

# Omar Rota-Stabelli

## List of Publications by Year in descending order

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Version: 2024-02-01

60  
papers

4,383  
citations

159585

30  
h-index

138484

58  
g-index

71  
all docs

71  
docs citations

71  
times ranked

5470  
citing authors

#	ARTICLE	IF	CITATIONS
1	On the Origin and Propagation of the COVID-19 Outbreak in the Italian Province of Trento, a Tourist Region of Northern Italy. <i>Viruses</i> , 2022, 14, 580.	3.3	1
2	The Impact of Fast Radiation on the Phylogeny of <i>Bactrocera</i> Fruit Flies as Revealed by Multiple Evolutionary Models and Mutation Rate-Calibrated Clock. <i>Insects</i> , 2022, 13, 603.	2.2	4
3	Chronological Incongruences between Mitochondrial and Nuclear Phylogenies of <i>Aedes</i> Mosquitoes. <i>Life</i> , 2021, 11, 181.	2.4	14
4	Pre-Cambrian roots of novel Antarctic cryptoendolithic bacterial lineages. <i>Microbiome</i> , 2021, 9, 63.	11.1	17
5	Reconstruction of ancient microbial genomes from the human gut. <i>Nature</i> , 2021, 594, 234-239.	27.8	139
6	Phylogenomics of Opsin Genes in Diptera Reveals Lineage-Specific Events and Contrasting Evolutionary Dynamics in <i>Anopheles</i> and <i>Drosophila</i> . <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	16
7	Divergence and hybridization in sea turtles: Inferences from genome data show evidence of ancient gene flow between species. <i>Molecular Ecology</i> , 2021, 30, 6178-6192.	3.9	24
8	Metagenomic analysis of ancient dental calculus reveals unexplored diversity of oral archaeal <i>Methanobrevibacter</i> . <i>Microbiome</i> , 2021, 9, 197.	11.1	18
9	<i>Drosophila</i> Evolution over Space and Time (DEST): A New Population Genomics Resource. <i>Molecular Biology and Evolution</i> , 2021, 38, 5782-5805.	8.9	37
10	Viviparity and habitat restrictions may influence the evolution of male reproductive genes in tsetse fly ( <i>Glossina</i> ) species. <i>BMC Biology</i> , 2021, 19, 211.	3.8	5
11	The evolution of insect biodiversity. <i>Current Biology</i> , 2021, 31, R1299-R1311.	3.9	39
12	Hallstatt miners consumed blue cheese and beer during the Iron Age and retained a non-Westernized gut microbiome until the Baroque period. <i>Current Biology</i> , 2021, 31, 5149-5162.e6.	3.9	22
13	Distinct genotypes and phenotypes in European and American strains of <i>Drosophila suzukii</i> : implications for biology and management of an invasive organism. <i>Journal of Pest Science</i> , 2020, 93, 77-89.	3.7	29
14	On the correct interpretation of similarity index in codon usage studies: Comparison with four other metrics and implications for Zika and West Nile virus. <i>Virus Research</i> , 2020, 286, 198097.	2.2	7
15	Large scale genome reconstructions illuminate <i>Wolbachia</i> evolution. <i>Nature Communications</i> , 2020, 11, 5235.	12.8	71
16	Structural and transcriptional evidence of mechanotransduction in the <i>Drosophila suzukii</i> ovipositor. <i>Journal of Insect Physiology</i> , 2020, 125, 104088.	2.0	22
17	Age, tissue, genotype and virus infection regulate <i>Wolbachia</i> levels in <i>Drosophila</i> . <i>Molecular Ecology</i> , 2020, 29, 2063-2079.	3.9	22
18	Sensory Neuroscience: A Taste for Light and the Origin of Animal Vision. <i>Current Biology</i> , 2020, 30, R773-R775.	3.9	7

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19	Complete mitochondrial genomes from transcriptomes: assessing pros and cons of data mining for assembling new mitogenomes. <i>Scientific Reports</i> , 2019, 9, 14806.	3.3	14
20	The <i>Prevotella copri</i> Complex Comprises Four Distinct Clades Underrepresented in Westernized Populations. <i>Cell Host and Microbe</i> , 2019, 26, 666-679.e7.	11.0	274
21	A chromosome-level genome assembly of <i>Cydia pomonella</i> provides insights into chemical ecology and insecticide resistance. <i>Nature Communications</i> , 2019, 10, 4237.	12.8	102
22	Survival and divergence in a small group: The extraordinary genomic history of the endangered Apennine brown bear stragglers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E9589-E9597.	7.1	140
23	Improved Modeling of Compositional Heterogeneity Supports Sponges as Sister to All Other Animals. <i>Current Biology</i> , 2017, 27, 3864-3870.e4.	3.9	244
24	Insertion sequence polymorphism and genomic rearrangements uncover hidden <i>Wolbachia</i> diversity in <i>Drosophila suzukii</i> and <i>D. subpulchrella</i> . <i>Scientific Reports</i> , 2017, 7, 14815.	3.3	15
25	Application of the consolidated species concept to identify the causal agent of strawberry anthracnose in Iran and initial molecular dating of the <i>Colletotrichum acutatum</i> species complex. <i>European Journal of Plant Pathology</i> , 2017, 147, 375-387.	1.7	19
26	Genome comparisons indicate recent transfer of <i>Wolbachia</i> between sister species <i>Drosophila suzukii</i> and <i>D. subpulchrella</i> . <i>Ecology and Evolution</i> , 2017, 7, 9391-9404.	1.9	49
27	Evolutionary scenarios for the origin of an Antarctic tardigrade species based on molecular clock analyses and biogeographic data. <i>Contributions To Zoology</i> , 2017, 86, 97-110.	0.5	26
28	Extracting spatio-temporal patterns in animal trajectories: an ecological application of sequence analysis methods. <i>Methods in Ecology and Evolution</i> , 2016, 7, 369-379.	5.2	35
29	Evolutionary Insights into Taste Perception of the Invasive Pest <i>Drosophila suzukii</i> . <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 4185-4196.	1.8	35
30	Identification and Characterization of two new Fungal Pathogens of <i>Polygonatum odoratum</i> (Angular Solomon's seal) in Italy. <i>Journal of Phytopathology</i> , 2016, 164, 1075-1084.	1.0	7
31	Multiple lines of evidence for reproductive winter diapause in the invasive pest <i>Drosophila suzukii</i> : useful clues for control strategies. <i>Journal of Pest Science</i> , 2016, 89, 689-700.	3.7	98
32	TRPA5, an Ankyrin Subfamily Insect TRP Channel, is Expressed in Antennae of <i>Cydia pomonella</i> (Lepidoptera: Tortricidae) in Multiple Splice Variants. <i>Journal of Insect Science</i> , 2016, 16, 83.	1.5	13
33	Relaxed selective constraints drove functional modifications in peripheral photoreception of the cavefish <i>P. andruzzii</i> and provide insight into the time of cave colonization. <i>Heredity</i> , 2016, 117, 383-392.	2.6	35
34	The Evolution of Olfactory Gene Families in <i>Drosophila</i> and the Genomic Basis of chemical-Ecological Adaptation in <i>Drosophila suzukii</i> . <i>Genome Biology and Evolution</i> , 2016, 8, 2297-2311.	2.5	76
35	Reply to Halanych et al.: Ctenophore misplacement is corroborated by independent datasets. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E948-9.	7.1	14
36	<i>Wolbachia</i> in European Populations of the Invasive Pest <i>Drosophila suzukii</i> : Regional Variation in Infection Frequencies. <i>PLoS ONE</i> , 2016, 11, e0147766.	2.5	37

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37	Loss of <i>Drosophila</i> pheromone reverses its role in sexual communication in <i>Drosophila suzukii</i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2015, 282, 20143018.	2.6	70
38	Olfactory responses of <i>Drosophila suzukii</i> females to host plant volatiles. <i>Physiological Entomology</i> , 2015, 40, 54-64.	1.5	87
39	Genomic data do not support comb jellies as the sister group to all other animals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 15402-15407.	7.1	286
40	Molecular-based estimate of species number, phylogenetic relationships and divergence times for the genus <i>Stenotaenia</i> (Chilopoda, Geophilomorpha) in the Italian region. <i>ZooKeys</i> , 2015, 510, 31-47.	1.1	7
41	The Comb Jelly Opsins and the Origins of Animal Phototransduction. <i>Genome Biology and Evolution</i> , 2014, 6, 1964-1971.	2.5	62
42	Interkingdom Transfer of the Acne-Causing Agent, <i>Propionibacterium acnes</i> , from Human to Grapevine. <i>Molecular Biology and Evolution</i> , 2014, 31, 1059-1065.	8.9	54
43	<i>Drosophila suzukii</i> . <i>Current Biology</i> , 2013, 23, R8-R9.	3.9	137
44	Molecular Timetrees Reveal a Cambrian Colonization of Land and a New Scenario for Ecdysozoan Evolution. <i>Current Biology</i> , 2013, 23, 392-398.	3.9	322
45	Bioinformatics methods for the comparative analysis of metazoan mitochondrial genome sequences. <i>Molecular Phylogenetics and Evolution</i> , 2013, 69, 320-327.	2.7	31
46	Serine Codon-Usage Bias in Deep Phylogenomics: Pancrustacean Relationships as a Case Study. <i>Systematic Biology</i> , 2013, 62, 121-133.	5.6	124
47	Draft Genome Sequence of the <i>Wolbachia</i> Endosymbiont of <i>Drosophila suzukii</i> . <i>Genome Announcements</i> , 2013, 1, .	0.8	37
48	Gibberellin metabolism in <i>Vitis vinifera</i> L. during bloom and fruit-set: functional characterization and evolution of grapevine gibberellin oxidases. <i>Journal of Experimental Botany</i> , 2013, 64, 4403-4419.	4.8	102
49	Linking Genomics and Ecology to Investigate the Complex Evolution of an Invasive <i>Drosophila</i> Pest. <i>Genome Biology and Evolution</i> , 2013, 5, 745-757.	2.5	138
50	An Overview of Arthropod Genomics, Mitogenomics, and the Evolutionary Origins of the Arthropod Proteome. , 2013, , 41-61.		10
51	An Overview of Arthropod Genomics, Mitogenomics, and the Evolutionary Origins of the Arthropod Proteome. , 2013, , 41-61.		3
52	A congruent solution to arthropod phylogeny: phylogenomics, microRNAs and morphology support monophyletic Mandibulata. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2011, 278, 298-306.	2.6	227
53	MicroRNAs and phylogenomics resolve the relationships of Tardigrada and suggest that velvet worms are the sister group of Arthropoda. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 15920-15924.	7.1	212
54	Ecdysozoan Mitogenomics: Evidence for a Common Origin of the Legged Invertebrates, the Panarthropoda. <i>Genome Biology and Evolution</i> , 2010, 2, 425-440.	2.5	154

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55	The mitochondrial genome structure of <i>Xenoturbella bocki</i> (phylum Xenoturbellida) is ancestral within the deuterostomes. <i>BMC Evolutionary Biology</i> , 2009, 9, 107.	3.2	36
56	MtZoa: A general mitochondrial amino acid substitutions model for animal evolutionary studies. <i>Molecular Phylogenetics and Evolution</i> , 2009, 52, 268-272.	2.7	105
57	The origins and evolution of the Ecdysozoa. , 2009, , 71-79.		2
58	A multi criterion approach for the selection of optimal outgroups in phylogeny: Recovering some support for Mandibulata over Myriochelata using mitogenomics. <i>Molecular Phylogenetics and Evolution</i> , 2008, 48, 103-111.	2.7	117
59	The evolution of the Ecdysozoa. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2008, 363, 1529-1537.	4.0	203
60	Mitogenomics and phylogenomics reveal priapulid worms as extant models of the ancestral Ecdysozoan. <i>Evolution &amp; Development</i> , 2006, 8, 502-510.	2.0	88