

Samia N Naccache

List of Publications by Year in descending order

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34
papers

5,012
citations

218677

26
h-index

377865

34
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37
all docs

37
docs citations

37
times ranked

6946
citing authors

#	ARTICLE	IF	CITATIONS
1	Metagenomic Next-Generation Sequencing of the 2014 Ebola Virus Disease Outbreak in the Democratic Republic of the Congo. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	3.9	17
2	Evaluation of Oxacillin and Cefoxitin Disk Diffusion and Microbroth Dilution Methods for Detecting <i>mecA</i> -Mediated β -Lactam Resistance in Contemporary <i>Staphylococcus epidermidis</i> Isolates. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	3.9	17
3	Clinical Metagenomic Sequencing for Diagnosis of Meningitis and Encephalitis. <i>New England Journal of Medicine</i> , 2019, 380, 2327-2340.	27.0	644
4	Laboratory validation of a clinical metagenomic sequencing assay for pathogen detection in cerebrospinal fluid. <i>Genome Research</i> , 2019, 29, 831-842.	5.5	349
5	The Brief Case: Inherited Chromosomally Integrated Human Herpesvirus 6 (HHV-6) in the Age of Multiplex HHV-6 Testing. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	3.9	4
6	Closing the Brief Case: Inherited Chromosomally Integrated Human Herpesvirus 6 (HHV-6) in the Age of Multiplex HHV-6 Testing. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	3.9	3
7	Metagenomics to Assist in the Diagnosis of Bloodstream Infection. <i>journal of applied laboratory medicine</i> , The, 2019, 3, 643-653.	1.3	49
8	One Year in the Life of a Rapid Syndromic Panel for Meningitis/Encephalitis: a Pediatric Tertiary Care Facility's Experience. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	3.9	47
9	The Brief Case: Retropharyngeal Abscess in a 14-Year-Old Caused by <i>Fusobacterium necrophorum</i> . <i>Journal of Clinical Microbiology</i> , 2018, 56, .	3.9	1
10	Closing the Brief Case: Retropharyngeal Abscess in a 14-Year-Old Caused by <i>Fusobacterium necrophorum</i> . <i>Journal of Clinical Microbiology</i> , 2018, 56, .	3.9	1
11	Neurobrucellosis: Unexpected Answer From Metagenomic Next-Generation Sequencing. <i>Journal of the Pediatric Infectious Diseases Society</i> , 2017, 6, piw066.	1.3	62
12	Viral Surveillance in Serum Samples From Patients With Acute Liver Failure By Metagenomic Next-Generation Sequencing. <i>Clinical Infectious Diseases</i> , 2017, 65, 1477-1485.	5.8	76
13	The eukaryotic gut virome in hematopoietic stem cell transplantation: new clues in enteric graft-versus-host disease. <i>Nature Medicine</i> , 2017, 23, 1080-1085.	30.7	109
14	Diagnosis of Fatal Human Case of St. Louis Encephalitis Virus Infection by Metagenomic Sequencing, California, 2016. <i>Emerging Infectious Diseases</i> , 2017, 23, 1964-1968.	4.3	76
15	Distinct Zika Virus Lineage in Salvador, Bahia, Brazil. <i>Emerging Infectious Diseases</i> , 2016, 22, 1788-1792.	4.3	45
16	Two human immunodeficiency virus Type 2 cases in US blood donors including serologic, molecular, and genomic characterization of an epidemiologically unusual case. <i>Transfusion</i> , 2016, 56, 1560-1568.	1.6	8
17	Use of a Molecular Panel To Aid in Diagnosis of Culture-Negative Meningitis. <i>Journal of Clinical Microbiology</i> , 2016, 54, 3069-3070.	3.9	11
18	Coinfections of Zika and Chikungunya Viruses in Bahia, Brazil, Identified by Metagenomic Next-Generation Sequencing. <i>Journal of Clinical Microbiology</i> , 2016, 54, 2348-2353.	3.9	106

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19	Rapid metagenomic identification of viral pathogens in clinical samples by real-time nanopore sequencing analysis. <i>Genome Medicine</i> , 2015, 7, 99.	8.2	456
20	Utility of Metagenomic Next-Generation Sequencing for Characterization of HIV and Human Pegivirus Diversity. <i>PLoS ONE</i> , 2015, 10, e0141723.	2.5	37
21	Discovery of a Novel Human Pegivirus in Blood Associated with Hepatitis C Virus Co-Infection. <i>PLoS Pathogens</i> , 2015, 11, e1005325.	4.7	74
22	Genomic Assays for Identification of Chikungunya Virus in Blood Donors, Puerto Rico, 2014. <i>Emerging Infectious Diseases</i> , 2015, 21, 1409-1413.	4.3	39
23	Clinical metagenomic identification of Balamuthia mandrillaris encephalitis and assembly of the draft genome: the continuing case for reference genome sequencing. <i>Genome Medicine</i> , 2015, 7, 113.	8.2	102
24	Diagnosis of Neuroinvasive Astrovirus Infection in an Immunocompromised Adult With Encephalitis by Unbiased Next-Generation Sequencing. <i>Clinical Infectious Diseases</i> , 2015, 60, 919-923.	5.8	262
25	An ensemble strategy that significantly improves de novo assembly of microbial genomes from metagenomic next-generation sequencing data. <i>Nucleic Acids Research</i> , 2015, 43, e46-e46.	14.5	213
26	A novel outbreak enterovirus D68 strain associated with acute flaccid myelitis cases in the USA (2012-14): a retrospective cohort study. <i>Lancet Infectious Diseases</i> , The, 2015, 15, 671-682.	9.1	348
27	Concerns over the origin of NIH-CQV, a novel virus discovered in Chinese patients with seronegative hepatitis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E976-E976.	7.1	34
28	A cloud-compatible bioinformatics pipeline for ultrarapid pathogen identification from next-generation sequencing of clinical samples. <i>Genome Research</i> , 2014, 24, 1180-1192.	5.5	421
29	Actionable Diagnosis of Neuroleptospirosis by Next-Generation Sequencing. <i>New England Journal of Medicine</i> , 2014, 370, 2408-2417.	27.0	760
30	A novel bocavirus in canine liver. <i>Virology Journal</i> , 2013, 10, 54.	3.4	47
31	The Perils of Pathogen Discovery: Origin of a Novel Parvovirus-Like Hybrid Genome Traced to Nucleic Acid Extraction Spin Columns. <i>Journal of Virology</i> , 2013, 87, 11966-11977.	3.4	216
32	The Genome Sequence of Lone Star Virus, a Highly Divergent Bunyavirus Found in the Amblyomma americanum Tick. <i>PLoS ONE</i> , 2013, 8, e62083.	2.5	50
33	Myosin VI altered at threonine 406 stabilizes actin filaments in vivo. <i>Cytoskeleton</i> , 2006, 63, 633-645.	4.4	15
34	Binding of internalized receptors to the PDZ domain of GIPC/synectin recruits myosin VI to endocytic vesicles. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 12735-12740.	7.1	126