Tyler S Alioto

List of Publications by Year
in descending order

53 papers	34,282 citations	136950 32 h-index	175258 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. Nature, 2012, 489, 57-74.	27.8	15,516
2	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. Nature, 2007, 447, 799-816.	27.8	4,709
3	Landscape of transcription in human cells. Nature, 2012, 489, 101-108.	27.8	4,484
4	The tomato genome sequence provides insights into fleshy fruit evolution. Nature, 2012, 485, 635-641.	27.8	2,860
5	A User's Guide to the Encyclopedia of DNA Elements (ENCODE). PLoS Biology, 2011, 9, e1001046.	5.6	1,257
6	The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution. Science, 2009, 324, 522-528.	12.6	1,038
7	Assessment of transcript reconstruction methods for RNA-seq. Nature Methods, 2013, 10, 1177-1184.	19.0	679
8	The genome of melon (Cucumis melo L.). Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 11872-11877.	7.1	654
9	Systematic evaluation of spliced alignment programs for RNA-seq data. Nature Methods, 2013, 10, 1185-1191.	19.0	467
10	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. Nature Communications, 2015, 6, 10001.	12.8	266
11	Genome sequence of the olive tree, Olea europaea. GigaScience, 2016, 5, 29.	6.4	201
12	Prominent use of distal 5' transcription start sites and discovery of a large number of additional exons in ENCODE regions. Genome Research, 2007, 17, 746-759.	5.5	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. Genome Biology, 2016, 17, 32.	8.8	166
14	U12DB: a database of orthologous U12-type spliceosomal introns. Nucleic Acids Research, 2007, 35, D110-D115.	14.5	151
15	Whole genome sequencing of turbot (Scophthalmus maximus; Pleuronectiformes): a fish adapted to demersal life. DNA Research, 2016, 23, 181-192.	3.4	150
16	The odorant receptor repertoire of teleost fish. BMC Genomics, 2005, 6, 173.	2.8	140
17	Extreme genomic erosion after recurrent demographic bottlenecks in the highly endangered Iberian lynx. Genome Biology, 2016, 17, 251.	8.8	131
18	Using geneid to Identify Genes. Current Protocols in Bioinformatics, 2018, 64, e56.	25.8	112

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19	Massive gene presence-absence variation shapes an open pan-genome in the Mediterranean mussel. Genome Biology, 2020, 21, 275.	8.8	105
20	Transposons played a major role in the diversification between the closely related almond and peach genomes: results from the almond genome sequence. Plant Journal, 2020, 101, 455-472.	5.7	94
21	Selective single molecule sequencing and assembly of a human Y chromosome of African origin. Nature Communications, 2019, 10, 4.	12.8	90
22	Identifying protein-coding genes in genomic sequences. Genome Biology, 2009, 10, 201.	9.6	82
23	A nuclear lamin is required for cytoplasmic organization and egg polarity in Drosophila. Nature Cell Biology, 2001, 3, 848-851.	10.3	77
24	The repertoire of olfactory C family G protein-coupled receptors in zebrafish: candidate chemosensory receptors for amino acids. BMC Genomics, 2006, 7, 309.	2.8	76
25	The Origins, Evolution, and Functional Potential of Alternative Splicing in Vertebrates. Molecular Biology and Evolution, 2011, 28, 2949-2959.	8.9	74
26	nGASP â€“ the nematode genome annotation assessment project. BMC Bioinformatics, 2008, 9, 549.	2.6	61
27	Genomic adaptations to aquatic and aerial life in mayflies and the origin of insect wings. Nature Communications, 2020, 11, 2631.	12.8	57
28	A Reference Genome Sequence for the European Silver Fir (Abies albaMill.): A Community-Generated Genomic Resource. G3: Genes, Genomes, Genetics, 2019, 9, 2039-2049.	1.8	53
29	Genomic evidence for recurrent genetic admixture during the domestication of Mediterranean olive trees (Olea europaea L.). BMC Biology, 2020, 18, 148.	3.8	39
30	Epigenetic regulation of gene expression in Chinese Hamster Ovary cells in response to the changing environment of a batch culture. Biotechnology and Bioengineering, 2019, 116, 677-692.	3.3	37
31	European sea bass brain DLB-1â€¯cell line is susceptible to nodavirus: A transcriptomic study. Fish and Shellfish Immunology, 2019, 86, 14-24.	3.6	35
32	Innate Cell-Mediated Cytotoxic Activity of European Sea Bass Leucocytes Against Nodavirus-Infected Cells: A Functional and RNA-seq Study. Scientific Reports, 2017, 7, 15396.	3.3	33
33	Phylogenomics Identifies an Ancestral Burst of Gene Duplications Predating the Diversification of Aphidomorpha. Molecular Biology and Evolution, 2020, 37, 730-756.	8.9	29
34	Septin 3 Gene Polymorphism in Alzheimerâ€™s Disease. Gene Expression, 2003, 11, 263-270.	1.2	24
35	A 3-way hybrid approach to generate a new high-quality chimpanzee reference genome (Pan_tro_3.0). GigaScience, 2017, 6, 1-6.	6.4	17
36	Gene Prediction. Methods in Molecular Biology, 2012, 855, 175-201.	0.9	14

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37	The High-Quality Genome Sequence of the Oceanic Island Endemic Species Drosophila guanche Reveals Signals of Adaptive Evolution in Genes Related to Flight and Genome Stability. Genome Biology and Evolution, 2018, 10, 1956-1969.	2.5	14
38	Chromosome anchoring in Senegalese sole (Solea senegalensis) reveals sex-associated markers and genome rearrangements in flatfish. Scientific Reports, 2021, 11, 13460.	3.3	14
39	The Genome Sequence of the Eastern Woodchuck (Marmota monax) â€“ A Preclinical Animal Model for Chronic Hepatitis B. G3: Genes, Genomes, Genetics, 2019, 9, 3943-3952.	1.8	13
40	Genome Sequence of Plesiomonas shigelloides Strain 302-73 (Serotype O1). Genome Announcements, 2013, 1, .	0.8	12
41	Emergence of 16S rRNA methyltransferases among carbapenemase-producing Enterobacterales in Spain studied by whole-genome sequencing. International Journal of Antimicrobial Agents, 2022, 59, 106456.	2.5	11
42	An Improved Matrix-Assisted Laser Desorption Ionizationâ€“Time of Flight Mass Spectrometry Data Analysis Pipeline for the Identification of Carbapenemase-Producing Klebsiella pneumoniae. Journal of Clinical Microbiology, 2021, 59, e0080021.	3.9	9
43	ASPic-GeneID: A Lightweight Pipeline for Gene Prediction and Alternative Isoforms Detection. BioMed Research International, 2013, 2013, 1-11.	1.9	8
44	Tetracycline resistance transmission in Campylobacter is promoted at temperatures resembling the avian reservoir. Veterinary Microbiology, 2020, 244, 108652.	1.9	7
45	The Genome Sequence of the Octocoral Paramuricea clavata â€“ A Key Resource To Study the Impact of Climate Change in the Mediterranean. G3: Genes, Genomes, Genetics, 2020, 10, 2941-2952.	1.8	6
46	Occurrence of the p019 Gene in the bla _{KPC} -Harboring Plasmids: Adverse Clinical Impact for Direct Tracking of KPC-Producing Klebsiella pneumoniae by Matrix-Assisted Laser Desorption Ionizationâ€“Time of Flight Mass Spectrometry. Journal of Clinical Microbiology, 2021, 59, e0023821.	3.9	6
47	De Novo Assembly and Annotation of the Larval Transcriptome of Two Spadefoot Toads Widely Divergent in Developmental Rate. G3: Genes, Genomes, Genetics, 2019, 9, 2647-2655.	1.8	5
48	Linking omics and ecology to dissect interactions between the apple proliferation phytoplasma and its psyllid vector Cacopsylla melanoneura. Insect Biochemistry and Molecular Biology, 2020, 127, 103474.	2.7	5
49	Alteration in the Culex pipiens transcriptome reveals diverse mechanisms of the mosquito immune system implicated upon Rift Valley fever phlebovirus exposure. PLoS Neglected Tropical Diseases, 2020, 14, e0008870.	3.0	4
50	Combining Nanopore and Illumina Sequencing Permits Detailed Analysis of Insertion Mutations and Structural Variations Produced by PEG-Mediated Transformation in Ostreococcus tauri. Cells, 2021, 10, 664.	4.1	3
51	Whole-Genome Sequencing Recommendations. , 2016, , 13-41.		2
52	Genotypingâ€byâ€sequencing resolves relationships in Polygonaceae tribe Eriogoneae. Taxon, 2021, 70, 826-841.	0.7	2
53	Chromosome-level assembly, annotation and phylome of Pelobates cultripes, the western spadefoot toad. DNA Research, 2022, 29, .	3.4	1