

Xuhua Xia

List of Publications by Year in descending order

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155
papers

10,416
citations

76196

40
h-index

53109

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.	1.2	1,315
3	DAMBE5: A Comprehensive Software Package for Data Analysis in Molecular Biology and Evolution. Molecular Biology and Evolution, 2013, 30, 1720-1728.	3.5	992
4	DAMBE7: New and Improved Tools for Data Analysis in Molecular Biology and Evolution. Molecular Biology and Evolution, 2018, 35, 1550-1552.	3.5	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.	1.0	318
7	Evolution and expression of FOXL2. Journal of Medical Genetics, 2002, 39, 916-921.	1.5	247
8	Domains and Functions of Spike Protein in SARS-Cov-2 in the Context of Vaccine Design. Viruses, 2021, 13, 109.	1.5	223
9	An evolutionary and functional analysis of FoxL2 in rainbow trout gonad differentiation. Journal of Molecular Endocrinology, 2004, 33, 705-715.	1.1	178
10	The goldfish (<i>Carassius auratus</i>) as a model for neuroendocrine signaling. Molecular and Cellular Endocrinology, 2008, 293, 43-56.	1.6	147
11	Mating system of the meadow vole, <i>Microtus pennsylvanicus</i> . Behavioral Ecology, 1993, 4, 83-89.	1.0	144
12	A General Model of Codon Bias Due to GC Mutational Bias. PLoS ONE, 2010, 5, e13431.	1.1	144
13	Extreme Genomic CpG Deficiency in SARS-CoV-2 and Evasion of Host Antiviral Defense. Molecular Biology and Evolution, 2020, 37, 2699-2705.	3.5	136
14	Bioinformatics and Drug Discovery. Current Topics in Medicinal Chemistry, 2017, 17, 1709-1726.	1.0	128
15	Structure, evolution and expression of the FOXL2 transcription unit. Cytogenetic and Genome Research, 2003, 101, 206-211.	0.6	125
16	Effects of fluoxetine on the reproductive axis of female goldfish (<i>Carassius auratus</i>). Physiological Genomics, 2008, 35, 273-282.	1.0	124
17	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
18	Maximizing Transcription Efficiency Causes Codon Usage Bias. Genetics, 1996, 144, 1309-1320.	1.2	112

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19	What Amino Acid Properties Affect Protein Evolution?. <i>Journal of Molecular Evolution</i> , 1998, 47, 557-564.	0.8	98
20	HIV-1 Modulates the tRNA Pool to Improve Translation Efficiency. <i>Molecular Biology and Evolution</i> , 2011, 28, 1827-1834.	3.5	94
21	NeXML: Rich, Extensible, and Verifiable Representation of Comparative Data and Metadata. <i>Systematic Biology</i> , 2012, 61, 675-689.	2.7	90
22	Detailed Dissection and Critical Evaluation of the Pfizer/BioNTech and Moderna mRNA Vaccines. <i>Vaccines</i> , 2021, 9, 734.	2.1	89
23	18S Ribosomal RNA and Tetrapod Phylogeny. <i>Systematic Biology</i> , 2003, 52, 283-295.	2.7	85
24	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
25	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
26	Uncertainty of Paternity Can Select Against Paternal Care. <i>American Naturalist</i> , 1992, 139, 1126-1129.	1.0	73
27	An Improved Implementation of Effective Number of Codons (Nc). <i>Molecular Biology and Evolution</i> , 2013, 30, 191-196.	3.5	71
28	Mutation and selection on the anticodon of tRNA genes in vertebrate mitochondrial genomes. <i>Gene</i> , 2005, 345, 13-20.	1.0	66
29	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
30	The rate heterogeneity of nonsynonymous substitutions in mammalian mitochondrial genes. <i>Molecular Biology and Evolution</i> , 1998, 15, 336-344.	3.5	58
31	Phylogenetic Relationship Among Horseshoe Crab Species: Effect of Substitution Models on Phylogenetic Analyses. <i>Systematic Biology</i> , 2000, 49, 87-100.	2.7	58
32	Evolution of the highly networked deubiquitinating enzymes USP4, USP15, and USP11. <i>BMC Evolutionary Biology</i> , 2015, 15, 230.	3.2	56
33	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
34	GC skew in protein-coding genes between the leading and lagging strands in bacterial genomes: New substitution models incorporating strand bias. <i>Journal of Theoretical Biology</i> , 2008, 253, 508-513.	0.8	54
35	Strong Eukaryotic IRESs Have Weak Secondary Structure. <i>PLoS ONE</i> , 2009, 4, e4136.	1.1	54
36	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

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37	Functional insight into Maelstrom in the germline piRNA pathway: a unique domain homologous to the DnaQ-H 3'→5' exonuclease, its lineage-specific expansion/loss and evolutionarily active site switch. <i>Biology Direct</i> , 2008, 3, 48.	1.9	49
38	An Improved Implementation of Codon Adaptation Index. <i>Evolutionary Bioinformatics</i> , 2007, 3, 117693430700300.	0.6	48
39	DNA Replication and Strand Asymmetry in Prokaryotic and Mitochondrial Genomes. <i>Current Genomics</i> , 2012, 13, 16-27.	0.7	48
40	Preservation of Genes Involved in Sterol Metabolism in Cholesterol Auxotrophs: Facts and Hypotheses. <i>PLoS ONE</i> , 2008, 3, e2883.	1.1	48
41	A Major Controversy in Codon-Anticodon Adaptation Resolved by a New Codon Usage Index. <i>Genetics</i> , 2015, 199, 573-579.	1.2	47
42	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
43	The Effect of Mutation and Selection on Codon Adaptation in Escherichia coli Bacteriophage. <i>Genetics</i> , 2014, 197, 301-315.	1.2	42
44	On transition bias in mitochondrial genes of pocket gophers. <i>Journal of Molecular Evolution</i> , 1996, 43, 32-40.	0.8	41
45	MBEToolbox: a MATLAB toolbox for sequence data analysis in molecular biology and evolution. <i>BMC Bioinformatics</i> , 2005, 6, 64.	1.2	41
46	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
47	Mural granulosa cell gene expression associated with oocyte developmental competence. <i>Journal of Ovarian Research</i> , 2010, 3, 6.	1.3	40
48	The +4G Site in Kozak Consensus Is Not Related to the Efficiency of Translation Initiation. <i>PLoS ONE</i> , 2007, 2, e188.	1.1	39
49	Differential Codon Adaptation between dsDNA and ssDNA Phages in Escherichia coli. <i>Molecular Biology and Evolution</i> , 2014, 31, 1606-1617.	3.5	39
50	Defining Global Neuroendocrine Gene Expression Patterns Associated with Reproductive Seasonality in Fish. <i>PLoS ONE</i> , 2009, 4, e5816.	1.1	39
51	Paternal behavior by <i>Peromyscus leucopus</i> in enclosures. <i>Canadian Journal of Zoology</i> , 1988, 66, 1184-1187.	0.4	38
52	Using Generalized Procrustes Analysis (GPA) for normalization of cDNA microarray data. <i>BMC Bioinformatics</i> , 2008, 9, 25.	1.2	38
53	An improved implementation of codon adaptation index. <i>Evolutionary Bioinformatics</i> , 2007, 3, 53-8.	0.6	38
54	Genetic evidence of promiscuity in <i>Peromyscus leucopus</i> . <i>Behavioral Ecology and Sociobiology</i> , 1991, 28, 171.	0.6	37

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55	A distance-based least-square method for dating speciation events. <i>Molecular Phylogenetics and Evolution</i> , 2011, 59, 342-353.	1.2	37
56	Morphological Changes of <i>Pseudomonas pseudoalcaligenes</i> in Response to Temperature Selection. <i>Current Microbiology</i> , 2003, 46, 120-123.	1.0	34
57	An Extensive Study of Mutation and Selection on the Wobble Nucleotide in tRNA Anticodons in Fungal Mitochondrial Genomes. <i>Journal of Molecular Evolution</i> , 2008, 66, 484-493.	0.8	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. <i>Molecular Phylogenetics and Evolution</i> , 2009, 52, 665-676.	1.2	30
60	The cost of wobble translation in fungal mitochondrial genomes: integration of two traditional hypotheses. <i>BMC Evolutionary Biology</i> , 2008, 8, 211.	3.2	29
61	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
62	Coevolution between Stop Codon Usage and Release Factors in Bacterial Species. <i>Molecular Biology and Evolution</i> , 2016, 33, 2357-2367.	3.5	29
63	The Evolution and Functional Diversification of the Deubiquitinating Enzyme Superfamily. <i>Genome Biology and Evolution</i> , 2017, 9, 558-573.	1.1	29
64	<i>Escherichia coli</i> and <i>Staphylococcus</i> 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
65	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
66	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
67	Factors Affecting Splicing Strength of Yeast Genes. <i>Comparative and Functional Genomics</i> , 2011, 2011, 1-13.	2.0	27
68	The evolution of genomic GC content undergoes a rapid reversal within the genus <i>Plasmodium</i> . <i>Genome</i> , 2014, 57, 507-511.	0.9	26
69	Coronavirus genomes carry the signatures of their habitats. <i>PLoS ONE</i> , 2020, 15, e0244025.	1.1	25
70	DNA Methylation and <i>Mycoplasma</i> Genomes. <i>Journal of Molecular Evolution</i> , 2003, 57, S21-S28.	0.8	24
71	Selection preserves Ubiquitin Specific Protease 4 alternative exon skipping in therian mammals. <i>Scientific Reports</i> , 2016, 6, 20039.	1.6	24
72	Conflict between Translation Initiation and Elongation in Vertebrate Mitochondrial Genomes. <i>PLoS ONE</i> , 2007, 2, e227.	1.1	24

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73	How Changes in Anti-SD Sequences Would Affect SD Sequences in <i>Escherichia coli</i> and <i>Bacillus subtilis</i> . <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1607-1615.	0.8	23
74	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
75	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
76	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
77	The Role of +4U as an Extended Translation Termination Signal in Bacteria. <i>Genetics</i> , 2017, 205, 539-549.	1.2	22
78	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. <i>Scientific Reports</i> , 2017, 7, 17639.	1.6	22
79	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
80	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
81	Measuring Temporal Variability of Population Density: A Critique. <i>American Naturalist</i> , 1992, 140, 883-892.	1.0	18
82	Genomic Adaptation to Acidic Environment: Evidence from <i>Helicobacter pylori</i> . <i>American Naturalist</i> , 2005, 166, 776-784.	1.0	18
83	Self-Organizing Map for Characterizing Heterogeneous Nucleotide and Amino Acid Sequence Motifs. <i>Computation</i> , 2017, 5, 43.	1.0	18
84	Rapid evolution of animal mitochondrial DNA. , 2012, , 73-82.		18
85	Dating the origin of the major lineages of Branchiopoda. <i>Palaeoworld</i> , 2016, 25, 303-317.	0.5	17
86	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
87	ARSDA: A New Approach for Storing, Transmitting and Analyzing Transcriptomic Data. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3839-3848.	0.8	16
88	<i>Aeromonas</i> phages encode tRNAs for their overused codons. <i>International Journal of Computational Biology and Drug Design</i> , 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. <i>Viruses</i> , 2021, 13, 1790.	1.5	15
90	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

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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 <i>Pseudomonas pseudoalcaligenes</i> after ten months culturing at increasing temperature. FEMS Microbiology Ecology, 2003, 45, 127-134.	1.3	12
94	RNA-Seq approach for accurate characterization of splicing efficiency of yeast introns. Methods, 2020, 176, 25-33.	1.9	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.	1.8	10
96	Unique Shineâ€Dalgarno Sequences in Cyanobacteria and Chloroplasts Reveal Evolutionary Differences in Their Translation Initiation. Genome Biology and Evolution, 2019, 11, 3194-3206.	1.1	10
97	Infestations of Wild <i>Peromyscus leucopus</i> by Bot Fly Larvae. Journal of Mammalogy, 1990, 71, 255-258.	0.6	8
98	Morphological variation in deer mice in relation to sex and habitat. Canadian Journal of Zoology, 1987, 65, 527-533.	0.4	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.	1.6	7
101	Dispersion of adult male <i>Peromyscus leucopus</i> in relation to female reproductive status. Canadian Journal of Zoology, 1989, 67, 1047-1052.	0.4	6
102	Topological Bias in Distance-Based Phylogenetic Methods: Problems with Over- and Underestimated Genetic Distances. Evolutionary Bioinformatics, 2006, 2, 117693430600200.	0.6	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.	1.8	6
104	Sex-related dispersion of breeding deer mice in the Kananaskis Valley, Alberta. Canadian Journal of Zoology, 1986, 64, 933-936.	0.4	5
105	Imputing missing distances in molecular phylogenetics. PeerJ, 2018, 6, e5321.	0.9	5
106	Conservation of griseofulvin genes in the <i>gsf</i> gene cluster among fungal genomes. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	5
107	RNA-Seq-Based Analysis Reveals Heterogeneity in Mature 16S rRNA 3â€Termini and Extended Anti-Shine-Dalgarno Motifs in Bacterial Species. G3: Genes, Genomes, Genetics, 2018, 8, 3973-3979.	0.8	4
108	Drug efficacy and toxicity prediction: an innovative application of transcriptomic data. Cell Biology and Toxicology, 2020, 36, 591-602.	2.4	4

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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	Offspring Recognition by Male <i>Peromyscus maniculatus</i> . <i>Journal of Mammalogy</i> , 1988, 69, 811-813.	0.6	3
111	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
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	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. <i>Global Ecology and Biogeography</i> , 2019, 28, 1195-1199.	2.7	3
117	Applications of Protein Secondary Structure Algorithms in SARS-CoV-2 Research. <i>Journal of Proteome Research</i> , 2021, 20, 1457-1463.	1.8	3
118	Comparative Genomics. , 2011, , 567-600.		3
119	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
120	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
121	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
122	Molecular Phylogenetics: Mathematical Framework and Unsolved Problems. <i>Biological and Medical Physics Series</i> , 2007, , 169-189.	0.3	2
123	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
124	Beyond Trees: Regulons and Regulatory Motif Characterization. <i>Genes</i> , 2020, 11, 995.	1.0	2
125	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
126	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

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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.	1.1	1
132	Editorial for the special issue "RNA-Seq: Methods and applications" Methods, 2020, 176, 1-3.	1.9	1
133	Marsh Spot Disease and Its Causal Factor, Manganese Deficiency in Plants: A Historical and Prospective Review. Agricultural Sciences, 2021, 12, 928-948.	0.2	1
134	Does <i>Saccharomyces cerevisiae</i> Require Specific Post-Translational Silencing against Leaky Translation of Hac1up?. Microorganisms, 2021, 9, 620.	1.6	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.	1.0	1
137	Post-Alignment Adjustment and Its Automation. Genes, 2021, 12, 1809.	1.0	1
138	A Full Sibling is not as Valuable as an Offspring: On Hamilton's Rule. American Naturalist, 1993, 142, 174-185.	1.0	0
139	The genus <i>Schevoderia</i> Borchmann: Phylogeny and historical biogeography, with description of a new species (Coleoptera: Tenebrionidae: Lagriinae). Oriental Insects, 2001, 35, 3-27.	0.1	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 <i>Pyrococcus Horikoshii</i> : 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