Abderrahman Hachani

List of Publications by Year
in descending order

32	2,618	331670 21	414414 32
papers	citations	h-index	g-index

37	37	37	3042
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The bacterial type VI secretion machine: yet another player for protein transport across membranes. Microbiology (United Kingdom), 2008, 154, 1570-1583.	1.8	319
2	Agrobacterium tumefaciens Deploys a Superfamily of Type VI Secretion DNase Effectors as Weapons for Interbacterial Competition In Planta. Cell Host and Microbe, 2014, 16, 94-104.	11.0	295
3	Type VI secretion and anti-host effectors. Current Opinion in Microbiology, 2016, 29, 81-93.	5.1	242
4	The Second Type VI Secretion System of Pseudomonas aeruginosa Strain PAO1 Is Regulated by Quorum Sensing and Fur and Modulates Internalization in Epithelial Cells. Journal of Biological Chemistry, 2012, 287, 27095-27105.	3.4	191
5	The VgrG Proteins Are â€œÃ la Carteâ€•Delivery Systems for Bacterial Type VI Effectors. Journal of Biological Chemistry, 2014, 289, 17872-17884.	3.4	185
6	The p110Î´ isoform of the kinase PI(3)K controls the subcellular compartmentalization of TLR4 signaling and protects from endotoxic shock. Nature Immunology, 2012, 13, 1045-1054.	14.5	163
7	Type VI Secretion System in Pseudomonas aeruginosa. Journal of Biological Chemistry, 2011, 286, 12317-12327.	3.4	150
8	Regulatory RNAs and the HptB/RetS signalling pathways fine-tune Pseudomonas aeruginosa pathogenesis. Molecular Microbiology, 2010, 76, 1427-1443.	2.5	133
9	Internalization of Pseudomonas aeruginosa Strain PAO1 into Epithelial Cells Is Promoted by Interaction of a T6SS Effector with the Microtubule Network. MBio, 2015, 6, e00712.	4.1	121
10	High-level antibiotic resistance in Pseudomonas aeruginosa biofilm: the ndvB gene is involved in the production of highly glycerol-phosphorylated Â-(1->3)-glucans, which bind aminoglycosides. Glycobiology, 2010, 20, 895-904.	2.5	101
11	Spa32 Regulates a Switch in Substrate Specificity of the Type III Secreton of Shigella flexneri from Needle Components to Ipa Proteins. Journal of Bacteriology, 2002, 184, 3433-3441.	2.2	92
12	The Pseudomonas aeruginosa T6SS Delivers a Periplasmic Toxin that Disrupts Bacterial Cell Morphology. Cell Reports, 2019, 29, 187-201.e7.	6.4	82
13	Cross Talk between Type III Secretion and Flagellar Assembly Systems in Pseudomonas aeruginosa. Journal of Bacteriology, 2007, 189, 3124-3132.	2.2	70
14	Unstable chromosome rearrangements in Staphylococcus aureus cause phenotype switching associated with persistent infections. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 20135-20140.	7.1	69
15	IpgB1 and IpgB2, two homologous effectors secreted via the Mxi-Spa type III secretion apparatus, cooperate to mediate polarized cell invasion and inflammatory potential of Shigella flexenri. Microbes and Infection, 2008, 10, 260-268.	1.9	55
16	The Campylobacter jejuni Type VI Secretion System Enhances the Oxidative Stress Response and Host Colonization. Frontiers in Microbiology, 2019, 10, 2864.	3.5	39
17	Klebsiella pneumoniae induces host metabolic stress that promotes tolerance to pulmonary infection. Cell Metabolism, 2022, 34, 761-774.e9.	16.2	36
18	A Visual Assay to Monitor T6SS-mediated Bacterial Competition. Journal of Visualized Experiments, 2013, , e50103.	0.3	35

#	Article	IF	Citations
19	Intracellular<scp>Staphylococcus aureus</scp>and host cell death pathways. Cellular Microbiology, 2021, 23, e13317.	2.1	31
20	An rhs Gene Linked to the Second Type VI Secretion Cluster Is a Feature of the Pseudomonas aeruginosa Strain PA14. Journal of Bacteriology, 2014, 196, 800-810.	2.2	30
21	Spa13 of Shigella flexneri has a dual role: chaperone escort and export gate-activator switch of the type III secretion system. Microbiology (United Kingdom), 2014, 160, 130-141.	1.8	27
22	Transcriptional slippage controls production of type III secretion apparatus components in Shigella flexneri. Molecular Microbiology, 2006, 62, 1460-1468.	2.5	25
23	From Welfare to Warfare: The Arbitration of Host-Microbiota Interplay by the Type VI Secretion System. Frontiers in Cellular and Infection Microbiology, 2020, 10, 587948.	3.9	21
24	Niche-specific genome degradation and convergent evolution shaping Staphylococcus aureus adaptation during severe infections. ELife, 0, 11, .	6.0	18
25	Air-Liquid-Interface Differentiated Human Nose Epithelium: A Robust Primary Tissue Culture Model of SARS-CoV-2 Infection. International Journal of Molecular Sciences, 2022, 23, 835.	4.1	15
26	Biogenesis of the Spacious Coxiella -Containing Vacuole Depends on Host Transcription Factors TFEB and TFE3. Infection and Immunity, 2020, 88, .	2.2	12
27	Organoid Models of SARS-CoV-2 Infection: What Have We Learned about COVID-19?. Organoids, 2022, 1, 2-27.	3.1	12
28	Characterization of a new periplasmic single-domain rhodanese encoded by a sulfur-regulated gene in a hyperthermophilic bacterium Aquifex aeolicus. Biochimie, 2010, 92, 388-397.	2.6	11
29	Bioinformatic Analysis of the Campylobacter jejuni Type VI Secretion System and Effector Prediction. Frontiers in Microbiology, 2021, 12, 694824.	3.5	10
30	Reprogramming of Cell Death Pathways by Bacterial Effectors as a Widespread Virulence Strategy. Infection and Immunity, 2022, 90, e0061421.	2.2	10
31	EirA Is a Novel Protein Essential for Intracellular Replication of Coxiella burnetii. Infection and Immunity, 2020, 88, .	2.2	7
32	Inhibition of the master regulator of Listeria monocytogenes virulence enables bacterial clearance from spacious replication vacuoles in infected macrophages. PLoS Pathogens, 2022, 18, e1010166.	4.7	7