

Kamel Jabbari

List of Publications by Year in descending order

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Version: 2024-02-01

50
papers

11,898
citations

172457

29
h-index

189892

50
g-index

52
all docs

52
docs citations

52
times ranked

13274
citing authors

#	ARTICLE	IF	CITATIONS
1	DNA sequence-dependent chromatin architecture and nuclear hubs formation. <i>Scientific Reports</i> , 2019, 9, 14646.	3.3	25
2	A common genomic code for chromatin architecture and recombination landscape. <i>PLoS ONE</i> , 2019, 14, e0213278.	2.5	18
3	Exome-wide analysis of mutational burden in patients with typical and atypical Rolandic epilepsy. <i>European Journal of Human Genetics</i> , 2018, 26, 258-264.	2.8	22
4	Rare gene deletions in genetic generalized and Rolandic epilepsies. <i>PLoS ONE</i> , 2018, 13, e0202022.	2.5	6
5	The Diverging Routes of BORIS and CTCF: An Interactomic and Phylogenomic Analysis. <i>Life</i> , 2018, 8, 4.	2.4	9
6	Rare coding variants in genes encoding GABAA receptors in genetic generalised epilepsies: an exome-based case-control study. <i>Lancet Neurology</i> , The, 2018, 17, 699-708.	10.2	67
7	An Isochore Framework Underlies Chromatin Architecture. <i>PLoS ONE</i> , 2017, 12, e0168023.	2.5	55
8	A genomic view on epilepsy and autism candidate genes. <i>Genomics</i> , 2016, 108, 31-36.	2.9	11
9	Leveraging the Power of High Performance Computing for Next Generation Sequencing Data Analysis: Tricks and Twists from a High Throughput Exome Workflow. <i>PLoS ONE</i> , 2015, 10, e0126321.	2.5	37
10	The Streamlined Genome of <i>Phytomonas</i> spp. Relative to Human Pathogenic Kinetoplastids Reveals a Parasite Tailored for Plants. <i>PLoS Genetics</i> , 2014, 10, e1004007.	3.5	66
11	<i>DEPDC5</i> mutations in genetic focal epilepsies of childhood. <i>Annals of Neurology</i> , 2014, 75, 788-792.	5.3	105
12	Sequencing of diverse mandarin, pummelo and orange genomes reveals complex history of admixture during citrus domestication. <i>Nature Biotechnology</i> , 2014, 32, 656-662.	17.5	572
13	Early allopolyploid evolution in the post-Neolithic <i>Brassica napus</i> oilseed genome. <i>Science</i> , 2014, 345, 950-953.	12.6	2,089
14	Genome structure and metabolic features in the red seaweed <i>Chondrus crispus</i> shed light on evolution of the Archaeplastida. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 5247-5252.	7.1	307
15	The <i>Ectocarpus</i> Genome and Brown Algal Genomics. <i>Advances in Botanical Research</i> , 2012, 64, 141-184.	1.1	18
16	The banana (<i>Musa acuminata</i>) genome and the evolution of monocotyledonous plants. <i>Nature</i> , 2012, 488, 213-217.	27.8	1,049
17	Transcription factor families inferred from genome sequences of photosynthetic stramenopiles. <i>New Phytologist</i> , 2010, 188, 52-66.	7.3	126
18	The <i>Ectocarpus</i> genome and the independent evolution of multicellularity in brown algae. <i>Nature</i> , 2010, 465, 617-621.	27.8	774

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19	The <i>Phaeodactylum</i> genome reveals the evolutionary history of diatom genomes. <i>Nature</i> , 2008, 456, 239-244.	27.8	1,458
20	The tiny eukaryote <i>Ostreococcus</i> provides genomic insights into the paradox of plankton speciation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 7705-7710.	7.1	563
21	Simple proteomic checks for detecting noncoding RNA. <i>Proteomics</i> , 2007, 7, 361-363.	2.2	6
22	IDENTIFICATION AND COMPARATIVE GENOMIC ANALYSIS OF SIGNALING AND REGULATORY COMPONENTS IN THE DIATOM <i>THALASSIOSIRA PSEUDONANA</i> . <i>Journal of Phycology</i> , 2007, 43, 585-604.	2.3	87
23	The <i>Chlamydomonas</i> Genome Reveals the Evolution of Key Animal and Plant Functions. <i>Science</i> , 2007, 318, 245-250.	12.6	2,354
24	Genome analysis of the smallest free-living eukaryote <i>Ostreococcus tauri</i> unveils many unique features. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 11647-11652.	7.1	809
25	The evolution of introns in human duplicated genes. <i>Gene</i> , 2006, 365, 41-47.	2.2	12
26	Comparative Genomics of the Pennate Diatom <i>Phaeodactylum tricornutum</i> . <i>Plant Physiology</i> , 2005, 137, 500-513.	4.8	122
27	Compositional Gene Landscapes in Vertebrates. <i>Genome Research</i> , 2004, 14, 886-892.	5.5	16
28	Comparative genomics of <i>Anopheles gambiae</i> and <i>Drosophila melanogaster</i> . <i>Gene</i> , 2004, 333, 183-186.	2.2	8
29	Incorrectly predicted genes in rice?. <i>Gene</i> , 2004, 333, 187-188.	2.2	12
30	Cytosine methylation and CpG, TpG (CpA) and TpA frequencies. <i>Gene</i> , 2004, 333, 143-149.	2.2	233
31	Body temperature and evolutionary genomics of vertebrates: a lesson from the genomes of <i>Takifugu rubripes</i> and <i>Tetraodon nigroviridis</i> . <i>Gene</i> , 2004, 333, 179-181.	2.2	18
32	The new genes of rice: a closer look. <i>Trends in Plant Science</i> , 2004, 9, 281-285.	8.8	33
33	The correlation between GC3 and hydropathy in human genes. <i>Gene</i> , 2003, 317, 137-140.	2.2	13
34	GC3 heterogeneity and body temperature in vertebrates. <i>Gene</i> , 2003, 317, 161-163.	2.2	10
35	The major shifts of human duplicated genes. <i>Gene</i> , 2003, 317, 203-208.	2.2	15
36	Compositional features of eukaryotic genomes for checking predicted genes. <i>Briefings in Bioinformatics</i> , 2003, 4, 43-52.	6.5	18

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37	Isochore conservation between MHC regions on human chromosome 6 and mouse chromosome 17. <i>FEBS Letters</i> , 2002, 511, 175-177.	2.8	17
38	Similar integration but different stability of Alus and LINEs in the human genome. <i>Gene</i> , 2001, 276, 39-45.	2.2	101
39	Gene Expression, Amino Acid Conservation, and Hydrophobicity Are the Main Factors Shaping Codon Preferences in <i>Mycobacterium tuberculosis</i> and <i>Mycobacterium leprae</i> . <i>Journal of Molecular Evolution</i> , 2000, 50, 45-55.	1.8	49
40	The distribution of genes in the <i>Drosophila</i> genome. <i>Gene</i> , 2000, 247, 287-292.	2.2	31
41	Evolutionary Genomics of Vertebrates and Its Implications. <i>Annals of the New York Academy of Sciences</i> , 1999, 870, 81-94.	3.8	34
42	Synonymous Codon Choices in the Extremely GC-Poor Genome of <i>Plasmodium falciparum</i> : Compositional Constraints and Translational Selection. <i>Journal of Molecular Evolution</i> , 1999, 49, 27-35.	1.8	61
43	Synonymous and Nonsynonymous Substitutions in Genes from Gramineae: Intragenic Correlations. <i>Journal of Molecular Evolution</i> , 1999, 49, 330-342.	1.8	12
44	The correlation of protein hydropathy with the base composition of coding sequences. <i>Gene</i> , 1999, 238, 3-14.	2.2	82
45	Correlations of nucleotide substitution rates and base composition of mammalian coding sequences with protein structure. <i>Gene</i> , 1999, 238, 23-31.	2.2	28
46	Synonymous and Nonsynonymous Substitutions in Mammalian Genes: Intragenic Correlations. <i>Journal of Molecular Evolution</i> , 1998, 46, 37-44.	1.8	53
47	Compositional Properties of Homologous Coding Sequences from Plants. <i>Journal of Molecular Evolution</i> , 1998, 46, 45-53.	1.8	65
48	CpG doublets, CpG islands and Alu repeats in long human DNA sequences from different isochore families. <i>Gene</i> , 1998, 224, 123-128.	2.2	97
49	Evolutionary changes in CpG and methylation levels in the genome of vertebrates. <i>Gene</i> , 1997, 205, 109-118.	2.2	98
50	Methylation patterns in the isochores of vertebrate genomes. <i>Gene</i> , 1997, 205, 119-124.	2.2	26