

# Tyler S Alioto

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3813182/publications.pdf>

Version: 2024-02-01

53  
papers

34,282  
citations

136740

32  
h-index

174990

52  
g-index

58  
all docs

58  
docs citations

58  
times ranked

55852  
citing authors

#	ARTICLE	IF	CITATIONS
1	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012, 489, 57-74.	13.7	15,516
2	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007, 447, 799-816.	13.7	4,709
3	Landscape of transcription in human cells. <i>Nature</i> , 2012, 489, 101-108.	13.7	4,484
4	The tomato genome sequence provides insights into fleshy fruit evolution. <i>Nature</i> , 2012, 485, 635-641.	13.7	2,860
5	A User's Guide to the Encyclopedia of DNA Elements (ENCODE). <i>PLoS Biology</i> , 2011, 9, e1001046.	2.6	1,257
6	The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution. <i>Science</i> , 2009, 324, 522-528.	6.0	1,038
7	Assessment of transcript reconstruction methods for RNA-seq. <i>Nature Methods</i> , 2013, 10, 1177-1184.	9.0	679
8	The genome of melon ( <i>Cucumis melo</i> L.). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 11872-11877.	3.3	654
9	Systematic evaluation of spliced alignment programs for RNA-seq data. <i>Nature Methods</i> , 2013, 10, 1185-1191.	9.0	467
10	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. <i>Nature Communications</i> , 2015, 6, 10001.	5.8	266
11	Genome sequence of the olive tree, <i>Olea europaea</i> . <i>GigaScience</i> , 2016, 5, 29.	3.3	201
12	Prominent use of distal 5' transcription start sites and discovery of a large number of additional exons in ENCODE regions. <i>Genome Research</i> , 2007, 17, 746-759.	2.4	173
13	Genome and transcriptome analysis of the Mesoamerican common bean and the role of gene duplications in establishing tissue and temporal specialization of genes. <i>Genome Biology</i> , 2016, 17, 32.	3.8	166
14	U12DB: a database of orthologous U12-type spliceosomal introns. <i>Nucleic Acids Research</i> , 2007, 35, D110-D115.	6.5	151
15	Whole genome sequencing of turbot ( <i>Scophthalmus maximus</i> ; Pleuronectiformes): a fish adapted to demersal life. <i>DNA Research</i> , 2016, 23, 181-192.	1.5	150
16	The odorant receptor repertoire of teleost fish. <i>BMC Genomics</i> , 2005, 6, 173.	1.2	140
17	Extreme genomic erosion after recurrent demographic bottlenecks in the highly endangered Iberian lynx. <i>Genome Biology</i> , 2016, 17, 251.	3.8	131
18	Using geneid to Identify Genes. <i>Current Protocols in Bioinformatics</i> , 2018, 64, e56.	25.8	112

#	ARTICLE	IF	CITATIONS
19	Massive gene presence-absence variation shapes an open pan-genome in the Mediterranean mussel. <i>Genome Biology</i> , 2020, 21, 275.	3.8	105
20	Transposons played a major role in the diversification between the closely related almond and peach genomes: results from the almond genome sequence. <i>Plant Journal</i> , 2020, 101, 455-472.	2.8	94
21	Selective single molecule sequencing and assembly of a human Y chromosome of African origin. <i>Nature Communications</i> , 2019, 10, 4.	5.8	90
22	Identifying protein-coding genes in genomic sequences. <i>Genome Biology</i> , 2009, 10, 201.	13.9	82
23	A nuclear lamin is required for cytoplasmic organization and egg polarity in <i>Drosophila</i> . <i>Nature Cell Biology</i> , 2001, 3, 848-851.	4.6	77
24	The repertoire of olfactory C family G protein-coupled receptors in zebrafish: candidate chemosensory receptors for amino acids. <i>BMC Genomics</i> , 2006, 7, 309.	1.2	76
25	The Origins, Evolution, and Functional Potential of Alternative Splicing in Vertebrates. <i>Molecular Biology and Evolution</i> , 2011, 28, 2949-2959.	3.5	74
26	nGASP – the nematode genome annotation assessment project. <i>BMC Bioinformatics</i> , 2008, 9, 549.	1.2	61
27	Genomic adaptations to aquatic and aerial life in mayflies and the origin of insect wings. <i>Nature Communications</i> , 2020, 11, 2631.	5.8	57
28	A Reference Genome Sequence for the European Silver Fir ( <i>Abies alba</i> Mill.): A Community-Generated Genomic Resource. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2039-2049.	0.8	53
29	Genomic evidence for recurrent genetic admixture during the domestication of Mediterranean olive trees ( <i>Olea europaea</i> L.). <i>BMC Biology</i> , 2020, 18, 148.	1.7	39
30	Epigenetic regulation of gene expression in Chinese Hamster Ovary cells in response to the changing environment of a batch culture. <i>Biotechnology and Bioengineering</i> , 2019, 116, 677-692.	1.7	37
31	European sea bass brain DLB-1 cell line is susceptible to nodavirus: A transcriptomic study. <i>Fish and Shellfish Immunology</i> , 2019, 86, 14-24.	1.6	35
32	Innate Cell-Mediated Cytotoxic Activity of European Sea Bass Leucocytes Against Nodavirus-Infected Cells: A Functional and RNA-seq Study. <i>Scientific Reports</i> , 2017, 7, 15396.	1.6	33
33	Phylogenomics Identifies an Ancestral Burst of Gene Duplications Predating the Diversification of Aphidomorpha. <i>Molecular Biology and Evolution</i> , 2020, 37, 730-756.	3.5	29
34	<i>Septin 3</i> Gene Polymorphism in Alzheimer's Disease. <i>Gene Expression</i> , 2003, 11, 263-270.	0.5	24
35	A 3-way hybrid approach to generate a new high-quality chimpanzee reference genome (Pan_tro_3.0). <i>GigaScience</i> , 2017, 6, 1-6.	3.3	17
36	Gene Prediction. <i>Methods in Molecular Biology</i> , 2012, 855, 175-201.	0.4	14

#	ARTICLE	IF	CITATIONS
37	The High-Quality Genome Sequence of the Oceanic Island Endemic Species <i>Drosophila guanche</i> Reveals Signals of Adaptive Evolution in Genes Related to Flight and Genome Stability. <i>Genome Biology and Evolution</i> , 2018, 10, 1956-1969.	1.1	14
38	Chromosome anchoring in Senegalese sole ( <i>Solea senegalensis</i> ) reveals sex-associated markers and genome rearrangements in flatfish. <i>Scientific Reports</i> , 2021, 11, 13460.	1.6	14
39	The Genome Sequence of the Eastern Woodchuck ( <i>Marmota monax</i> ) – A Preclinical Animal Model for Chronic Hepatitis B. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3943-3952.	0.8	13
40	Genome Sequence of <i>Plesiomonas shigelloides</i> Strain 302-73 (Serotype O1). <i>Genome Announcements</i> , 2013, 1, .	0.8	12
41	Emergence of 16S rRNA methyltransferases among carbapenemase-producing Enterobacterales in Spain studied by whole-genome sequencing. <i>International Journal of Antimicrobial Agents</i> , 2022, 59, 106456.	1.1	11
42	An Improved Matrix-Assisted Laser Desorption Ionization–Time of Flight Mass Spectrometry Data Analysis Pipeline for the Identification of Carbapenemase-Producing <i>Klebsiella pneumoniae</i> . <i>Journal of Clinical Microbiology</i> , 2021, 59, e0080021.	1.8	9
43	ASPic-GenelD: A Lightweight Pipeline for Gene Prediction and Alternative Isoforms Detection. <i>BioMed Research International</i> , 2013, 2013, 1-11.	0.9	8
44	Tetracycline resistance transmission in <i>Campylobacter</i> is promoted at temperatures resembling the avian reservoir. <i>Veterinary Microbiology</i> , 2020, 244, 108652.	0.8	7
45	The Genome Sequence of the Octocoral <i>Paramuricea clavata</i> – A Key Resource To Study the Impact of Climate Change in the Mediterranean. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2941-2952.	0.8	6
46	Occurrence of the <i>pO19</i> Gene in the <i>bla</i> <sub>KPC</sub> -Harboring Plasmids: Adverse Clinical Impact for Direct Tracking of KPC-Producing <i>Klebsiella pneumoniae</i> by Matrix-Assisted Laser Desorption Ionization–Time of Flight Mass Spectrometry. <i>Journal of Clinical Microbiology</i> , 2021, 59, e0023821.	1.8	6
47	<i>De Novo</i> Assembly and Annotation of the Larval Transcriptome of Two Spadefoot Toads Widely Divergent in Developmental Rate. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2647-2655.	0.8	5
48	Linking omics and ecology to dissect interactions between the apple proliferation phytoplasma and its psyllid vector <i>Cacopsylla melanoneura</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2020, 127, 103474.	1.2	5
49	Alteration in the <i>Culex pipiens</i> transcriptome reveals diverse mechanisms of the mosquito immune system implicated upon Rift Valley fever phlebovirus exposure. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008870.	1.3	4
50	Combining Nanopore and Illumina Sequencing Permits Detailed Analysis of Insertion Mutations and Structural Variations Produced by PEG-Mediated Transformation in <i>Ostreococcus tauri</i> . <i>Cells</i> , 2021, 10, 664.	1.8	3
51	Whole-Genome Sequencing Recommendations. , 2016, , 13-41.		2
52	Genotyping-by-sequencing resolves relationships in Polygonaceae tribe Eriogoneae. <i>Taxon</i> , 2021, 70, 826-841.	0.4	2
53	Chromosome-level assembly, annotation and phylome of <i>Pelobates cultripes</i> , the western spadefoot toad. <i>DNA Research</i> , 2022, 29, .	1.5	1