6
104	Sex-related dispersion of breeding deer mice in the Kananaskis Valley, Alberta. Canadian Journal of Zoology, 1986, 64, 933-936.	1.0	5
105	Imputing missing distances in molecular phylogenetics. PeerJ, 2018, 6, e5321.	2.0	5
106	Conservation of griseofulvin genes in the<i>gsf</i>gene cluster among fungal genomes. G3: Genes, Genomes, Genetics, 2022, 12, .	1.8	5
107	RNA-Seq-Based Analysis Reveals Heterogeneity in Mature 16S rRNA 3â€² Termini and Extended Anti-Shine-Dalgarno Motifs in Bacterial Species. G3: Genes, Genomes, Genetics, 2018, 8, 3973-3979.	1.8	4
108	Drug efficacy and toxicity prediction: an innovative application of transcriptomic data. Cell Biology and Toxicology, 2020, 36, 591-602.	5.3	4

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109	MBEToolbox 2.0: an enhanced version of a MATLAB toolbox for molecular biology and evolution. Evolutionary Bioinformatics, 2007, 2, 179-82.	1.2	4
110	Offspring Recognition by Male Peromyscus maniculatus. Journal of Mammalogy, 1988, 69, 811-813.	1.3	3
111	Genetic Variation in Clones of Pseudomonas pseudoalcaligenes After Ten Months of Selection in Different Thermal Environments in the Laboratory. Current Microbiology, 2005, 50, 238-245.	2.2	3
112	MBEToolbox 2.0: An enhanced version of a MATLAB toolbox for Molecular Biology and Evolution. Evolutionary Bioinformatics, 2006, 2, 117693430600200.	1.2	3
113	Nucleotide Substitution Models and Evolutionary Distances. , 2018, , 269-314.		3
114	Distance-Based Phylogenetic Methods. , 2018, , 343-379.		3
115	Maximum Likelihood in Molecular Phylogenetics. , 2018, , 381-395.		3
116	PGT: Visualizing temporal and spatial biogeographic patterns. Global Ecology and Biogeography, 2019, 28, 1195-1199.	5.8	3
117	Applications of Protein Secondary Structure Algorithms in SARS-CoV-2 Research. Journal of Proteome Research, 2021, 20, 1457-1463.	3.7	3
118	Comparative Genomics. , 2011, , 567-600.		3
119	Topological bias in distance-based phylogenetic methods: problems with over- and underestimated genetic distances. Evolutionary Bioinformatics, 2007, 2, 333-45.	1.2	3
120	Codon-based detection of positive selection can be biased by heterogeneous distribution of polar amino acids along protein sequences. Computational Systems Bioinformatics / Life Sciences Society Computational Systems Bioinformatics Conference, 2006, , 335-40.	0.4	3
121	Quantitative Trait Locus Mapping of Marsh Spot Disease Resistance in Cranberry Common Bean (Phaseolus vulgaris L.). International Journal of Molecular Sciences, 2022, 23, 7639.	4.1	3
122	Molecular Phylogenetics: Mathematical Framework and Unsolved Problems. Biological and Medical Physics Series, 2007, , 169-189.	0.4	2
123	Correlations between recombination rate and intron distributions along chromosomes of C. elegans. Progress in Natural Science: Materials International, 2009, 19, 517-522.	4.4	2
124	Beyond Trees: Regulons and Regulatory Motif Characterization. Genes, 2020, 11, 995.	2.4	2
125	Inheritance of marsh spot disease resistance in cranberry common bean (Phaseolus vulgaris L.). Crop Journal, 2022, 10, 456-467.	5.2	2
126	Deriving Transition Probabilities and Evolutionary Distances from Substitution Rate Matrix by Probability Reasoning. Journal of Genetics and Genome Research, 2017, 4, .	0.3	2

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127	Bioinformatics and Translation Termination in Bacteria. , 2018, , 239-254.		1
128	Hidden Markov Models and Protein Secondary Structure Prediction. , 2018, , 145-172.		1
129	Bioinformatics and Translation Elongation. , 2018, , 197-238.		1
130	Genomic Features: Content Sensors, Nucleotide Skew Plot, Strand Asymmetry, and DNA Methylation. , 2018, , 255-268.		1
131	Improving Phylogenetic Signals of Mitochondrial Genes Using a New Method of Codon Degeneration. Life, 2020, 10, 171.	2.4	1
132	Editorial for the special issue â€œRNA-Seq: Methods and applicationsâ€• Methods, 2020, 176, 1-3.	3.8	1
133	Marsh Spot Disease and Its Causal Factor, Manganese Deficiency in Plants: A Historical and Prospective Review. Agricultural Sciences, 2021, 12, 928-948.	0.3	1
134	Does Saccharomyces cerevisiae Require Specific Post-Translational Silencing against Leaky Translation of Hac1up?. Microorganisms, 2021, 9, 620.	3.6	1
135	Starless bias and parameter-estimation bias in the likelihood-based phylogenetic method. AIMS Genetics, 2018, 05, 212-223.	1.9	1
136	Revisiting Hamilton's Rule. American Naturalist, 1995, 145, 483-492.	2.1	1
137	Post-Alignment Adjustment and Its Automation. Genes, 2021, 12, 1809.	2.4	1
138	A Full Sibling is not as Valuable as an Offspring: On Hamilton's Rule. American Naturalist, 1993, 142, 174-185.	2.1	0
139	The genus<i>Schevodera</i>Borchmann: Phylogeny and historical biogeography, with description of a new species (Coleoptera: Tenebrionidae: Lagriinae). Oriental Insects, 2001, 35, 3-27.	0.3	0
140	Bioinformatic Approach to Identify Penultimate Amino Acids Efficient for N-Terminal Methionine Excision. , 2007, , .		0
141	Internal ribosomal entry site lacks secondary structure. Nature Precedings, 2007, , .	0.1	0
142	Non-AUG initiation codon and downstream inframe AUG in Pyrococcus Horikoshii: Evaluating two hypotheses. , 2011, , .		0
143	A comparative study of codon adaptation in ssDNA and dsDNA phages. , 2012, , .		0
144	String Mathematics, BLAST, and FASTA. , 2018, , 1-31.		0

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145	Bioinformatics and In Silico 2D Gel Electrophoresis. , 2018, , 413-420.		0
146	Sequence Alignment. , 2018, , 33-75.		0
147	Position weight matrix and Perceptron. , 2018, , 77-98.		0
148	Transcriptomics and RNA-Seq Data Analysis. , 2018, , 113-128.		0
149	Self-Organizing Map and Other Clustering Methods in Transcriptomics. , 2018, , 129-144.		0
150	Bioinformatics and Translation Initiation. , 2018, , 173-195.		0
151	Protein Substitution Model and Evolutionary Distance. , 2018, , 315-326.		0
152	Protein Isoelectric Point and Helicobacter pylori. , 2018, , 397-412.		0
153	Fundamentals of Proteomics. , 2018, , 421-436.		0
154	Gibbs sampler. , 2018, , 99-111.		0
155	Bioinformatic Approaches for Repurposing and Repositioning Antibiotics, Antiprotozoals, and Antivirals. , 2019, , 679-700.		0