

# Keith A Crandall

## List of Publications by Year in descending order

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Version: 2024-02-01

350  
papers

59,688  
citations

8755

75  
h-index

1009

236  
g-index

395  
all docs

395  
docs citations

395  
times ranked

42554  
citing authors

#	ARTICLE	IF	CITATIONS
1	Deep Ancestral Introgression Shapes Evolutionary History of Dragonflies and Damselflies. <i>Systematic Biology</i> , 2022, 71, 526-546.	5.6	32
2	Dominant clade-featured SARS-CoV-2 co-occurring mutations reveal plausible epistasis: An in silico based hypothetical model. <i>Journal of Medical Virology</i> , 2022, 94, 1035-1049.	5.0	16
3	The Earth BioGenome Project 2020: Starting the clock. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	124
4	Standards recommendations for the Earth BioGenome Project. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	33
5	Why sequence all eukaryotes?. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	51
6	Chromosome-level genome assembly, annotation, and phylogenomics of the gooseneck barnacle <i>Pollicipes pollicipes</i> . <i>GigaScience</i> , 2022, 11, .	6.4	8
7	Association of Early Aspirin Use With In-Hospital Mortality in Patients With Moderate COVID-19. <i>JAMA Network Open</i> , 2022, 5, e223890.	5.9	31
8	Unlocking capacities of genomics for the COVID-19 response and future pandemics. <i>Nature Methods</i> , 2022, 19, 374-380.	19.0	35
9	Composition, Structure and Diversity of Soil Bacterial Communities before, during and after Transit through the Gut of the Earthworm <i>Aporrectodea caliginosa</i> . <i>Microorganisms</i> , 2022, 10, 1025.	3.6	12
10	Comparative Analysis of Metagenomics and Metataxonomics for the Characterization of Vermicompost Microbiomes. <i>Frontiers in Microbiology</i> , 2022, 13, .	3.5	3
11	The Origin, Epidemiology, and Phylodynamics of Human Immunodeficiency Virus Type 1 CRF47_BF. <i>Frontiers in Microbiology</i> , 2022, 13, .	3.5	1
12	Metabolite, protein, and tissue dysfunction associated with COVID-19 disease severity. <i>Scientific Reports</i> , 2022, 12, .	3.3	11
13	Induction of mastitis by cow-to-mouse fecal and milk microbiota transplantation causes microbiome dysbiosis and genomic functional perturbation in mice. <i>Animal Microbiome</i> , 2022, 4, .	3.8	18
14	The HIV Latency Reversal Agent HODHBt Enhances NK Cell Effector and Memory-Like Functions by Increasing Interleukin-15-Mediated STAT Activation. <i>Journal of Virology</i> , 2022, 96, .	3.4	5
15	Each patient is a research biorepository: informatics-enabled research on surplus clinical specimens via the living BioBank. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2021, 28, 138-143.	4.4	4
16	Exon probe sets and bioinformatics pipelines for all levels of fish phylogenomics. <i>Molecular Ecology Resources</i> , 2021, 21, 816-833.	4.8	18
17	A New Morphotype of the Crayfish <i>Cambarus hubrichti</i> (Decapoda: Cambaridae) from a Karst Spring Cave System, with Comments on Its Ecology. , 2021, , 445-468.		1
18	The evolutionary diversity of barnacles, with an updated classification of fossil and living forms. <i>Zoological Journal of the Linnean Society</i> , 2021, 193, 789-846.	2.3	62

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19	Inflammation in children with cystic fibrosis: contribution of bacterial production of long-chain fatty acids. <i>Pediatric Research</i> , 2021, 90, 99-108.	2.3	13
20	Entangled Aeglidae (Decapoda, Anomura): Additional evidence for cryptic species. <i>Zoologica Scripta</i> , 2021, 50, 473-484.	1.7	4
21	Expression of Human Endogenous Retroviruses in Systemic Lupus Erythematosus: Multiomic Integration With Gene Expression. <i>Frontiers in Immunology</i> , 2021, 12, 661437.	4.8	14
22	COVID-19 biomarkers and their overlap with comorbidities in a disease biomarker data model. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	11
23	Locus-Specific Characterization of Human Endogenous Retrovirus Expression in Prostate, Breast, and Colon Cancers. <i>Cancer Research</i> , 2021, 81, 3449-3460.	0.9	20
24	Su579 ALDH2 DEFICIENCY TOGETHER WITH DISRUPTION OF TGF- $\beta^2$ SIGNALING DRIVES OBESITY AND METABOLIC SYNDROME THROUGH A LIVER- BRAIN-GUT MICROBIOME AXIS. <i>Gastroenterology</i> , 2021, 160, S-746.	1.3	0
25	Importance of beta-lactam pharmacokinetics and pharmacodynamics on the recovery of microbial diversity in the airway of persons with cystic fibrosis. <i>Journal of Investigative Medicine</i> , 2021, 69, 1350-1359.	1.6	6
26	Omics community detection using multi-resolution clustering. <i>Bioinformatics</i> , 2021, 37, 3588-3594.	4.1	6
27	Abstract 2910: A TGF- $\beta^2$ -ALDH2 axis controls liver- brain-gut microbiome driven obesity, metabolic syndrome and cancer. , 2021, , .		0
28	Earthworms drastically change fungal and bacterial communities during vermicomposting of sewage sludge. <i>Scientific Reports</i> , 2021, 11, 15556.	3.3	32
29	Clinical Characterization and Prediction of Clinical Severity of SARS-CoV-2 Infection Among US Adults Using Data From the US National COVID Cohort Collaborative. <i>JAMA Network Open</i> , 2021, 4, e2116901.	5.9	179
30	Impact of Anaerobic Antibacterial Spectrum on Cystic Fibrosis Airway Microbiome Diversity and Pulmonary Function. <i>Pediatric Infectious Disease Journal</i> , 2021, Publish Ahead of Print, 962-968.	2.0	4
31	The genus <i>Creaserinus</i> Hobbs, 1973 (Decapoda: Cambaridae) in Texas. <i>Zootaxa</i> , 2021, 5017, 1-84.	0.5	3
32	A synthesis tree of the Copepoda: integrating phylogenetic and taxonomic data reveals multiple origins of parasitism. <i>PeerJ</i> , 2021, 9, e12034.	2.0	15
33	Felsenstein Phylogenetic Likelihood. <i>Journal of Molecular Evolution</i> , 2021, 89, 134-145.	1.8	9
34	HAPHIPIE: Haplotype Reconstruction and Phylodynamics for Deep Sequencing of Intrahost Viral Populations. <i>Molecular Biology and Evolution</i> , 2021, 38, 1677-1690.	8.9	9
35	Associations between HIV infection and clinical spectrum of COVID-19: a population level analysis based on US National COVID Cohort Collaborative (N3C) data. <i>Lancet HIV</i> , the, 2021, 8, e690-e700.	4.7	106
36	Epidemiological associations with genomic variation in SARS-CoV-2. <i>Scientific Reports</i> , 2021, 11, 23023.	3.3	5

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37	SARS-CoV-2 infection reduces human nasopharyngeal commensal microbiome with inclusion of pathobionts. <i>Scientific Reports</i> , 2021, 11, 24042.	3.3	32
38	Mutated CEACAMs Disrupt Transforming Growth Factor Beta Signaling and Alter the Intestinal Microbiome to Promote Colorectal Carcinogenesis. <i>Gastroenterology</i> , 2020, 158, 238-252.	1.3	46
39	ReQTL: identifying correlations between expressed SNVs and gene expression using RNA-sequencing data. <i>Bioinformatics</i> , 2020, 36, 1351-1359.	4.1	13
40	A new molecular phylogeny-based taxonomy of parasitic barnacles (Crustacea: Cirripedia): Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 622 Td	2.3	25
41	Microbiome dynamics and genomic determinants of bovine mastitis. <i>Genomics</i> , 2020, 112, 5188-5203.	2.9	41
42	Validation of Variant Assembly Using HAPHIPE with Next-Generation Sequence Data from Viruses. <i>Viruses</i> , 2020, 12, 758.	3.3	4
43	Tu1929 ANTIMICROBIAL RESISTANCE GENE BURDEN DECREASES OVER TIME IN PRETERM INFANTS RECEIVING BREAST MILK. <i>Gastroenterology</i> , 2020, 158, S-1222.	1.3	0
44	Airway microbial diversity is decreased in young children with cystic fibrosis compared to healthy controls but improved with CFTR modulation. <i>Heliyon</i> , 2020, 6, e04104.	3.2	11
45	Human Endogenous Retrovirus Expression Is Associated with Head and Neck Cancer and Differential Survival. <i>Viruses</i> , 2020, 12, 956.	3.3	20
46	Genome-wide analysis of SARS-CoV-2 virus strains circulating worldwide implicates heterogeneity. <i>Scientific Reports</i> , 2020, 10, 14004.	3.3	242
47	Hemiptera phylogenomic resources: Tree-based orthology prediction and conserved exon identification. <i>Molecular Ecology Resources</i> , 2020, 20, 1346-1360.	4.8	5
48	Drug Resistance Prediction Using Deep Learning Techniques on HIV-1 Sequence Data. <i>Viruses</i> , 2020, 12, 560.	3.3	32
49	Sampling bias and incorrect rooting make phylogenetic network tracing of SARS-COV-2 infections unreliable. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 12522-12523.	7.1	68
50	Variants in the Kisspeptin-GnRH Pathway Modulate the Hormonal Profile and Reproductive Outcomes. <i>DNA and Cell Biology</i> , 2020, 39, 1012-1022.	1.9	3
51	Environmental DNA survey captures patterns of fish and invertebrate diversity across a tropical seascape. <i>Scientific Reports</i> , 2020, 10, 6729.	3.3	60
52	Longitudinal Associations of the Cystic Fibrosis Airway Microbiome and Volatile Metabolites: A Case Study. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 174.	3.9	19
53	Testing the "Grandma Hypothesis": Characterizing Skin Microbiome Diversity as a Project-Based Learning Approach to Genomics. <i>Journal of Microbiology and Biology Education</i> , 2020, 21, .	1.0	4
54	A cross-sectional study to characterize local HIV-1 dynamics in Washington, DC using next-generation sequencing. <i>Scientific Reports</i> , 2020, 10, 1989.	3.3	9

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55	The Cancer Microbiome: Distinguishing Direct and Indirect Effects Requires a Systemic View. Trends in Cancer, 2020, 6, 192-204.	7.4	162
56	Evaluation of haplotype callers for next-generation sequencing of viruses. Infection, Genetics and Evolution, 2020, 82, 104277.	2.3	29
57	Insights Into the Resistome of Bovine Clinical Mastitis Microbiome, a Key Factor in Disease Complication. Frontiers in Microbiology, 2020, 11, 860.	3.5	56
58	Consumption of Diet Soda Sweetened with Sucralose and Acesulfameâ€Potassium Alters Inflammatory Transcriptome Pathways in Females with Overweight and Obesity. Molecular Nutrition and Food Research, 2020, 64, e1901166.	3.3	15
59	Epitope-based chimeric peptide vaccine design against S, M and E proteins of SARS-CoV-2 etiologic agent of global pandemic COVID-19: an in silico approach. PeerJ, 2020, 8, e9572.	2.0	108
60	Evaluation of computational methods for human microbiome analysis using simulated data. PeerJ, 2020, 8, e9688.	2.0	14
61	Machine learning approaches to predict lupus disease activity from gene expression data. Scientific Reports, 2019, 9, 9617.	3.3	58
62	Transcriptomic analysis of human endogenous retroviruses in systemic lupus erythematosus. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 21350-21351.	7.1	13
63	Baseline human gut microbiota profile in healthy people and standard reporting template. PLoS ONE, 2019, 14, e0206484.	2.5	133
64	Metagenomic deep sequencing reveals association of microbiome signature with functional biases in bovine mastitis. Scientific Reports, 2019, 9, 13536.	3.3	97
65	Fecal Transplant in Children With Clostridioides difficile Gives Sustained Reduction in Antimicrobial Resistance and Potential Pathogen Burden. Open Forum Infectious Diseases, 2019, 6, ofz379.	0.9	32
66	Telescope: Characterization of the retrotranscriptome by accurate estimation of transposable element expression. PLoS Computational Biology, 2019, 15, e1006453.	3.2	99
67	Gut microbiome differences between wild and captive black rhinoceros â€“ implications for rhino health. Scientific Reports, 2019, 9, 7570.	3.3	97
68	A phylogenomic framework, evolutionary timeline and genomic resources for comparative studies of decapod crustaceans. Proceedings of the Royal Society B: Biological Sciences, 2019, 286, 20190079.	2.6	126
69	Transcriptome patterns in hidradenitis suppurativa: support for the role of antimicrobial peptides and interferon pathways in disease pathogenesis. Clinical and Experimental Dermatology, 2019, 44, 882-892.	1.3	39
70	Changes in microbiome diversity following beta-lactam antibiotic treatment are associated with therapeutic versus subtherapeutic antibiotic exposure in cystic fibrosis. Scientific Reports, 2019, 9, 2534.	3.3	17
71	A 28-Year History of HIV-1 Drug Resistance and Transmission in Washington, DC. Frontiers in Microbiology, 2019, 10, 369.	3.5	7
72	2573. Impact of Anaerobic Antibacterial Spectrum on Cystic Fibrosis Lung Microbiome Diversity and Pulmonary Function. Open Forum Infectious Diseases, 2019, 6, S894-S894.	0.9	0

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73	Towards a barnacle tree of life: integrating diverse phylogenetic efforts into a comprehensive hypothesis of thecostracan evolution. <i>PeerJ</i> , 2019, 7, e7387.	2.0	19
74	Earth BioGenome Project: Sequencing life for the future of life. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 4325-4333.	7.1	652
75	Phylogeography reveals unexpectedly low genetic diversity in a widely distributed species: the case of the freshwater crab <i>Aegla platensis</i> (Decapoda: Anomura). <i>Biological Journal of the Linnean Society</i> , 2018, 123, 578-592.	1.6	7
76	Looks can be deceiving: species delimitation reveals hidden diversity in the freshwater crab <i>Aegla longirostri</i> (Decapoda: Anomura). <i>Zoological Journal of the Linnean Society</i> , 2018, 182, 24-37.	2.3	18
77	More evolution underground: Accelerated mitochondrial substitution rate in Australian burrowing freshwater crayfishes (Decapoda: Parastacidae). <i>Molecular Phylogenetics and Evolution</i> , 2018, 118, 88-98.	2.7	19
78	Microbial diversity within the airway microbiome in chronic pediatric lung diseases. <i>Infection, Genetics and Evolution</i> , 2018, 63, 316-325.	2.3	23
79	Pediatric asthma comprises different phenotypic clusters with unique nasal microbiotas. <i>Microbiome</i> , 2018, 6, 179.	11.1	45
80	Antibiotic multidrug resistance in the cystic fibrosis airway microbiome is associated with decreased diversity. <i>Heliyon</i> , 2018, 4, e00795.	3.2	31
81	Kisspeptin/GPR54 System: What Do We Know About Its Role in Human Reproduction?. <i>Cellular Physiology and Biochemistry</i> , 2018, 49, 1259-1276.	1.6	83
82	The Evolution of Gene Expression Underlying Vision Loss in Cave Animals. <i>Molecular Biology and Evolution</i> , 2018, 35, 2005-2014.	8.9	28
83	Phototransduction Gene Expression and Evolution in Cave and Surface Crayfishes. <i>Integrative and Comparative Biology</i> , 2018, 58, 398-410.	2.0	17
84	Systematic pan-cancer analysis of somatic allele frequency. <i>Scientific Reports</i> , 2018, 8, 7735.	3.3	21
85	Benchmark Evaluation of True Single Molecular Sequencing to Determine Cystic Fibrosis Airway Microbiome Diversity. <i>Frontiers in Microbiology</i> , 2018, 9, 1069.	3.5	7
86	De novo transcriptome assembly of <i>Pueraria montana</i> var. <i>lobata</i> and <i>Neustanthus phaseoloides</i> for the development of eSSR and SNP markers: narrowing the US origin(s) of the invasive kudzu. <i>BMC Genomics</i> , 2018, 19, 439.	2.8	11
87	Seminal Simian Immunodeficiency Virus in Chronically Infected <i>Cynomolgus</i> Macaques Is Dominated by Virus Originating from Multiple Genital Organs. <i>Journal of Virology</i> , 2018, 92, .	3.4	20
88	Images are not and should not ever be type specimens: a rebuttal to Garraffoni & Freitas. <i>Zootaxa</i> , 2017, 4269, 455-459.	0.5	15
89	Advancing genomics through the Global Invertebrate Genomics Alliance (GIGA). <i>Invertebrate Systematics</i> , 2017, 31, 1.	1.3	22
90	Overexpressed somatic alleles are enriched in functional elements in Breast Cancer. <i>Scientific Reports</i> , 2017, 7, 8287.	3.3	3

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91	An updated classification of the freshwater crayfishes (Decapoda: Astacidea) of the world, with a complete species list. <i>Journal of Crustacean Biology</i> , 2017, 37, 615-653.	0.8	196
92	Phylogenetic evidence from freshwater crayfishes that cave adaptation is not an evolutionary dead-end. <i>Evolution; International Journal of Organic Evolution</i> , 2017, 71, 2522-2532.	2.3	38
93	Corrigendum to: Advancing genomics through the Global Invertebrate Genomics Alliance (GIGA). <i>Invertebrate Systematics</i> , 2017, 31, 231.	1.3	2
94	Nasopharyngeal Microbiome Diversity Changes over Time in Children with Asthma. <i>PLoS ONE</i> , 2017, 12, e0170543.	2.5	55
95	DNA Barcoding analysis of seafood accuracy in Washington, D.C. restaurants. <i>PeerJ</i> , 2017, 5, e3234.	2.0	15
96	Characterization of HIV diversity, phylodynamics and drug resistance in Washington, DC. <i>PLoS ONE</i> , 2017, 12, e0185644.	2.5	20
97	Metataxonomic and Metagenomic Approaches vs. Culture-Based Techniques for Clinical Pathology. <i>Frontiers in Microbiology</i> , 2016, 7, 484.	3.5	78
98	Two sampling methods yield distinct microbial signatures in the nasopharynxes of asthmatic children. <i>Microbiome</i> , 2016, 4, 25.	11.1	31
99	Collecting and processing freshwater crayfishes. <i>Journal of Crustacean Biology</i> , 2016, 36, 761-766.	0.8	7
100	Global Diversity and Conservation of Freshwater Crayfish (Crustacea: Decapoda: Astacoidea). , 2016, , 65-114.		7
101	Fish-T1K (Transcriptomes of 1,000 Fishes) Project: large-scale transcriptome data for fish evolution studies. <i>GigaScience</i> , 2016, 5, 18.	6.4	44
102	Comparison of two commercial DNA extraction kits for the analysis of nasopharyngeal bacterial communities. <i>AIMS Microbiology</i> , 2016, 2, 108-119.	2.2	18
103	Phylogenetic Estimate of the Freshwater Crayfish (Decapoda: Astacidea) using Morphology and Molecules. , 2015, , 298-310.		3
104	Three new species of Aeglidae ( Aegla Leach, 1820) from Paraná State, Brazil. <i>Journal of Crustacean Biology</i> , 2015, 35, 839-849.	0.8	15
105	Climate oscillations, glacial refugia, and dispersal ability: factors influencing the genetic structure of the least salmonfly, <i>Pteronarcissa badia</i> (Plecoptera), in Western North America. <i>BMC Evolutionary Biology</i> , 2015, 15, 279.	3.2	21
106	Multiple drivers of decline in the global status of freshwater crayfish (Decapoda: Astacidea). <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140060.	4.0	225
107	Phylogeny, extinction and conservation: embracing uncertainties in a time of urgency. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140002.	4.0	49
108	A synthetic phylogeny of freshwater crayfish: insights for conservation. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140009.	4.0	38

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109	Integrating microbial and host transcriptomics to characterize asthma-associated microbial communities. BMC Medical Genomics, 2015, 8, 50.	1.5	63
110	Synthesis of phylogeny and taxonomy into a comprehensive tree of life. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 12764-12769.	7.1	584
111	The native South American crayfishes (Crustacea, Parastacidae): state of knowledge and conservation status. Aquatic Conservation: Marine and Freshwater Ecosystems, 2015, 25, 288-301.	2.0	20
112	Dual Transcriptomic Profiling of Host and Microbiota during Health and Disease in Pediatric Asthma. PLoS ONE, 2015, 10, e0131819.	2.5	87
113	Composition, taxonomy and functional diversity of the oropharynx microbiome in individuals with schizophrenia and controls. PeerJ, 2015, 3, e1140.	2.0	222
114	Concordance and discordance of sequence survey methods for molecular epidemiology. PeerJ, 2015, 3, e761.	2.0	5
115	Using phylogenetically-informed annotation (PIA) to search for light-interacting genes in transcriptomes from non-model organisms. BMC Bioinformatics, 2014, 15, 350.	2.6	62
116	PathoScope 2.0: a complete computational framework for strain identification in environmental or clinical sequencing samples. Microbiome, 2014, 2, 33.	11.1	206
117	Characteristics and Prediction of RNA Structure. BioMed Research International, 2014, 2014, 1-10.	1.9	5
118	On stabilising the names of the infraorders of thalassinidean shrimps, Axiidea de Saint Laurent, 1979 and Gebiidea de Saint Laurent, 1979 (Decapoda). Crustaceana, 2014, 87, 1258-1272.	0.3	19
119	Characteristics of equipartition for RNA structure. BMC Proceedings, 2014, 8, S3.	1.6	0
120	The Global Invertebrate Genomics Alliance (GIGA): Developing Community Resources to Study Diverse Invertebrate Genomes. Journal of Heredity, 2014, 105, 1-18.	2.4	96
121	Single-Molecule Long-Read 16S Sequencing To Characterize the Lung Microbiome from Mechanically Ventilated Patients with Suspected Pneumonia. Journal of Clinical Microbiology, 2014, 52, 3913-3921.	3.9	69
122	Molecular phylogeny, systematics and morphological evolution of the acorn barnacles (Thoracica: Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	2.7	40
123	Whole genome single-nucleotide variation profile-based phylogenetic tree building methods for analysis of viral, bacterial and human genomes. Genomics, 2014, 104, 1-7.	2.9	19
124	Clinical PathoScope: rapid alignment and filtration for accurate pathogen identification in clinical samples using unassembled sequencing data. BMC Bioinformatics, 2014, 15, 262.	2.6	55
125	Life in extreme environments: microbial diversity in Great Salt Lake, Utah. Extremophiles, 2014, 18, 525-535.	2.3	67
126	Biodiversity only makes sense in the light of evolution. Journal of Biosciences, 2014, 39, 333-337.	1.1	9

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127	The Emergence of Lobsters: Phylogenetic Relationships, Morphological Evolution and Divergence Time Comparisons of an Ancient Group (Decapoda: Achelata, Astacidea, Glypheidea, Polychelida). <i>Systematic Biology</i> , 2014, 63, 457-479.	5.6	124
128	Status, distribution, and genetics of Blair's fencing crayfish, <i>Faxonella blairi</i> (Decapoda: Tj ETQq0 0 0 rgBT /Overlock 1Q Tf 50 702	0.1	1
129	A comprehensive and integrative reconstruction of evolutionary history for Anomura (Crustacea: Tj ETQq1 1 0.784314 rgBT /Overlock	3.2	113
130	Molecular phylogenetics of the burrowing crayfish genus <i>Fallicambarus</i> (Decapoda: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 622 Td	1.7	15
131	Pathogen typing in the genomics era: MLST and the future of molecular epidemiology. <i>Infection, Genetics and Evolution</i> , 2013, 16, 38-53.	2.3	157
132	Failed species, innominate forms, and the vain search for species limits: cryptic diversity in dusky salamanders ( <i>Desmognathus</i> ) of eastern Tennessee. <i>Ecology and Evolution</i> , 2013, 3, 2547-2567.	1.9	18
133	<i>Pathoscope</i> : Species identification and strain attribution with unassembled sequencing data. <i>Genome Research</i> , 2013, 23, 1721-1729.	5.5	132
134	Lost Branches on the Tree of Life. <i>PLoS Biology</i> , 2013, 11, e1001636.	5.6	58
135	New species and records of the genus <i>Aegla</i> Leach, 1820 (Crustacea, Anomura, Aeglidae) from the West-Central region of Rio Grande do Sul, Brazil. <i>Nauplius</i> , 2013, 21, 211-223.	0.3	19
136	Population Genomics and Phylogeography of an Australian Dairy Factory Derived Lytic Bacteriophage. <i>Genome Biology and Evolution</i> , 2012, 4, 382-393.	2.5	36
137	Molecular phylogeny and character evolution of the chthamaloid barnacles (Cirripedia: Thoracica). <i>Molecular Phylogenetics and Evolution</i> , 2012, 65, 329-334.	2.7	12
138	Genetic diversity and molecular epidemiology of HIV transmission. <i>Future Virology</i> , 2012, 7, 239-252.	1.8	11
139	A new species of burrowing crayfish, <i>Virilastacus jarai</i> (Crustacea, Decapoda, Parastacidae) from central-southern Chile. <i>Proceedings of the Biological Society of Washington</i> , 2012, 125, 258-275.	0.3	16
140	All the better to see you with: a review of odonate color vision with transcriptomic insight into the odonate eye. <i>Organisms Diversity and Evolution</i> , 2012, 12, 241-250.	1.6	51
141	Phylogenetic relationships, character evolution, and taxonomic implications within the slipper lobsters (Crustacea: Decapoda: Scyllaridae). <i>Molecular Phylogenetics and Evolution</i> , 2012, 62, 237-250.	2.7	33
142	The evolution of HIV: Inferences using phylogenetics. <i>Molecular Phylogenetics and Evolution</i> , 2012, 62, 777-792.	2.7	79
143	Three new species of <i>Aegla</i> (Anomura) freshwater crabs from the upper Uruguay River hydrographic basin in Brazil. <i>Journal of Crustacean Biology</i> , 2012, 32, 529-540.	0.8	28
144	Phylogenetics links monster larva to deep-sea shrimp. <i>Ecology and Evolution</i> , 2012, 2, 2367-2373.	1.9	37

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145	Deep Phylogeny and Character Evolution in Thecostraca (Crustacea: Maxillopoda). Integrative and Comparative Biology, 2012, 52, 430-442.	2.0	17
146	Insights into origins of Human T-cell Lymphotropic Virus Type 1 based on new strains from aboriginal people of Canada. Infection, Genetics and Evolution, 2012, 12, 1822-1830.	2.3	5
147	Phylogenetic search through partial tree mixing. BMC Bioinformatics, 2012, 13, S8.	2.6	2
148	A Genomic Island in Salmonella enterica ssp. salamae Provides New Insights on the Genealogy of the Locus of Enterocyte Effacement. PLoS ONE, 2012, 7, e41615.	2.5	14
149	Testing Phylogenetic Hypotheses of the Subgenera of the Freshwater Crayfish Genus Cambarus (Decapoda: Cambaridae). PLoS ONE, 2012, 7, e46105.	2.5	29
150	Conflicting Evolutionary Patterns Due to Mitochondrial Introgression and Multilocus Phylogeography of the Patagonian Freshwater Crab Aegla neuquensis. PLoS ONE, 2012, 7, e37105.	2.5	24
151	Phylogeny and Evolutionary Patterns in the Dwarf Crayfish Subfamily (Decapoda: Cambarellinae). PLoS ONE, 2012, 7, e48233.	2.5	21
152	Multilocus Sequence Typing of Pathogens. , 2011, , 503-521.		5
153	Targeted Amplicon Sequencing (TAS): A Scalable Next-Gen Approach to Multilocus, Multitaxa Phylogenetics. Genome Biology and Evolution, 2011, 3, 1312-1323.	2.5	196
154	Phyldynamics of HIV-1 from a Phase III AIDS Vaccine Trial in Bangkok, Thailand. PLoS ONE, 2011, 6, e16902.	2.5	34
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