

# Fatma Z Guerfali

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5732992/publications.pdf>

Version: 2024-02-01

22  
papers

4,674  
citations

840119

11  
h-index

794141

19  
g-index

22  
all docs

22  
docs citations

22  
times ranked

10001  
citing authors

#	ARTICLE	IF	CITATIONS
1	In silico prediction of protein-protein interactions in human macrophages. BMC Research Notes, 2014, 7, 157.	0.6	3,274
2	Role of Human Macrophage Polarization in Inflammation during Infectious Diseases. International Journal of Molecular Sciences, 2018, 19, 1801.	1.8	859
3	MicroRNA Expression Profile in Human Macrophages in Response to Leishmania major Infection. PLoS Neglected Tropical Diseases, 2013, 7, e2478.	1.3	125
4	Transcriptomic Signature of Leishmania Infected Mice Macrophages: A Metabolic Point of View. PLoS Neglected Tropical Diseases, 2012, 6, e1763.	1.3	103
5	<i>Leishmania</i> Genome Dynamics during Environmental Adaptation Reveal Strain-Specific Differences in Gene Copy Number Variation, Karyotype Instability, and Telomeric Amplification. MBio, 2018, 9, .	1.8	82
6	Simultaneous gene expression profiling in human macrophages infected with Leishmania major parasites using SAGE. BMC Genomics, 2008, 9, 238.	1.2	68
7	Designing a course model for distance-based online bioinformatics training in Africa: The H3ABioNet experience. PLoS Computational Biology, 2017, 13, e1005715.	1.5	29
8	Application of Multi-SOM clustering approach to macrophage gene expression analysis. Infection, Genetics and Evolution, 2009, 9, 328-336.	1.0	24
9	Comparative analysis of resistant and susceptible macrophage gene expression response to Leishmania major parasite. BMC Genomics, 2013, 14, 723.	1.2	22
10	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.	1.0	19
11	Comparative genomics of Tunisian Leishmania major isolates causing human cutaneous leishmaniasis with contrasting clinical severity. Infection, Genetics and Evolution, 2017, 50, 110-120.	1.0	16
12	MicroRNAs in diagnosis and therapeutics. , 2019, , 137-177.		13
13	EuPathDomains: The divergent domain database for eukaryotic pathogens. Infection, Genetics and Evolution, 2011, 11, 698-707.	1.0	8
14	Genetic micro-heterogeneity of Leishmania major in emerging foci of zoonotic cutaneous leishmaniasis in Tunisia. Infection, Genetics and Evolution, 2016, 43, 179-185.	1.0	7
15	Designing and running an advanced Bioinformatics and genome analyses course in Tunisia. PLoS Computational Biology, 2019, 15, e1006373.	1.5	6
16	Identification of Divergent Protein Domains by Combining HMM-HMM Comparisons and Co-Occurrence Detection. PLoS ONE, 2014, 9, e95275.	1.1	6
17	Treatment with synthetic lipophilic tyrosyl ester controls Leishmania major infection by reducing parasite load in BALB/c mice. Parasitology, 2016, 143, 1615-1621.	0.7	4
18	Ten simple rules for organizing a bioinformatics training course in low- and middle-income countries. PLoS Computational Biology, 2021, 17, e1009218.	1.5	4

#	ARTICLE	IF	CITATIONS
19	Methodology optimizing SAGE library tag-to-gene mapping: application to Leishmania. BMC Research Notes, 2012, 5, 74.	0.6	3
20	Letter to the Editor: Hypoxia inducible factor 1 $\alpha$ : A critical factor for the immune response to pathogens and Leishmania. Cellular Immunology, 2016, 310, 211.	1.4	2
21	Differentially expressed Leishmania major genes might discriminate between clinical isolates of contrasted virulence. International Journal of Infectious Diseases, 2012, 16, e160-e161.	1.5	0
22	Integrated MicroRNA-mRNA analysis of human innate immune cells upon leishmania major infection. International Journal of Infectious Diseases, 2014, 21, 159.	1.5	0