

# Marcos Perez-Losada

## List of Publications by Year in descending order

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168  
papers

5,872  
citations

87401

40  
h-index

120465

65  
g-index

176  
all docs

176  
docs citations

176  
times ranked

7638  
citing authors

#	ARTICLE	IF	CITATIONS
1	Reef Location and Client Diversity Influence the Skin Microbiome of the Caribbean Cleaner Goby <i>Elacatinus evelynae</i> . <i>Microbial Ecology</i> , 2023, 85, 372-382.	1.4	2
2	Monitoring Infection and Antibiotic Treatment in the Skin Microbiota of Farmed European Seabass ( <i>Dicentrarchus Labrax</i> ) Fingerlings. <i>Microbial Ecology</i> , 2022, 83, 789-797.	1.4	4
3	Chromosome-level genome assembly, annotation, and phylogenomics of the gooseneck barnacle <i>Pollicipes pollicipes</i> . <i>GigaScience</i> , 2022, 11, .	3.3	8
4	Nasopharyngeal metatranscriptome profiles of infants with bronchiolitis and risk of childhood asthma: a multicentre prospective study. <i>European Respiratory Journal</i> , 2022, 60, 2102293.	3.1	23
5	Bacterial Succession during Vermicomposting of Silver Wattle ( <i>Acacia dealbata</i> Link). <i>Microorganisms</i> , 2022, 10, 65.	1.6	9
6	Nasopharyngeal airway dual-transcriptome of infants with severe bronchiolitis and risk of childhood asthma: A multicenter prospective study. <i>Journal of Allergy and Clinical Immunology</i> , 2022, 150, 806-816.	1.5	19
7	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.	1.6	12
8	Comparative Analysis of Metagenomics and Metataxonomics for the Characterization of Vermicompost Microbiomes. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	3
9	The Origin, Epidemiology, and Phylodynamics of Human Immunodeficiency Virus Type 1 CRF47_BF. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	1
10	A single intravesical instillation of <i>Lactobacillus rhamnosus</i> GG is safe in children and adults with neuropathic bladder: A phase Ia clinical trial. <i>Journal of Spinal Cord Medicine</i> , 2021, 44, 62-69.	0.7	15
11	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.	1.0	62
12	Entangled Aeglididae (Decapoda, Anomura): Additional evidence for cryptic species. <i>Zoologica Scripta</i> , 2021, 50, 473-484.	0.7	4
13	Expression of Human Endogenous Retroviruses in Systemic Lupus Erythematosus: Multiomic Integration With Gene Expression. <i>Frontiers in Immunology</i> , 2021, 12, 661437.	2.2	14
14	Identification of CRF89_BF, a new member of an HIV-1 circulating BF intersubtype recombinant form family widely spread in South America. <i>Scientific Reports</i> , 2021, 11, 11442.	1.6	9
15	Longitudinal sampling of external mucosae in farmed European seabass reveals the impact of water temperature on bacterial dynamics. <i>ISME Communications</i> , 2021, 1, .	1.7	10
16	Integrated omics endotyping of infants with respiratory syncytial virus bronchiolitis and risk of childhood asthma. <i>Nature Communications</i> , 2021, 12, 3601.	5.8	65
17	Earthworms drastically change fungal and bacterial communities during vermicomposting of sewage sludge. <i>Scientific Reports</i> , 2021, 11, 15556.	1.6	32
18	Comparative analysis of the bronchoalveolar microbiome in Portuguese patients with different chronic lung disorders. <i>Scientific Reports</i> , 2021, 11, 15042.	1.6	5

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19	Effects of aging on the skin and gill microbiota of farmed seabass and seabream. <i>Animal Microbiome</i> , 2021, 3, 10.	1.5	23
20	HAPHIPE: Haplotype Reconstruction and Phylodynamics for Deep Sequencing of Intra-host Viral Populations. <i>Molecular Biology and Evolution</i> , 2021, 38, 1677-1690.	3.5	9
21	Epidemiological associations with genomic variation in SARS-CoV-2. <i>Scientific Reports</i> , 2021, 11, 23023.	1.6	5
22	Bacterial Signatures of Paediatric Respiratory Disease: An Individual Participant Data Meta-Analysis. <i>Frontiers in Microbiology</i> , 2021, 12, 711134.	1.5	5
23	In infants with severe bronchiolitis: dual-transcriptomic profiling of nasopharyngeal microbiome and host response. <i>Pediatric Research</i> , 2020, 88, 144-146.	1.1	9
24	Geographical isolation and restricted gene flow drive speciation of <i>Aegla singularis</i> (Decapoda: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 54 177-189.	0.7	8
25	Review of otitis media microbiome studies: What do they tell us?. <i>Laryngoscope Investigative Otolaryngology</i> , 2020, 5, 936-940.	0.6	5
26	Validation of Variant Assembly Using HAPHIPE with Next-Generation Sequence Data from Viruses. <i>Viruses</i> , 2020, 12, 758.	1.5	4
27	Human Endogenous Retrovirus Expression Is Associated with Head and Neck Cancer and Differential Survival. <i>Viruses</i> , 2020, 12, 956.	1.5	20
28	Temporal Dynamics of Bacterial Communities in a Pilot-Scale Vermireactor Fed with Distilled Grape Marc. <i>Microorganisms</i> , 2020, 8, 642.	1.6	14
29	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, .	0.5	4
30	The effects of environment and ontogeny on the skin microbiome of two <i>Stegastes</i> damselfishes (Pomacentridae) from the eastern Caribbean Sea. <i>Marine Biology</i> , 2020, 167, 1.	0.7	12
31	Innate IFN $\lambda$ responses to dsRNA in the human infant airway epithelium and clinical regulatory factors during viral respiratory infections in early life. <i>Clinical and Experimental Allergy</i> , 2020, 50, 1044-1054.	1.4	13
32	A cross-sectional study to characterize local HIV-1 dynamics in Washington, DC using next-generation sequencing. <i>Scientific Reports</i> , 2020, 10, 1989.	1.6	9
33	Evaluation of haplotype callers for next-generation sequencing of viruses. <i>Infection, Genetics and Evolution</i> , 2020, 82, 104277.	1.0	29
34	High-throughput sequencing (HTS) for the analysis of viral populations. <i>Infection, Genetics and Evolution</i> , 2020, 80, 104208.	1.0	35
35	The Urine Microbiome of Healthy Men and Women Differs by Urine Collection Method. <i>International Neurourology Journal</i> , 2020, 24, 41-51.	0.5	66
36	Evaluation of computational methods for human microbiome analysis using simulated data. <i>PeerJ</i> , 2020, 8, e9688.	0.9	14

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37	Changes in the composition and function of bacterial communities during vermicomposting may explain beneficial properties of vermicompost. <i>Scientific Reports</i> , 2019, 9, 9657.	1.6	69
38	Rapid Bacterial Community Changes during Vermicomposting of Grape Marc Derived from Red Winemaking. <i>Microorganisms</i> , 2019, 7, 473.	1.6	19
39	Fecal Transplant in Children With <i>Clostridioides difficile</i> Gives Sustained Reduction in Antimicrobial Resistance and Potential Pathogen Burden. <i>Open Forum Infectious Diseases</i> , 2019, 6, ofz379.	0.4	32
40	Telescope: Characterization of the retrotranscriptome by accurate estimation of transposable element expression. <i>PLoS Computational Biology</i> , 2019, 15, e1006453.	1.5	99
41	Altered Middle Ear Microbiome in Children With Chronic Otitis Media With Effusion and Respiratory Illnesses. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 339.	1.8	19
42	Bacterial succession and functional diversity during vermicomposting of the white grape marc <i>Vitis vinifera</i> v. <i>Albariño</i> . <i>Scientific Reports</i> , 2019, 9, 7472.	1.6	32
43	A Risky Business? Habitat and Social Behavior Impact Skin and Gut Microbiomes in Caribbean Cleaning Gobies. <i>Frontiers in Microbiology</i> , 2019, 10, 716.	1.5	22
44	Validation of publicly-available software used in analyzing NGS data for HIV-1 drug resistance mutations and transmission networks in a Washington, DC, Cohort. <i>PLoS ONE</i> , 2019, 14, e0214820.	1.1	10
45	Microbiome dynamics during cast ageing in the earthworm <i>Aporrectodea caliginosa</i> . <i>Applied Soil Ecology</i> , 2019, 139, 56-63.	2.1	33
46	Multigene phylogeny reveals a new Iranian earthworm genus (Lumbricidae: Philomontanus) with three new species. <i>PLoS ONE</i> , 2019, 14, e0208904.	1.1	11
47	A 28-Year History of HIV-1 Drug Resistance and Transmission in Washington, DC. <i>Frontiers in Microbiology</i> , 2019, 10, 369.	1.5	7
48	Effects of disease, antibiotic treatment and recovery trajectory on the microbiome of farmed seabass ( <i>Dicentrarchus labrax</i> ). <i>Scientific Reports</i> , 2019, 9, 18946.	1.6	54
49	Characterization of the skin and gill microbiomes of the farmed seabass ( <i>Dicentrarchus labrax</i> ) and seabream ( <i>Sparus aurata</i> ). <i>Aquaculture</i> , 2019, 500, 57-64.	1.7	69
50	Towards a barnacle tree of life: integrating diverse phylogenetic efforts into a comprehensive hypothesis of thecostracan evolution. <i>PeerJ</i> , 2019, 7, e7387.	0.9	19
51	Tracheal Microbiota in Patients With a Tracheostomy Before, During and After an Acute Respiratory Infection. <i>Pediatric Infectious Disease Journal</i> , 2018, 37, e269-e271.	1.1	13
52	Glucocorticoids modulate gastrointestinal microbiome in a wild bird. <i>Royal Society Open Science</i> , 2018, 5, 171743.	1.1	83
53	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.	0.7	7
54	Diversity, structure and sources of bacterial communities in earthworm cocoons. <i>Scientific Reports</i> , 2018, 8, 6632.	1.6	20

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55	Multigene phylogeny reveals two new isolated and relic earthworm genera (Oligochaeta): <i>Tj ETQq1</i> and <i>rgBT/Overlock</i> . <i>Trends in Microbiology</i> , 2018, 16, 107-114.	0.784314	10
56	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.	1.0	18
57	Mutation and recombination in pathogen evolution: Relevance, methods and controversies. <i>Infection, Genetics and Evolution</i> , 2018, 63, 295-306.	1.0	32
58	Microbial sequence typing in the genomic era. <i>Infection, Genetics and Evolution</i> , 2018, 63, 346-359.	1.0	50
59	Microbial diversity within the airway microbiome in chronic pediatric lung diseases. <i>Infection, Genetics and Evolution</i> , 2018, 63, 316-325.	1.0	23
60	RSV vs. rhinovirus bronchiolitis: difference in nasal airway microRNA profiles and NF $\kappa$ B signaling. <i>Pediatric Research</i> , 2018, 83, 606-614.	1.1	42
61	Identification of <i>Burkholderia fungorum</i> in the urine of an individual with spinal cord injury and augmentation cystoplasty using 16S sequencing: copathogen or innocent bystander?. <i>Spinal Cord Series and Cases</i> , 2018, 4, 85.	0.3	9
62	Pediatric asthma comprises different phenotypic clusters with unique nasal microbiotas. <i>Microbiome</i> , 2018, 6, 179.	4.9	45
63	Characterization of mucoid and serous middle ear effusions from patients with chronic otitis media: implication of different biological mechanisms?. <i>Pediatric Research</i> , 2018, 84, 296-305.	1.1	27
64	Phylogenetic analysis of apicomplexan parasites infecting commercially valuable species from the North-East Atlantic reveals high levels of diversity and insights into the evolution of the group. <i>Parasites and Vectors</i> , 2018, 11, 63.	1.0	21
65	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, .	1.5	20
66	Relationship of the Middle Ear Effusion Microbiome to Secretory Mucin Production in Pediatric Patients With Chronic Otitis Media. <i>Pediatric Infectious Disease Journal</i> , 2017, 36, 635-640.	1.1	32
67	Nasopharyngeal Microbiome in Premature Infants and Stability during Rhinovirus Infection. <i>Journal of Investigative Medicine</i> , 2017, 65, 984-990.	0.7	16
68	Nasopharyngeal Microbiome Diversity Changes over Time in Children with Asthma. <i>PLoS ONE</i> , 2017, 12, e0170543.	1.1	55
69	Multilocus Sequence Typing of Pathogens. , 2017, , 383-404.		12
70	The temporal dynamics of the tracheal microbiome in tracheostomised patients with and without lower respiratory infections. <i>PLoS ONE</i> , 2017, 12, e0182520.	1.1	24
71	Characterization of HIV diversity, phylodynamics and drug resistance in Washington, DC. <i>PLoS ONE</i> , 2017, 12, e0185644.	1.1	20
72	Metataxonomic and Metagenomic Approaches vs. Culture-Based Techniques for Clinical Pathology. <i>Frontiers in Microbiology</i> , 2016, 7, 484.	1.5	78

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73	Two sampling methods yield distinct microbial signatures in the nasopharynges of asthmatic children. <i>Microbiome</i> , 2016, 4, 25.	4.9	31
74	Different next generation sequencing platforms produce different microbial profiles and diversity in cystic fibrosis sputum. <i>Journal of Microbiological Methods</i> , 2016, 130, 95-99.	0.7	39
75	Nasopharynx Microbiome Composition Varies over Time in Pediatric Asthma. <i>Journal of Investigative Medicine</i> , 2016, 64, 815-815.	0.7	0
76	Redefining Healthy Urine: A Cross-Sectional Exploratory Metagenomic Study of People With and Without Bladder Dysfunction. <i>Journal of Urology</i> , 2016, 196, 579-587.	0.2	58
77	Characterization of the bacterial communities of casts from <i>Eisenia andrei</i> fed with different substrates. <i>Applied Soil Ecology</i> , 2016, 98, 103-111.	2.1	56
78	DNA barcoding of earthworms ( <i>Eisenia fetida/andrei</i> complex) from 28 ecotoxicological test laboratories. <i>Applied Soil Ecology</i> , 2016, 104, 3-11.	2.1	38
79	Proteomic Characterization of Middle Ear Fluid Confirms Neutrophil Extracellular Traps as a Predominant Innate Immune Response in Chronic Otitis Media. <i>PLoS ONE</i> , 2016, 11, e0152865.	1.1	38
80	Comparison of two commercial DNA extraction kits for the analysis of nasopharyngeal bacterial communities. <i>AIMS Microbiology</i> , 2016, 2, 108-119.	1.0	18
81	MP20-08 PYLURIA AND ASYMPTOMATIC BACTERIURIA IS ASSOCIATED WITH NOVEL AND SPECIFIC URINE MICROBIOMES. <i>Journal of Urology</i> , 2015, 193, .	0.2	2
82	MP20-07 ALL ASYMPTOMATIC BACTERIURIA, ALL THE TIME. <i>Journal of Urology</i> , 2015, 193, .	0.2	0
83	Three new species of Aeglidae ( Aegla Leach, 1820) from Paraná State, Brazil. <i>Journal of Crustacean Biology</i> , 2015, 35, 839-849.	0.3	15
84	Recombination in viruses: Mechanisms, methods of study, and evolutionary consequences. <i>Infection, Genetics and Evolution</i> , 2015, 30, 296-307.	1.0	255
85	Feeding on microbiomes: effects of detritivory on the taxonomic and phylogenetic bacterial composition of animal manures. <i>FEMS Microbiology Ecology</i> , 2015, 91, fiv117.	1.3	53
86	Integrating microbial and host transcriptomics to characterize asthma-associated microbial communities. <i>BMC Medical Genomics</i> , 2015, 8, 50.	0.7	63
87	Underground evolution: New roots for the old tree of lumbricid earthworms. <i>Molecular Phylogenetics and Evolution</i> , 2015, 83, 7-19.	1.2	69
88	Dual Transcriptomic Profiling of Host and Microbiota during Health and Disease in Pediatric Asthma. <i>PLoS ONE</i> , 2015, 10, e0131819.	1.1	87
89	Phylogeny and Phylogeography of a Recent HIV-1 Subtype F Outbreak among Men Who Have Sex with Men in Spain Deriving from a Cluster with a Wide Geographic Circulation in Western Europe. <i>PLoS ONE</i> , 2015, 10, e0143325.	1.1	29
90	Composition, taxonomy and functional diversity of the oropharynx microbiome in individuals with schizophrenia and controls. <i>PeerJ</i> , 2015, 3, e1140.	0.9	222

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91	Multiplexing of novel microsatellite loci for the vulnerable slipper lobster <i>Scyllarus arctus</i> (Linnaeus, 1758). <i>Journal of Experimental Zoology</i> , 2014, 321, 119-123.	1.2	2
92	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, 3913-3921.	1.8	69
93	Molecular phylogeny, systematics and morphological evolution of the acorn barnacles (Thoracica: Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.2	40
94	Molecular phylogenetic analysis of the coccidian cephalopod parasites <i>Aggregata octopiana</i> and <i>Aggregata eberthi</i> (Apicomplexa: Aggregatidae) from the NE Atlantic coast using 18S rRNA sequences. <i>European Journal of Protistology</i> , 2013, 49, 373-380.	0.5	14
95	Pathogen typing in the genomics era: MLST and the future of molecular epidemiology. <i>Infection, Genetics and Evolution</i> , 2013, 16, 38-53.	1.0	157
96	Panmixia in the endangered slipper lobster <i>Scyllarides latus</i> from the northeastern Atlantic and western Mediterranean. <i>Journal of Crustacean Biology</i> , 2013, 33, 557-566.	0.3	8
97	<strong>Phylogenetic relationships of the family Sphaeromatidae Latreille, 1825 (Crustacea: Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.2	22
98	New species and records of the genus <i>Aegla</i> Leach, 1820 (Crustacea, Anomura, Aeglididae) from the West-Central region of Rio Grande do Sul, Brazil. <i>Nauplius</i> , 2013, 21, 211-223.	0.3	19
99	Molecular phylogeny and character evolution of the chthamaloid barnacles (Cirripedia: Thoracica). <i>Molecular Phylogenetics and Evolution</i> , 2012, 65, 329-334.	1.2	12
100	Genetic diversity and molecular epidemiology of HIV transmission. <i>Future Virology</i> , 2012, 7, 239-252.	0.9	11
101	The evolution of HIV: Inferences using phylogenetics. <i>Molecular Phylogenetics and Evolution</i> , 2012, 62, 777-792.	1.2	79
102	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.	0.3	28
103	Taxonomic assessment of Lumbricidae (Oligochaeta) earthworm genera using DNA barcodes. <i>European Journal of Soil Biology</i> , 2012, 48, 41-47.	1.4	35
104	Deep Phylogeny and Character Evolution in Thecostraca (Crustacea: Maxillopoda). <i>Integrative and Comparative Biology</i> , 2012, 52, 430-442.	0.9	17
105	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, 1822-1830.	1.0	5
106	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.	1.1	24
107	How Long Does Evolution of the Troglomorphic Form Take? Estimating Divergence Times in <i>Astyanax Mexicanus</i> . <i>Acta Carsologica</i> , 2012, 36, .	0.3	22
108	Multilocus Sequence Typing of Pathogens. , 2011, , 503-521.		5

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109	Phylodynamics of HIV-1 from a Phase III AIDS Vaccine Trial in Bangkok, Thailand. PLoS ONE, 2011, 6, e16902.	1.1	34
110	An Earthworm Riddle: Systematics and Phylogeography of the Spanish Lumbricid Postandrilus. PLoS ONE, 2011, 6, e28153.	1.1	38
111	Comparing phylogeographic patterns across the Patagonian Andes in twofreshwater crabs of the		



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127	Aegla manuiflata, a new species of freshwater anomuran (Decapoda: Anomura: Aegliidae) from Brazil, determined by morphological and molecular characters. <i>Zootaxa</i> , 2009, 2088, 31-40.	0.2	28
128	The Timing of the Diversification of the Freshwater Crayfishes. <i>Crustacean Issues</i> , 2009, , 343-355.	0.9	25
129	Assessing the conservation status of the land snail <i>Oreohelix peripherica wasatchensis</i> (Family) Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.8	10
130	Global diversity of crabs (Aegliidae: Anomura: Decapoda) in freshwater. <i>Hydrobiologia</i> , 2008, 595, 267-273.	1.0	68
131	Disease progression and evolution of the HIV-1 env gene in 24 infected infants. <i>Infection, Genetics and Evolution</i> , 2008, 8, 110-120.	1.0	21
132	The tempo and mode of barnacle evolution. <i>Molecular Phylogenetics and Evolution</i> , 2008, 46, 328-346.	1.2	127
133	Methods for Analyzing Viral Evolution. , 2008, , 165-204.		5
134	New methods for inferring population dynamics from microbial sequences. <i>Infection, Genetics and Evolution</i> , 2007, 7, 24-43.	1.0	18
135	Temporal trends in gonococcal population genetics in a high prevalence urban community. <i>Infection, Genetics and Evolution</i> , 2007, 7, 271-278.	1.0	36
136	Testing hypotheses of population structuring in the Northeast Atlantic Ocean and Mediterranean Sea using the common cuttlefish <i>Sepia officinalis</i> . <i>Molecular Ecology</i> , 2007, 16, 2667-2679.	2.0	97
137	Distinguishing importation from diversification of quinolone-resistant <i>Neisseria gonorrhoeae</i> by molecular evolutionary analysis. <i>BMC Evolutionary Biology</i> , 2007, 7, 84.	3.2	12
138	Global diversity of crabs (Aegliidae: Anomura: Decapoda) in freshwater. , 2007, , 267-273.		2
139	Population genetics of microbial pathogens estimated from multilocus sequence typing (MLST) data. <i>Infection, Genetics and Evolution</i> , 2006, 6, 97-112.	1.0	135
140	Evolution of Afrotropical freshwater crab lineages obscured by morphological convergence. <i>Molecular Phylogenetics and Evolution</i> , 2006, 40, 227-235.	1.2	70
141	Comparing Phylogenetic Codivergence between Polyomaviruses and Their Hosts. <i>Journal of Virology</i> , 2006, 80, 5663-5669.	1.5	71
142	Longitudinal Population Analysis of Dual Infection with Recombination in Two Strains of HIV Type 1 Subtype B in an Individual from a Phase 3 HIV Vaccine Efficacy Trial. <i>AIDS Research and Human Retroviruses</i> , 2006, 22, 968-978.	0.5	8
143	Phylogenomics and Molecular Evolution of Polyomaviruses. <i>Advances in Experimental Medicine and Biology</i> , 2006, 577, 46-59.	0.8	12
144	Phylogeny and biogeography of the freshwater crayfish <i>Euastacus</i> (Decapoda: Parastacidae) based on nuclear and mitochondrial DNA. <i>Molecular Phylogenetics and Evolution</i> , 2005, 37, 249-263.	1.2	60

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145	Model-based multi-locus estimation of decapod phylogeny and divergence times. <i>Molecular Phylogenetics and Evolution</i> , 2005, 37, 355-369.	1.2	223
146	First genetic validation and diagnosis of the short-finned squid species of the genus <i>Illex</i> (Cephalopoda: Ommastrephidae). <i>Marine Biology</i> , 2005, 148, 97-108.	0.7	10
147	Population Genetics of <i>Neisseria gonorrhoeae</i> in a High-Prevalence Community Using a Hypervariable Outer Membrane porB and 13 Slowly Evolving Housekeeping Genes. <i>Molecular Biology and Evolution</i> , 2005, 22, 1887-1902.	3.5	40
148	Phylogenetic species delimitation of the earthworms <i>Eisenia fetida</i> (Savigny, 1826) and <i>Eisenia andrei</i> Bouché, 1972 (Oligochaeta, Lumbricidae) based on mitochondrial and nuclear DNA sequences. <i>Pedobiologia</i> , 2005, 49, 317-324.	0.5	101
149	Unraveling the Evolutionary Radiation of the Thoracican Barnacles Using Molecular and Morphological Evidence: A Comparison of Several Divergence Time Estimation Approaches. <i>Systematic Biology</i> , 2004, 53, 244-264.	2.7	112
150	Molecular Systematics and Biogeography of the Southern South American Freshwater Crabs <i>Aegla</i> (Decapoda: Anomura: Aeglidae) Using Multiple Heuristic Tree Search Approaches. <i>Systematic Biology</i> , 2004, 53, 767-780.	2.7	113
151	REANALYSIS OF THE RELATIONSHIPS AMONG THE CIRRIPIEDIA AND THE ASCOTHORACIDA AND THE PHYLOGENETIC POSITION OF THE FACETOTECTA (MAXILLOPODA: THECOSTRACA) USING 18S rDNA SEQUENCES. <i>Journal of Crustacean Biology</i> , 2002, 22, 661-669.	0.3	14
152	Phylogenetic Relationships among the Species of <i>Aegla</i> (Anomura: Aeglidae) Freshwater Crabs from Chile. <i>Journal of Crustacean Biology</i> , 2002, 22, 304-313.	0.3	25
153	Phylogenetic Position of the Freshwater Anomuran Family Aeglidae. <i>Journal of Crustacean Biology</i> , 2002, 22, 670-676.	0.3	19
154	Reanalysis of the Relationships among the Cirripedia and the Ascothoracida and the Phylogenetic Position of the Facetotecta (Maxillopoda: Thecostraca) Using 18S rDNA Sequences. <i>Journal of Crustacean Biology</i> , 2002, 22, 661-669.	0.3	27
155	PHYLOGENETIC POSITION OF THE FRESHWATER ANOMURAN FAMILY AEGLIDAE. <i>Journal of Crustacean Biology</i> , 2002, 22, 670-676.	0.3	26
156	PHYLOGENETIC RELATIONSHIPS AMONG THE SPECIES OF AEGLA (ANOMURA: AEGLIDAE) FRESHWATER CRABS FROM CHILE. <i>Journal of Crustacean Biology</i> , 2002, 22, 304-313.	0.3	34
157	Conservation phylogenetics of Chilean freshwater crabs <i>Aegla</i> (Anomura, Aeglidae): assigning priorities for aquatic habitat protection. <i>Biological Conservation</i> , 2002, 105, 345-353.	1.9	56
158	Extensive population subdivision of the cuttlefish <i>Sepia officinalis</i> (Mollusca: Cephalopoda) around the Iberian Peninsula indicated by microsatellite DNA variation. <i>Heredity</i> , 2002, 89, 417-424.	1.2	107
159	Molecular phylogenetics for conservation biology. , 2001, , 19-56.		12
160	Species differentiation of <i>Sepia officinalis</i> and <i>Sepia hierredda</i> (Cephalopoda: Sepiidae) based on morphological and allozyme analyses. <i>Journal of the Marine Biological Association of the United Kingdom</i> , 2001, 81, 271-281.	0.4	7
161	Polymorphic microsatellites in the common cuttlefish <i>Sepia officinalis</i> (Cephalopoda). <i>Molecular Ecology</i> , 2000, 9, 237-238.	2.0	20
162	Allozyme differentiation in the cuttlefish <i>Sepia officinalis</i> (Mollusca: Cephalopoda) from the NE Atlantic and Mediterranean. <i>Heredity</i> , 1999, 83, 280-289.	1.2	44

#	ARTICLE	IF	CITATIONS
163	Allozyme Evidence for Cryptic Speciation in Sympatric Populations of <i>Nassarius</i> spp. (Mollusca: Tj ETQq1 1 0,784314 rgBT /Overl 0,4 16	0,4	16
164	Allozyme electrophoretic technique and phylogenetic relationships in three species of Sepia (Cephalopoda: Sepiidae). Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology, 1996, 114, 11-18.	0.7	10
165	Genetic differentiation in three Sepia species (Mollusca: Cephalopoda) from Galician waters (north-west Iberian Peninsula). Marine Biology, 1996, 126, 253-259.	0.7	14
166	Aegla chilota, new species of anomuran freshwater crab from Chilo Island, western Patagonia. Nauplius, 0, 26, .	0.3	8
167	The Habitat Types of Freshwater Prawns (Palaemonidae: <i>Macrobrachium</i> ) with Abbreviated Larval Development in Mesoamerica (Mexico, Guatemala and Belize). , 0, , .		1
168	Epidemiological and Evolutionary Dynamics of Pathogens. , 0, , 21-30.		0