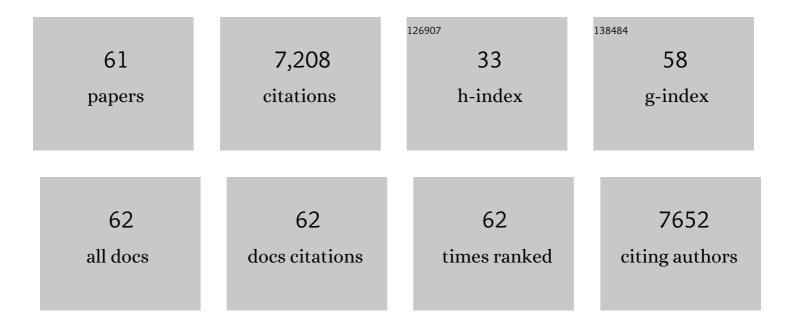
List of Publications by Year in descending order

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EDEDI TEKAIA

#	Article	IF	CITATIONS
1	Enhancing Bioinformatics and Genomics Courses: Building Capacity and Skills via Lab Meeting Activities. BioEssays, 2020, 42, 2000134.	2.5	0
2	Designing and running an advanced Bioinformatics and genome analyses course in Tunisia. PLoS Computational Biology, 2019, 15, e1006373.	3.2	6
3	Inferring Orthologs: Open Questions and Perspectives. Genomics Insights, 2016, 9, GEI.S37925.	3.0	50
4	Genome Data Exploration Using Correspondence Analysis. Bioinformatics and Biology Insights, 2016, 10, BBI.S39614.	2.0	18
5	Investigation of secreted protein transcripts as early biomarkers for type 1 diabetes in the mouse model. Gene, 2013, 512, 161-165.	2.2	3
6	Complete DNA Sequence of Kuraishia capsulata Illustrates Novel Genomic Features among Budding Yeasts (Saccharomycotina). Genome Biology and Evolution, 2013, 5, 2524-2539.	2.5	39
7	Detection and Characterization of Megasatellites in Orthologous and Nonorthologous Genes of 21 Fungal Genomes. Eukaryotic Cell, 2013, 12, 794-803.	3.4	12
8	SuperPartitions: Detection and classification of orthologs. Gene, 2012, 492, 199-211.	2.2	11
9	Use of Fine-Needle Aspiration for Diagnosis of <i>Mycobacterium ulcerans</i> Infection. Journal of Clinical Microbiology, 2010, 48, 2263-2264.	3.9	12
10	Promiscuous DNA in the nuclear genomes of hemiascomycetous yeasts. FEMS Yeast Research, 2008, 8, 846-857.	2.3	42
11	Seasonal increase of spontaneous histamine release in washed leucocytes from rhinitis patients sensitive to grass pollen. Clinical and Experimental Immunology, 2008, 79, 385-391.	2.6	7
12	Protection against Mycobacterium ulcerans Lesion Development by Exposure to Aquatic Insect Saliva. PLoS Medicine, 2007, 4, e64.	8.4	49
13	Reductive evolution and niche adaptation inferred from the genome of Mycobacterium ulcerans, the causative agent of Buruli ulcer. Genome Research, 2007, 17, 192-200.	5.5	345
14	Evolution of proteomes: fundamental signatures and global trends in amino acid compositions. BMC Genomics, 2006, 7, 307.	2.8	77
15	Genomic sequence of the pathogenic and allergenic filamentous fungus Aspergillus fumigatus. Nature, 2005, 438, 1151-1156.	27.8	1,272
16	Genome Trees from Conservation Profiles. PLoS Computational Biology, 2005, 1, e75.	3.2	24
17	A Human-Curated Annotation of the Candida albicans Genome. PLoS Genetics, 2005, 1, e1.	3.5	293
18	Aspergillus fumigatus: saprophyte or pathogen?. Current Opinion in Microbiology, 2005, 8, 385-392.	5.1	346

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19	Continued Colonization of the Human Genome by Mitochondrial DNA. PLoS Biology, 2004, 2, e273.	5.6	187
20	Genome evolution in yeasts. Nature, 2004, 430, 35-44.	27.8	1,498
21	A novel design of whole-genome microarray probes for Saccharomyces cerevisiae which minimizes cross-hybridization. BMC Genomics, 2003, 4, 38.	2.8	29
22	Novel Transporters from Hemiascomycete Yeasts. Journal of Molecular Microbiology and Biotechnology, 2003, 6, 19-28.	1.0	3
23	Expressed Sequence Tag Analysis of the Human Pathogen Paracoccidioides brasiliensis Yeast Phase: Identification of Putative Homologues of Candida albicans Virulence and Pathogenicity Genes. Eukaryotic Cell, 2003, 2, 34-48.	3.4	185
24	Otoancorin, an inner ear protein restricted to the interface between the apical surface of sensory epithelia and their overlying acellular gels, is defective in autosomal recessive deafness DFNB22. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 6240-6245.	7.1	163
25	Amino acid composition of genomes, lifestyles of organisms, and evolutionary trends: a global picture with correspondence analysis. Gene, 2002, 297, 51-60.	2.2	171
26	Transcript profiling in Candida albicans reveals new cellular functions for the transcriptional repressors CaTup1, CaMig1 and CaNrg1. Molecular Microbiology, 2001, 42, 981-993.	2.5	207
27	The decaying genome of <i>Mycobacterium leprae</i> . Leprosy Review, 2001, 72, .	0.3	31
28	Genomic Exploration of the Hemiascomycetous Yeasts: 1. A set of yeast species for molecular evolution studies1. FEBS Letters, 2000, 487, 3-12.	2.8	186
29	Genomic Exploration of the Hemiascomycetous Yeasts: 3. Methods and strategies used for sequence analysis and annotation. FEBS Letters, 2000, 487, 17-30.	2.8	37
30	Genomic Exploration of the Hemiascomycetous Yeasts: 4. The genome ofSaccharomyces cerevisiaerevisited. FEBS Letters, 2000, 487, 31-36.	2.8	75
31	Genomic Exploration of the Hemiascomycetous Yeasts: 8.Zygosaccharomyces rouxii1. FEBS Letters, 2000, 487, 52-55.	2.8	30
32	Genomic Exploration of the Hemiascomycetous Yeasts: 15.Pichia sorbitophila. FEBS Letters, 2000, 487, 87-90.	2.8	14
33	Genomic Exploration of the Hemiascomycetous Yeasts: 18. Comparative analysis of chromosome maps and synteny with <i>Saccharomyces cerevisiae</i> . FEBS Letters, 2000, 487, 101-112.	2.8	71
34	Genomic Exploration of the Hemiascomycetous Yeasts: 19. Ascomycetes-specific genes. FEBS Letters, 2000, 487, 113-121.	2.8	47
35	Genomic Exploration of the Hemiascomycetous Yeasts: 20. Evolution of gene redundancy compared to Saccharomyces cerevisiae. FEBS Letters, 2000, 487, 122-133.	2.8	49
36	Genomic Exploration of the Hemiascomycetous Yeasts: 21. Comparative functional classification of genes. FEBS Letters, 2000, 487, 134-149.	2.8	23

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37	Detection and genetic polymorphism of human herpes virus type 8 in endemic or epidemic Kaposi's sarcoma from West and Central Africa, and South America. International Journal of Cancer, 2000, 85, 166-170.	5.1	42
38	Pervasiveness of Gene Conservation and Persistence of Duplicates in Cellular Genomes. Journal of Molecular Evolution, 1999, 49, 591-600.	1.8	37
39	Analysis of the proteome of Mycobacterium tuberculosis in silico. Tubercle and Lung Disease, 1999, 79, 329-342.	2.1	277
40	Antigenic and genetic relationships between European very virulent infectious bursal disease viruses and an early West African isolate. Avian Pathology, 1999, 28, 36-46.	2.0	91
41	Seroepidemiological and Molecular Studies of Human T Cell Lymphotropic Virus Type II, Subtype b, in Isolated Groups of Mataco and Toba Indians of Northern Argentina. AIDS Research and Human Retroviruses, 1999, 15, 407-417.	1.1	37
42	The Genomic Tree as Revealed from Whole Proteome Comparisons. Genome Research, 1999, 9, 550-557.	5.5	213
43	Molecular Epidemiology of HTLV-II among United States Blood Donors and Intravenous Drug Users: An Age–Cohort Effect for HTLV-II RFLP Type a0. Virology, 1998, 242, 425-434.	2.4	35
44	Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence. Nature, 1998, 396, 190-190.	27.8	119
45	Random exploration of the Kluyveromyces lactis genome and comparison with that of Saccharomyces cerevisiae. Nucleic Acids Research, 1998, 26, 5511-5524.	14.5	45
46	Cloning and characterisation of a gene from Plasmodium vivax and P. knowlesi: homology with valine-tRNA synthetase. Gene, 1996, 173, 137-145.	2.2	2
47	Evidence in Gabon for an intrafamilial clustering with mother-to-child and sexual transmission of a new molecular variant of human T-lymphotropic virus type-II subtype B. , 1996, 48, 22-32.		29
48	Tempo of neurogenesis and synaptogenesis in the primate cingulate mesocortex: Comparison with the neocortex. Journal of Comparative Neurology, 1995, 360, 363-376.	1.6	63
49	Gag-Specific Cytotoxic Responses to HIV Type 1 Are Associated with a Decreased Risk of Progression to AIDS-Related Complex or AIDS. AIDS Research and Human Retroviruses, 1995, 11, 903-907.	1.1	162
50	Isolation from Human Brain of Six Previously Unreported cDNAs Related to the Reverse Transcriptase of Human Endogenous Retroviruses. AIDS Research and Human Retroviruses, 1995, 11, 231-237.	1.1	23
51	Isolation and molecular characterization of a human T-cell lymphotropic virus type II (HTLV-II), subtype B, from a healthy Pygmy living in a remote area of Cameroon: an ancient origin for HTLV-II in Africa Proceedings of the National Academy of Sciences of the United States of America, 1995, 92, 4041-4045.	7.1	96
52	A New HTLV Type II Subtype A Isolate in an HIV Type 1-Infected Prostitute from Cameroon, Central Africa. AIDS Research and Human Retroviruses, 1995, 11, 989-993.	1.1	33
53	Seroepidemiology, Viral Isolation, and Molecular Characterization of Human T Cell Leukemia/Lymphoma Virus Type I from La Réunion Island, Indian Ocean. AIDS Research and Human Retroviruses, 1994, 10, 745-752.	1.1	29
54	Molecular Epidemiology of HTLV Type I in Japan: Evidence for Two Distinct Ancestral Lineages with a Particular Geographical Distribution. AIDS Research and Human Retroviruses, 1994, 10, 1557-1566.	1.1	39

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55	Molecular characterization of the heat shock protein 90 gene of the human malaria parasite Plasmodium falciparum. Molecular and Biochemical Parasitology, 1994, 67, 157-170.	1.1	65
56	Electrophoretic patterns of esterases and lactate- and malate-dehydrogenases fromAlcaligenes species. Current Microbiology, 1993, 27, 79-84.	2.2	0
57	In-vitro susceptibility of Alcaligenes faecalis compared with those of other Alcaligenes spp. to antimicrobial agents including seven β-lactams. Journal of Antimicrobial Chemotherapy, 1993, 32, 907-910.	3.0	22
58	Guanine content and allergens in house dust samples. Journal of Allergy and Clinical Immunology, 1989, 83, 926-933.	2.9	32
59	T-immunogenic peptides are constituted of rare sequence patterns. Use in the identification of T epitopes in the human immunodeficiency virus gag protein. European Journal of Immunology, 1988, 18, 1547-1554.	2.9	83
60	Objective comparison of exon and intron sequences by the mean of 2-dimensional data analysis methods. Nucleic Acids Research, 1988, 16, 1729-1728.	14.5	17
61	Aspergillus fumigatus Specificities as Deduced from Comparative Genomics. , 0, , 29-38.		0