

Mohammed Sebahia

List of Publications by Year in descending order

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59
papers

9,340
citations

218381

26
h-index

168136

53
g-index

60
all docs

60
docs citations

60
times ranked

9790
citing authors

#	ARTICLE	IF	CITATIONS
1	Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18. Nature, 2001, 413, 848-852.	13.7	1,192
2	Genome sequence of Yersinia pestis, the causative agent of plague. Nature, 2001, 413, 523-527.	13.7	1,144
3	Comparative analysis of the genome sequences of Bordetella pertussis, Bordetella parapertussis and Bordetella bronchiseptica. Nature Genetics, 2003, 35, 32-40.	9.4	898
4	The multidrug-resistant human pathogen Clostridium difficile has a highly mobile, mosaic genome. Nature Genetics, 2006, 38, 779-786.	9.4	821
5	The Pangenome Structure of <i>Escherichia coli</i> : Comparative Genomic Analysis of <i>E. coli</i> Commensal and Pathogenic Isolates. Journal of Bacteriology, 2008, 190, 6881-6893.	1.0	763
6	Genomic plasticity of the causative agent of melioidosis, Burkholderia pseudomallei. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 14240-14245.	3.3	675
7	The complete genome, comparative and functional analysis of Stenotrophomonas maltophilia reveals an organism heavily shielded by drug resistance determinants. Genome Biology, 2008, 9, R74.	13.9	452
8	Comparative genome and phenotypic analysis of Clostridium difficile O27 strains provides insight into the evolution of a hypervirulent bacterium. Genome Biology, 2009, 10, R102.	13.9	431
9	Genome sequence of the enterobacterial phytopathogen Erwinia carotovora subsp. atroseptica and characterization of virulence factors. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 11105-11110.	3.3	366
10	Evolutionary dynamics of <i>Clostridium difficile</i> over short and long time scales. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 7527-7532.	3.3	346
11	The Genome of <i>Burkholderia cenocepacia</i> J2315, an Epidemic Pathogen of Cystic Fibrosis Patients. Journal of Bacteriology, 2009, 191, 261-277.	1.0	329
12	Complete Genome Sequence of Uropathogenic <i>Proteus mirabilis</i> , a Master of both Adherence and Motility. Journal of Bacteriology, 2008, 190, 4027-4037.	1.0	229
13	Genome sequence of a proteolytic (Group I) Clostridium botulinum strain Hall A and comparative analysis of the clostridial genomes. Genome Research, 2007, 17, 1082-1092.	2.4	228
14	Genome Evolution of Wolbachia Strain wPip from the Culex pipiens Group. Molecular Biology and Evolution, 2008, 25, 1877-1887.	3.5	210
15	Proteomic and Genomic Characterization of Highly Infectious <i>Clostridium difficile</i> 630 Spores. Journal of Bacteriology, 2009, 191, 5377-5386.	1.0	210
16	Complete Genome Sequence and Comparative Metabolic Profiling of the Prototypical Enteroaggregative Escherichia coli Strain O42. PLoS ONE, 2010, 5, e8801.	1.1	165
17	Genome Evolution and Plasticity of Serratia marcescens, an Important Multidrug-Resistant Nosocomial Pathogen. Genome Biology and Evolution, 2014, 6, 2096-2110.	1.1	155
18	Comparative genomics of the classical Bordetella subspecies: the evolution and exchange of virulence-associated diversity amongst closely related pathogens. BMC Genomics, 2012, 13, 545.	1.2	99

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19	Analysis of the carbapenem gene cluster of <i>Erwinia carotovora</i> : definition of the antibiotic biosynthetic genes and evidence for a novel β -lactam resistance mechanism. <i>Molecular Microbiology</i> , 1997, 26, 545-556.	1.2	91
20	The missing link: <i>Bordetella petrii</i> is endowed with both the metabolic versatility of environmental bacteria and virulence traits of pathogenic <i>Bordetellae</i> . <i>BMC Genomics</i> , 2008, 9, 449.	1.2	85
21	Comparison of the Genome Sequence of the Poultry Pathogen <i>Bordetella avium</i> with Those of <i>B. bronchiseptica</i> , <i>B. pertussis</i> , and <i>B. parapertussis</i> Reveals Extensive Diversity in Surface Structures Associated with Host Interaction. <i>Journal of Bacteriology</i> , 2006, 188, 6002-6015.	1.0	75
22	Carbapenem antibiotic biosynthesis in <i>Erwinia carotovora</i> is regulated by physiological and genetic factors modulating the quorum sensing-dependent control pathway. <i>Molecular Microbiology</i> , 2004, 55, 526-545.	1.2	73
23	Ankyrin repeat domain-encoding genes in the wPip strain of <i>Wolbachia</i> from the <i>Culex pipiens</i> group. <i>BMC Biology</i> , 2007, 5, 39.	1.7	60
24	Genomic and physiological variability within Group II (non-proteolytic) <i>Clostridium botulinum</i> . <i>BMC Genomics</i> , 2013, 14, 333.	1.2	49
25	<i>Erwinia carotovora</i> has two KdgR-like proteins belonging to the IclR family of transcriptional regulators: identification and characterization of the RexZ activator and the KdgR repressor of pathogenesis. <i>Microbiology (United Kingdom)</i> , 1999, 145, 1531-1545.	0.7	39
26	Cloning and sequence analysis of the glucose-6-phosphate dehydrogenase gene from the cyanobacterium <i>Synechococcus</i> PCC 7942. <i>Plant Molecular Biology</i> , 1992, 19, 877-880.	2.0	36
27	Array comparative hybridisation reveals a high degree of similarity between UK and European clinical isolates of hypervirulent <i>Clostridium difficile</i> . <i>BMC Genomics</i> , 2010, 11, 389.	1.2	23
28	<i>Pectobacterium carotovorum</i> subsp. <i>brasiliense</i> and <i>Pectobacterium carotovorum</i> subsp. <i>carotovorum</i> as causal agents of potato soft rot in Algeria. <i>European Journal of Plant Pathology</i> , 2018, 151, 1027-1034.	0.8	23
29	Production optimization, characterization, and covalent immobilization of a thermophilic <i>Serratia rubidaea</i> lipase isolated from an Algerian oil waste. <i>Molecular Biology Reports</i> , 2019, 46, 3167-3181.	1.0	12
30	The value of comparison. <i>Nature Reviews Microbiology</i> , 2003, 1, 11-12.	13.6	9
31	First molecular characterisation and PCR ribotyping of <i>Clostridium difficile</i> strains isolated in two Algerian Hospitals. <i>Journal of Infection in Developing Countries</i> , 2018, 12, 015-021.	0.5	9
32	Fishy business. <i>Nature Reviews Microbiology</i> , 2009, 7, 9-9.	13.6	5
33	Bacterial contamination of neglected hospital surfaces and equipment in an Algerian hospital: an important source of potential infection. <i>International Journal of Environmental Health Research</i> , 2022, 32, 1373-1381.	1.3	5
34	Lost and found. <i>Trends in Microbiology</i> , 2001, 9, 526-527.	3.5	3
35	Dynamic duos. <i>Trends in Microbiology</i> , 2001, 9, 579.	3.5	3
36	The devil is in the detail. <i>Trends in Microbiology</i> , 2003, 11, 256-258.	3.5	3

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37	Colonic irritation. Nature Reviews Microbiology, 2006, 4, 882-883.	13.6	3
38	Tales of the unexpected. Trends in Microbiology, 2002, 10, 261-262.	3.5	2
39	Genome giants. Trends in Microbiology, 2002, 10, 309-310.	3.5	2
40	The magnificent seven. Trends in Microbiology, 2003, 11, 12-14.	3.5	2
41	Shrinking genomics. Nature Reviews Microbiology, 2004, 2, 11-11.	13.6	2
42	GI genomes. Nature Reviews Microbiology, 2005, 3, 368-369.	13.6	2
43	Size matters?. Trends in Microbiology, 2001, 9, 359.	3.5	1
44	The Full Monty. Trends in Microbiology, 2001, 9, 411-412.	3.5	1
45	Sibling rivalry. Trends in Microbiology, 2002, 10, 396-397.	3.5	1
46	All walks of life. Trends in Microbiology, 2003, 11, 159-160.	3.5	1
47	The good, the bad and the ugly?. Trends in Microbiology, 2003, 11, 204-205.	3.5	1
48	A bad combination. Trends in Microbiology, 2003, 11, 297-299.	3.5	1
49	Sequencing the environment. Nature Reviews Microbiology, 2004, 2, 184-185.	13.6	1
50	Bacterial minimalism. Nature Reviews Microbiology, 2004, 2, 274-275.	13.6	1
51	Strength in diversity. Nature Reviews Microbiology, 2004, 2, 358-359.	13.6	1
52	Enemies within. Nature Reviews Microbiology, 2005, 3, 8-9.	13.6	1
53	Bacterial therapeutics. Nature Reviews Microbiology, 2007, 5, 170-171.	13.6	1
54	Of staphs, streps and other things. Trends in Microbiology, 2001, 9, 309.	3.5	0

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55	Split personalities. Trends in Microbiology, 2002, 10, 115.	3.5	0
56	Searching for clues. Trends in Microbiology, 2002, 10, 354-355.	3.5	0
57	Spot the difference. Trends in Microbiology, 2002, 10, 489-490.	3.5	0
58	Some like it hot. Nature Reviews Microbiology, 2004, 2, 690-691.	13.6	0
59	Livelihood hazards. Nature Reviews Microbiology, 2005, 3, 278-279.	13.6	0