

Keith A Crandall

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

353
papers

50,598
citations

69
h-index

223
g-index

395
ext. papers

55,086
ext. citations

5.2
avg, IF

7.84
L-index

#	Paper	IF	Citations
353	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,	11.5	15
352	Standards recommendations for the Earth BioGenome Project.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119,	11.5	4
351	Why sequence all eukaryotes?. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119,	11.5	6
350	Chromosome-level genome assembly, annotation, and phylogenomics of the gooseneck barnacle <i>Pollicipes pollicipes</i> .. <i>GigaScience</i> , 2022 , 11,	7.6	2
349	Association of Early Aspirin Use With In-Hospital Mortality in Patients With Moderate COVID-19.. <i>JAMA Network Open</i> , 2022 , 5, e223890	10.4	4
348	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	4.9	0
347	Epidemiological associations with genomic variation in SARS-CoV-2. <i>Scientific Reports</i> , 2021 , 11, 23023	4.9	0
346	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> , 2021 , 8, e690-e700	7.8	17
345	Dominant clade-featured SARS-CoV-2 co-occurring mutations reveal plausible epistasis: An in silico based hypothetical model. <i>Journal of Medical Virology</i> , 2021 , 94, 1035	19.7	3
344	HAPHPIPE: Haplotype Reconstruction and Phylodynamics for Deep Sequencing of Intrahost Viral Populations. <i>Molecular Biology and Evolution</i> , 2021 , 38, 1677-1690	8.3	3
343	Inflammation in children with cystic fibrosis: contribution of bacterial production of long-chain fatty acids. <i>Pediatric Research</i> , 2021 , 90, 99-108	3.2	2
342	Entangled Aeglididae (Decapoda, Anomura): Additional evidence for cryptic species. <i>Zoologica Scripta</i> , 2021 , 50, 473-484	2.5	0
341	Expression of Human Endogenous Retroviruses in Systemic Lupus Erythematosus: Multiomic Integration With Gene Expression. <i>Frontiers in Immunology</i> , 2021 , 12, 661437	8.4	4
340	COVID-19 biomarkers and their overlap with comorbidities in a disease biomarker data model. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	2
339	Locus-Specific Characterization of Human Endogenous Retrovirus Expression in Prostate, Breast, and Colon Cancers. <i>Cancer Research</i> , 2021 , 81, 3449-3460	10.1	4
338	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	2.9	4
337	Omics community detection using multi-resolution clustering. <i>Bioinformatics</i> , 2021 ,	7.2	2

336	Earthworms drastically change fungal and bacterial communities during vermicomposting of sewage sludge. <i>Scientific Reports</i> , 2021 , 11, 15556	4.9	9
335	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	8.6	1
334	Exon probe sets and bioinformatics pipelines for all levels of fish phylogenomics. <i>Molecular Ecology Resources</i> , 2021 , 21, 816-833	8.4	7
333	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		0
332	Deep ancestral introgression shapes evolutionary history of dragonflies and damselflies. <i>Systematic Biology</i> , 2021 ,	8.4	2
331	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	10.4	37
330	COVID-19 Disease Severity among People with HIV Infection or Solid Organ Transplant in the United States: A Nationally-representative, Multicenter, Observational Cohort Study 2021 ,		5
329	Impact of Anaerobic Antibacterial Spectrum on Cystic Fibrosis Airway Microbiome Diversity and Pulmonary Function. <i>Pediatric Infectious Disease Journal</i> , 2021 , 40, 962-968	3.4	2
328	The genus <i>Creaserinus</i> Hobbs, 1973 (Decapoda: Cambaridae) in Texas. <i>Zootaxa</i> , 2021 , 5017, 1-84	0.5	1
327	A synthesis tree of the Copepoda: integrating phylogenetic and taxonomic data reveals multiple origins of parasitism. <i>PeerJ</i> , 2021 , 9, e12034	3.1	0
326	Felsenstein Phylogenetic Likelihood. <i>Journal of Molecular Evolution</i> , 2021 , 89, 134-145	3.1	0
325	SARS-CoV-2 infection reduces human nasopharyngeal commensal microbiome with inclusion of pathobionts.. <i>Scientific Reports</i> , 2021 , 11, 24042	4.9	4
324	Hemiptera phylogenomic resources: Tree-based orthology prediction and conserved exon identification. <i>Molecular Ecology Resources</i> , 2020 , 20, 1346-1360	8.4	1
323	Drug Resistance Prediction Using Deep Learning Techniques on HIV-1 Sequence Data. <i>Viruses</i> , 2020 , 12,	6.2	15
322	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	11.5	46
321	Variants in the Kisspeptin-GnRH Pathway Modulate the Hormonal Profile and Reproductive Outcomes. <i>DNA and Cell Biology</i> , 2020 , 39, 1012-1022	3.6	2
320	Environmental DNA survey captures patterns of fish and invertebrate diversity across a tropical seascape. <i>Scientific Reports</i> , 2020 , 10, 6729	4.9	27
319	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	5.9	6

318	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,	1.3	2
317	A cross-sectional study to characterize local HIV-1 dynamics in Washington, DC using next-generation sequencing. <i>Scientific Reports</i> , 2020 , 10, 1989	4.9	7
316	The Cancer Microbiome: Distinguishing Direct and Indirect Effects Requires a Systemic View. <i>Trends in Cancer</i> , 2020 , 6, 192-204	12.5	79
315	Evaluation of haplotype callers for next-generation sequencing of viruses. <i>Infection, Genetics and Evolution</i> , 2020 , 82, 104277	4.5	20
314	COVID-19 Biomarkers in research: Extension of the OncoMX cancer biomarker data model to capture biomarker data from other diseases 2020 ,		2
313	Epitope-based chimeric peptide vaccine design against S, M and E proteins of SARS-CoV-2, the etiologic agent of COVID-19 pandemic: an in silico approach. <i>PeerJ</i> , 2020 , 8, e9572	3.1	61
312	Evaluation of computational methods for human microbiome analysis using simulated data. <i>PeerJ</i> , 2020 , 8, e9688	3.1	4
311	A new molecular phylogeny-based taxonomy of parasitic barnacles (Crustacea: Cirripedia: Rhizocephala). <i>Zoological Journal of the Linnean Society</i> , 2020 , 190, 632-653	2.4	12
310	Microbiome dynamics and genomic determinants of bovine mastitis. <i>Genomics</i> , 2020 , 112, 5188-5203	4.3	19
309	Validation of Variant Assembly Using HAPPIPE with Next-Generation Sequence Data from Viruses. <i>Viruses</i> , 2020 , 12,	6.2	1
308	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	3.6	3
307	Human Endogenous Retrovirus Expression Is Associated with Head and Neck Cancer and Differential Survival. <i>Viruses</i> , 2020 , 12,	6.2	3
306	Genome-wide analysis of SARS-CoV-2 virus strains circulating worldwide implicates heterogeneity. <i>Scientific Reports</i> , 2020 , 10, 14004	4.9	156
305	Mutated CEACAMs Disrupt Transforming Growth Factor Beta Signaling and Alter the Intestinal Microbiome to Promote Colorectal Carcinogenesis. <i>Gastroenterology</i> , 2020 , 158, 238-252	13.3	21
304	ReQTL: identifying correlations between expressed SNVs and gene expression using RNA-sequencing data. <i>Bioinformatics</i> , 2020 , 36, 1351-1359	7.2	8
303	Insights Into the Resistome of Bovine Clinical Mastitis Microbiome, a Key Factor in Disease Complication. <i>Frontiers in Microbiology</i> , 2020 , 11, 860	5.7	20
302	Consumption of Diet Soda Sweetened with Sucralose and Acesulfame-Potassium Alters Inflammatory Transcriptome Pathways in Females with Overweight and Obesity. <i>Molecular Nutrition and Food Research</i> , 2020 , 64, e1901166	5.9	9
301	Baseline human gut microbiota profile in healthy people and standard reporting template. <i>PLoS ONE</i> , 2019 , 14, e0206484	3.7	59

300	Metagenomic deep sequencing reveals association of microbiome signature with functional biases in bovine mastitis. <i>Scientific Reports</i> , 2019 , 9, 13536	4.9	39
299	Fecal Transplant in Children With Gives Sustained Reduction in Antimicrobial Resistance and Potential Pathogen Burden. <i>Open Forum Infectious Diseases</i> , 2019 , 6, ofz379	1	17
298	Telescope: Characterization of the retrotranscriptome by accurate estimation of transposable element expression. <i>PLoS Computational Biology</i> , 2019 , 15, e1006453	5	33
297	Gut microbiome differences between wild and captive black rhinoceros - implications for rhino health. <i>Scientific Reports</i> , 2019 , 9, 7570	4.9	47
296	A phylogenomic framework, evolutionary timeline and genomic resources for comparative studies of decapod crustaceans. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019 , 286, 20190079	4.4	67
295	Transcriptome patterns in hidradenitis suppurativa: support for the role of antimicrobial peptides and interferon pathways in disease pathogenesis. <i>Clinical and Experimental Dermatology</i> , 2019 , 44, 882-892	1.8	23
294	Changes in microbiome diversity following beta-lactam antibiotic treatment are associated with therapeutic versus subtherapeutic antibiotic exposure in cystic fibrosis. <i>Scientific Reports</i> , 2019 , 9, 2534	4.9	10
293	Machine learning approaches to predict lupus disease activity from gene expression data. <i>Scientific Reports</i> , 2019 , 9, 9617	4.9	31
292	Transcriptomic analysis of human endogenous retroviruses in systemic lupus erythematosus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 21350-21351	11.5	4
291	Evolutionary History and Phylogenetic Relationships of Aeglidae 2019 , 1-27		1
290	Towards a barnacle tree of life: integrating diverse phylogenetic efforts into a comprehensive hypothesis of thecostracan evolution. <i>PeerJ</i> , 2019 , 7, e7387	3.1	13
289	A 28-Year History of HIV-1 Drug Resistance and Transmission in Washington, DC. <i>Frontiers in Microbiology</i> , 2019 , 10, 369	5.7	5
288	2573. Impact of Anaerobic Antibacterial Spectrum on Cystic Fibrosis Lung Microbiome Diversity and Pulmonary Function. <i>Open Forum Infectious Diseases</i> , 2019 , 6, S894-S894	1	78
287	Claw asymmetry in crabs: approaching an old issue from a new point of view. <i>Biological Journal of the Linnean Society</i> , 2019 ,	1.9	5
286	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	11.5	334
285	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	1.9	6
284	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	2.4	12
283	More evolution underground: Accelerated mitochondrial substitution rate in Australian burrowing freshwater crayfishes (Decapoda: Parastacidae). <i>Molecular Phylogenetics and Evolution</i> , 2018 , 118, 88-98	4.1	10

282	Benchmark Evaluation of True Single Molecular Sequencing to Determine Cystic Fibrosis Airway Microbiome Diversity. <i>Frontiers in Microbiology</i> , 2018 , 9, 1069	5.7	3
281	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	4.5	5
280	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,	6.6	15
279	Microbial diversity within the airway microbiome in chronic pediatric lung diseases. <i>Infection, Genetics and Evolution</i> , 2018 , 63, 316-325	4.5	15
278	<i>Aegla chilota</i> , new species of anomuran freshwater crab from Chilo Island, western Patagonia. <i>Nauplius</i> , 2018 , 26,	1.3	6
277	Pediatric asthma comprises different phenotypic clusters with unique nasal microbiotas. <i>Microbiome</i> , 2018 , 6, 179	16.6	23
276	Invasion by non-indigenous freshwater decapods of Malta and Sicily, central Mediterranean Sea. <i>Journal of Crustacean Biology</i> , 2018 ,	0.8	7
275	Antibiotic multidrug resistance in the cystic fibrosis airway microbiome is associated with decreased diversity. <i>Heliyon</i> , 2018 , 4, e00795	3.6	20
274	Kisspeptin/GPR54 System: What Do We Know About Its Role in Human Reproduction?. <i>Cellular Physiology and Biochemistry</i> , 2018 , 49, 1259-1276	3.9	48
273	The Evolution of Gene Expression Underlying Vision Loss in Cave Animals. <i>Molecular Biology and Evolution</i> , 2018 , 35, 2005-2014	8.3	11
272	Phototransduction Gene Expression and Evolution in Cave and Surface Crayfishes. <i>Integrative and Comparative Biology</i> , 2018 , 58, 398-410	2.8	9
271	Systematic pan-cancer analysis of somatic allele frequency. <i>Scientific Reports</i> , 2018 , 8, 7735	4.9	13
270	Images are not and should not ever be type specimens: a rebuttal to Garraffoni & Freitas. <i>Zootaxa</i> , 2017 , 4269, 455-459	0.5	11
269	Advancing Genomics through the Global Invertebrate Genomics Alliance (GIGA). <i>Invertebrate Systematics</i> , 2017 , 31, 1-7	1.2	16
268	Overexpressed somatic alleles are enriched in functional elements in Breast Cancer. <i>Scientific Reports</i> , 2017 , 7, 8287	4.9	3
267	Nasopharyngeal Microbiome Diversity Changes over Time in Children with Asthma. <i>PLoS ONE</i> , 2017 , 12, e0170543	3.7	39
266	DNA Barcoding analysis of seafood accuracy in Washington, D.C. restaurants. <i>PeerJ</i> , 2017 , 5, e3234	3.1	14
265	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	126

264	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	3.8	20
263	Corrigendum to: Advancing genomics through the Global Invertebrate Genomics Alliance (GIGA). <i>Invertebrate Systematics</i> , 2017 , 31, 231	1.2	1
262	Characterization of HIV diversity, phylodynamics and drug resistance in Washington, DC. <i>PLoS ONE</i> , 2017 , 12, e0185644	3.7	15
261	Collecting and Processing Freshwater Crayfishes. <i>Journal of Crustacean Biology</i> , 2016 , 36, 761-766	0.8	6
260	Global Diversity and Conservation of Freshwater Crayfish (Crustacea: Decapoda: Astacoidea) 2016 , 65-114		5
259	Fish-T1K (Transcriptomes of 1,000 Fishes) Project: large-scale transcriptome data for fish evolution studies. <i>GigaScience</i> , 2016 , 5, 18	7.6	31
258	Comparison of two commercial DNA extraction kits for the analysis of nasopharyngeal bacterial communities. <i>AIMS Microbiology</i> , 2016 , 2, 108-119	4.5	11
257	Freshwater Prawns (Palaemonidae: Macrobrachium) with Abbreviated Larval Development in Rivers of Mexico: Uses, Management, and Conservation Opportunities 2016 ,		1
256	Metataxonomic and Metagenomic Approaches vs. Culture-Based Techniques for Clinical Pathology. <i>Frontiers in Microbiology</i> , 2016 , 7, 484	5.7	58
255	Two sampling methods yield distinct microbial signatures in the nasopharynges of asthmatic children. <i>Microbiome</i> , 2016 , 4, 25	16.6	21
254	Integrating microbial and host transcriptomics to characterize asthma-associated microbial communities. <i>BMC Medical Genomics</i> , 2015 , 8, 50	3.7	46
253	Synthesis of phylogeny and taxonomy into a comprehensive tree of life. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 12764-9	11.5	400
252	The native South American crayfishes (Crustacea, Parastacidae): state of knowledge and conservation status. <i>Aquatic Conservation: Marine and Freshwater Ecosystems</i> , 2015 , 25, 288-301	2.6	13
251	Phylogenetic Estimate of the Freshwater Crayfish (Decapoda: Astacidea) using Morphology and Molecules 2015 , 298-310		3
250	Three new species of Aeglidae (Aegla Leach, 1820) from Paraná State, Brazil. <i>Journal of Crustacean Biology</i> , 2015 , 35, 839-849	0.8	12
249	Climate oscillations, glacial refugia, and dispersal ability: factors influencing the genetic structure of the least salmonfly, <i>Pteronarcella badia</i> (Plecoptera), in Western North America. <i>BMC Evolutionary Biology</i> , 2015 , 15, 279	3	19
248	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	5.8	155
247	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	5.8	41

246	A synthetic phylogeny of freshwater crayfish: insights for conservation. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015 , 370, 20140009	5.8	30
245	Dual Transcriptomic Profiling of Host and Microbiota during Health and Disease in Pediatric Asthma. <i>PLoS ONE</i> , 2015 , 10, e0131819	3.7	68
244	Composition, taxonomy and functional diversity of the oropharynx microbiome in individuals with schizophrenia and controls. <i>PeerJ</i> , 2015 , 3, e1140	3.1	154
243	Concordance and discordance of sequence survey methods for molecular epidemiology. <i>PeerJ</i> , 2015 , 3, e761	3.1	5
242	Single-molecule long-read 16S sequencing to characterize the lung microbiome from mechanically ventilated patients with suspected pneumonia. <i>Journal of Clinical Microbiology</i> , 2014 , 52, 3913-21	9.7	44
241	Molecular phylogeny, systematics and morphological evolution of the acorn barnacles (Thoracica: Sessilia: Balanomorpha). <i>Molecular Phylogenetics and Evolution</i> , 2014 , 81, 147-58	4.1	31
240	Whole genome single-nucleotide variation profile-based phylogenetic tree building methods for analysis of viral, bacterial and human genomes. <i>Genomics</i> , 2014 , 104, 1-7	4.3	14
239	Clinical PathoScope: rapid alignment and filtration for accurate pathogen identification in clinical samples using unassembled sequencing data. <i>BMC Bioinformatics</i> , 2014 , 15, 262	3.6	43
238	Life in extreme environments: microbial diversity in Great Salt Lake, Utah. <i>Extremophiles</i> , 2014 , 18, 525-35		46
237	Biodiversity only makes sense in the light of evolution. <i>Journal of Biosciences</i> , 2014 , 39, 333-7	2.3	9
236	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, 457-79	8.4	89
235	Status, distribution, and genetics of Blair's fencing crayfish, <i>Faxonella blairi</i> (Decapoda: Cambaridae). <i>Southwestern Naturalist</i> , 2014 , 59, 244-250	0.3	1
234	Using phylogenetically-informed annotation (PIA) to search for light-interacting genes in transcriptomes from non-model organisms. <i>BMC Bioinformatics</i> , 2014 , 15, 350	3.6	47
233	PathoScope 2.0: a complete computational framework for strain identification in environmental or clinical sequencing samples. <i>Microbiome</i> , 2014 , 2, 33	16.6	124
232	Characteristics and prediction of RNA structure. <i>BioMed Research International</i> , 2014 , 2014, 690340	3	2
231	On stabilising the names of the infraorders of thalassinidean shrimps, Axiidea de Saint Laurent, 1979 and Gebiidea de Saint Laurent, 1979 (Decapoda). <i>Crustaceana</i> , 2014 , 87, 1258-1272	0.4	17
230	Characteristics of equipartition for RNA structure. <i>BMC Proceedings</i> , 2014 , 8, S3	2.3	
229	The Global Invertebrate Genomics Alliance (GIGA): developing community resources to study diverse invertebrate genomes. <i>Journal of Heredity</i> , 2014 , 105, 1-18	2.4	70

228	A comprehensive and integrative reconstruction of evolutionary history for Anomura (Crustacea: Decapoda). <i>BMC Evolutionary Biology</i> , 2013 , 13, 128	3	80
227	Molecular phylogenetics of the burrowing crayfish genus Fallicambarus (Decapoda: Cambaridae). <i>Zoologica Scripta</i> , 2013 , 42, 306-316	2.5	10
226	Pathogen typing in the genomics era: MLST and the future of molecular epidemiology. <i>Infection, Genetics and Evolution</i> , 2013 , 16, 38-53	4.5	120
225	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	2.8	16
224	Pathoscope: species identification and strain attribution with unassembled sequencing data. <i>Genome Research</i> , 2013 , 23, 1721-9	9.7	100
223	Lost branches on the tree of life. <i>PLoS Biology</i> , 2013 , 11, e1001636	9.7	45
222	New species and records of the genus <i>Aegla</i> Leach, 1820 (Crustacea, Anomura, Aegliidae) from the West-Central region of Rio Grande do Sul, Brazil. <i>Nauplius</i> , 2013 , 21, 211-223	1.3	16
221	Molecular phylogeny and character evolution of the chthamaloid barnacles (Cirripedia: Thoracica). <i>Molecular Phylogenetics and Evolution</i> , 2012 , 65, 329-34	4.1	7
220	Genetic diversity and molecular epidemiology of HIV transmission. <i>Future Virology</i> , 2012 , 7, 239-252	2.4	8
219	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	0.2	12
218	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	1.7	47
217	Phylogenetic relationships, character evolution, and taxonomic implications within the slipper lobsters (Crustacea: Decapoda: Scyllaridae). <i>Molecular Phylogenetics and Evolution</i> , 2012 , 62, 237-50	4.1	24
216	The evolution of HIV: inferences using phylogenetics. <i>Molecular Phylogenetics and Evolution</i> , 2012 , 62, 777-92	4.1	61
215	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	23
214	Phylogenetics links monster larva to deep-sea shrimp. <i>Ecology and Evolution</i> , 2012 , 2, 2367-73	2.8	29
213	Deep phylogeny and character evolution in Thecostraca (Crustacea: Maxillopoda). <i>Integrative and Comparative Biology</i> , 2012 , 52, 430-42	2.8	11
212	Insights into origins of Human T-cell Lymphotropic Virus Type 1 based on new strains from aboriginal people of Canada. <i>Infection, Genetics and Evolution</i> , 2012 , 12, 1822-30	4.5	5
211	Phylogenetic search through partial tree mixing. <i>BMC Bioinformatics</i> , 2012 , 13 Suppl 13, S8	3.6	2

210	A Genomic Island in <i>Salmonella enterica</i> ssp. <i>salamae</i> provides new insights on the genealogy of the locus of enterocyte effacement. <i>PLoS ONE</i> , 2012 , 7, e41615	3.7	10
209	Testing phylogenetic hypotheses of the subgenera of the freshwater crayfish genus <i>Cambarus</i> (Decapoda: Cambaridae). <i>PLoS ONE</i> , 2012 , 7, e46105	3.7	20
208	Population genomics and phylogeography of an Australian dairy factory derived lytic bacteriophage. <i>Genome Biology and Evolution</i> , 2012 , 4, 382-93	3.9	33
207	Conflicting evolutionary patterns due to mitochondrial introgression and multilocus phylogeography of the Patagonian freshwater crab <i>Aegla neuquensis</i> . <i>PLoS ONE</i> , 2012 , 7, e37105	3.7	23
206	Phylogeny and evolutionary patterns in the Dwarf crayfish subfamily (Decapoda: Cambarellinae). <i>PLoS ONE</i> , 2012 , 7, e48233	3.7	17
205	Multilocus Sequence Typing of Pathogens 2011 , 503-521		4
204	Targeted amplicon sequencing (TAS): a scalable next-gen approach to multilocus, multitaxa phylogenetics. <i>Genome Biology and Evolution</i> , 2011 , 3, 1312-23	3.9	156
203	Phylogenetics of HIV-1 from a phase III AIDS vaccine trial in Bangkok, Thailand. <i>PLoS ONE</i> , 2011 , 6, e16907	3.7	31
202	Comparing phylogeographic patterns across the Patagonian Andes in two freshwater crabs of the genus <i>Aegla</i> (Decapoda). <i>Crustacean Issues</i> , 2011 , 291-303		3
201	Population structure of two crayfish with diverse physiological requirements. <i>Crustacean Issues</i> , 2011 , 323-343		2
200	Shallow phylogeographic structure of Puerto Rico freshwater crabs. <i>Crustacean Issues</i> , 2011 , 345-365		
199	Cryptic genetic divergence in the giant Tasmanian freshwater crayfish <i>Astacopsis gouldi</i> (Decapoda: Parastacidae): implications for conservation. <i>Animal Conservation</i> , 2011 , 14, 87-97	3.2	10
198	Directed next generation sequencing for phylogenetics: An example using Decapoda (Crustacea). <i>Zoologischer Anzeiger</i> , 2011 , 250, 497-506	1.1	17
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