Fatma Z Guerfali

List of Publications by Year
in descending order

22 papers	4,674 citations	840776 11 h-index	794594 19 g-index
22 all docs	22 docs citations	22 times ranked	10001 citing authors

#	Article	IF	Citations
1	Ten simple rules for organizing a bioinformatics training course in low- and middle-income countries. PLoS Computational Biology, 2021, 17, e1009218.	3.2	4
2	Designing and running an advanced Bioinformatics and genome analyses course in Tunisia. PLoS Computational Biology, 2019, 15, e1006373.	3.2	6
3	MicroRNAs in diagnosis and therapeutics. , 2019, , 137-177.		13
4	*Leishmania* Genome Dynamics during Environmental Adaptation Reveal Strain-Specific Differences in Gene Copy Number Variation, Karyotype Instability, and Telomeric Amplification. MBio, 2018, 9, .	4.1	82
5	Role of Human Macrophage Polarization in Inflammation during Infectious Diseases. International Journal of Molecular Sciences, 2018, 19, 1801.	4.1	859
6	Comparative genomics of Tunisian Leishmania major isolates causing human cutaneous leishmaniasis with contrasting clinical severity. Infection, Genetics and Evolution, 2017, 50, 110-120.	2.3	16
7	Designing a course model for distance-based online bioinformatics training in Africa: The H3ABioNet experience. PLoS Computational Biology, 2017, 13, e1005715.	3.2	29
8	Treatment with synthetic lipophilic tyrosyl ester controls Leishmania major infection by reducing parasite load in BALB/c mice. Parasitology, 2016, 143, 1615-1621.	1.5	4
9	Letter to the Editor: Hypoxia inducible factor 1α: A critical factor for the immune response to pathogens and Leishmania. Cellular Immunology, 2016, 310, 211.	3.0	2
10	Genetic micro-heterogeneity of Leishmania major in emerging foci of zoonotic cutaneous leishmaniasis in Tunisia. Infection, Genetics and Evolution, 2016, 43, 179-185.	2.3	7
11	In silico prediction of protein-protein interactions in human macrophages. BMC Research Notes, 2014, 7, 157.	1.4	3,274
12	Integrated MicroRNA-mRNA analysis of human innate immune cells upon leishmania major infection. International Journal of Infectious Diseases, 2014, 21, 159.	3.3	0
13	Identification of Divergent Protein Domains by Combining HMM-HMM Comparisons and Co-Occurrence Detection. PLoS ONE, 2014, 9, e95275.	2.5	6
14	MicroRNA Expression Profile in Human Macrophages in Response to Leishmania major Infection. PLoS Neglected Tropical Diseases, 2013, 7, e2478.	3.0	125
15	Comparative analysis of resistant and susceptible macrophage gene expression response to Leishmania major parasite. BMC Genomics, 2013, 14, 723.	2.8	22
16	Transcriptomic Signature of Leishmania Infected Mice Macrophages: A Metabolic Point of View. PLoS Neglected Tropical Diseases, 2012, 6, e1763.	3.0	103
17	Differentially expressed Leishmania major genes might discriminate between clinical isolates of contrasted virulence. International Journal of Infectious Diseases, 2012, 16, e160-e161.	3.3	0
18	Methodology optimizing SAGE library tag-to-gene mapping: application to Leishmania. BMC Research Notes, 2012, 5, 74.	1.4	3

#	Article	IF	Citations
19	EuPathDomains: The divergent domain database for eukaryotic pathogens. Infection, Genetics and Evolution, 2011, 11, 698-707.	2.3	8
20	An in silico immunological approach for prediction of CD8+ T cell epitopes of Leishmania major proteins in susceptible BALB/c and resistant C57BL/6 murine models of infection. Infection, Genetics and Evolution, 2009, 9, 344-350.	2.3	19
21	Application of Multi-SOM clustering approach to macrophage gene expression analysis. Infection, Genetics and Evolution, 2009, 9, 328-336.	2.3	24
22	Simultaneous gene expression profiling in human macrophages infected with Leishmania major parasites using SAGE. BMC Genomics, 2008, 9, 238.	2.8	68