

Stephen J Salipante

List of Publications by Year in descending order

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88
papers

5,674
citations

147801
31
h-index

85541
71
g-index

97
all docs

97
docs citations

97
times ranked

10933
citing authors

#	ARTICLE	IF	CITATIONS
1	Classification and characterization of microsatellite instability across 18 cancer types. <i>Nature Medicine</i> , 2016, 22, 1342-1350.	30.7	726
2	Genetic Mechanisms of Immune Evasion in Colorectal Cancer. <i>Cancer Discovery</i> , 2018, 8, 730-749.	9.4	367
3	Microsatellite Instability Detection by Next Generation Sequencing. <i>Clinical Chemistry</i> , 2014, 60, 1192-1199.	3.2	333
4	Single molecule molecular inversion probes for targeted, high-accuracy detection of low-frequency variation. <i>Genome Research</i> , 2013, 23, 843-854.	5.5	292
5	Performance Comparison of Illumina and Ion Torrent Next-Generation Sequencing Platforms for 16S rRNA-Based Bacterial Community Profiling. <i>Applied and Environmental Microbiology</i> , 2014, 80, 7583-7591.	3.1	277
6	Application of Whole-Genome Sequencing for Bacterial Strain Typing in Molecular Epidemiology. <i>Journal of Clinical Microbiology</i> , 2015, 53, 1072-1079.	3.9	266
7	Validation and Implementation of Targeted Capture and Sequencing for the Detection of Actionable Mutation, Copy Number Variation, and Gene Rearrangement in Clinical Cancer Specimens. <i>Journal of Molecular Diagnostics</i> , 2014, 16, 56-67.	2.8	234
8	Complex MSH2 and MSH6 mutations in hypermutated microsatellite unstable advanced prostate cancer. <i>Nature Communications</i> , 2014, 5, 4988.	12.8	219
9	Gallium disrupts bacterial iron metabolism and has therapeutic effects in mice and humans with lung infections. <i>Science Translational Medicine</i> , 2018, 10, .	12.4	214
10	Rapid 16S rRNA Next-Generation Sequencing of Polymicrobial Clinical Samples for Diagnosis of Complex Bacterial Infections. <i>PLoS ONE</i> , 2013, 8, e65226.	2.5	186
11	ColoSeq Provides Comprehensive Lynch and Polyposis Syndrome Mutational Analysis Using Massively Parallel Sequencing. <i>Journal of Molecular Diagnostics</i> , 2012, 14, 357-366.	2.8	179
12	A Year of Infection in the Intensive Care Unit: Prospective Whole Genome Sequencing of Bacterial Clinical Isolates Reveals Cryptic Transmissions and Novel Microbiota. <i>PLoS Genetics</i> , 2015, 11, e1005413.	3.5	165
13	Large-scale genomic sequencing of extraintestinal pathogenic <i>Escherichia coli</i> strains. <i>Genome Research</i> , 2015, 25, 119-128.	5.5	158
14	Genomic analysis of bone marrow failure and myelodysplastic syndromes reveals phenotypic and diagnostic complexity. <i>Haematologica</i> , 2015, 100, 42-48.	3.5	108
15	Microsatellite instability in prostate cancer by PCR or next-generation sequencing. , 2018, 6, 29.		96
16	Phylogenetic fate mapping. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 5448-5453.	7.1	90
17	Digital PCR—An Emerging Technology with Broad Applications in Microbiology. <i>Clinical Chemistry</i> , 2020, 66, 117-123.	3.2	90
18	Characterization of the Mechanisms of Daptomycin Resistance among Gram-Positive Bacterial Pathogens by Multidimensional Lipidomics. <i>MSphere</i> , 2017, 2, .	2.9	87

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19	Improving performance of multigene panels for genomic analysis of cancer predisposition. <i>Genetics in Medicine</i> , 2016, 18, 974-981.	2.4	80
20	Clinical Next Generation Sequencing Outperforms Standard Microbiological Culture for Characterizing Polymicrobial Samples. <i>Clinical Chemistry</i> , 2016, 62, 1465-1473.	3.2	68
21	Evolved Aztreonam Resistance Is Multifactorial and Can Produce Hypervirulence in <i>Pseudomonas aeruginosa</i> . <i>MBio</i> , 2017, 8, .	4.1	65
22	Inadequacies of Minimum Spanning Trees in Molecular Epidemiology. <i>Journal of Clinical Microbiology</i> , 2011, 49, 3568-3575.	3.9	63
23	Discovery and Characterization of Spike N-Terminal Domain-Binding Aptamers for Rapid SARS-CoV-2 Detection. <i>Angewandte Chemie - International Edition</i> , 2021, 60, 21211-21215.	13.8	62
24	Mutations in a gene encoding a midbody kelch protein in familial and sporadic classical Hodgkin lymphoma lead to binucleated cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 14920-14925.	7.1	59
25	Accurate Pan-Cancer Molecular Diagnosis of Microsatellite Instability by Single-Molecule Molecular Inversion Probe Capture and High-Throughput Sequencing. <i>Clinical Chemistry</i> , 2018, 64, 950-958.	3.2	57
26	Traceless aptamer-mediated isolation of CD8+ T cells for chimeric antigen receptor T-cell therapy. <i>Nature Biomedical Engineering</i> , 2019, 3, 783-795.	22.5	56
27	Detection of minimal residual disease in NPM1-mutated acute myeloid leukemia by next-generation sequencing. <i>Modern Pathology</i> , 2014, 27, 1438-1446.	5.5	49
28	Efficient and Scalable Precision Genome Editing in <i>Staphylococcus aureus</i> through Conditional Recombineering and CRISPR/Cas9-Mediated Counterselection. <i>MBio</i> , 2018, 9, .	4.1	47
29	MSIplus for Integrated Colorectal Cancer Molecular Testing by Next-Generation Sequencing. <i>Journal of Molecular Diagnostics</i> , 2015, 17, 705-714.	2.8	46
30	CADD score has limited clinical validity for the identification of pathogenic variants in noncoding regions in a hereditary cancer panel. <i>Genetics in Medicine</i> , 2016, 18, 1269-1275.	2.4	45
31	In Vitro Activity of Delafloxacin against Clinical <i>Neisseria gonorrhoeae</i> Isolates and Selection of Gonococcal Delafloxacin Resistance. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 3106-3111.	3.2	36
32	Frequent PIK3CA Mutations in Colorectal and Endometrial Tumors With 2 or More Somatic Mutations in Mismatch Repair Genes. <i>Gastroenterology</i> , 2016, 151, 440-447.e1.	1.3	36
33	Coinfection of <i>Fusobacterium nucleatum</i> and <i>Actinomyces israelii</i> in Mastoiditis Diagnosed by Next-Generation DNA Sequencing. <i>Journal of Clinical Microbiology</i> , 2014, 52, 1789-1792.	3.9	35
34	Phylogenetic analysis of developmental and postnatal mouse cell lineages. <i>Evolution & Development</i> , 2010, 12, 84-94.	2.0	34
35	Polyclonality, Shared Strains, and Convergent Evolution in Chronic Cystic Fibrosis <i>Staphylococcus aureus</i> Airway Infection. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2021, 203, 1127-1137.	5.6	33
36	Combining Ivacaftor and Intensive Antibiotics Achieves Limited Clearance of Cystic Fibrosis Infections. <i>MBio</i> , 2021, 12, e0314821.	4.1	33

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37	Validation and implementation of a modular targeted capture assay for the detection of clinically significant molecular oncology alterations. <i>Practical Laboratory Medicine</i> , 2020, 19, e00153.	1.3	32
38	The Vaginal Microbiome of Transgender Men. <i>Clinical Chemistry</i> , 2019, 65, 199-207.	3.2	29
39	Occurrence of cross-resistance and β -lactam seesaw effect in glycopeptide-, lipopeptide- and lipoglycopeptide-resistant MRSA correlates with membrane phosphatidylglycerol levels. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 1182-1186.	3.0	29
40	Ultrasensitive detection of acute myeloid leukemia minimal residual disease using single molecule molecular inversion probes. <i>Haematologica</i> , 2017, 102, 1549-1557.	3.5	28
41	A Phylogenetic Approach to Mapping Cell Fate. <i>Current Topics in Developmental Biology</i> , 2007, 79, 157-184.	2.2	27
42	Whole-Genome Sequencing for High-Resolution Investigation of Methicillin-Resistant <i>Staphylococcus aureus</i> Epidemiology and Genome Plasticity. <i>Journal of Clinical Microbiology</i> , 2014, 52, 2787-2796.	3.9	27
43	Pattern associated leukemia immunophenotypes and measurable disease detection in acute myeloid leukemia or myelodysplastic syndrome with mutated <i>NPM1</i> . <i>Cytometry Part B - Clinical Cytometry</i> , 2019, 96, 67-72.	1.5	26
44	Aptamer Sandwich Lateral Flow Assay (AptaFlow) for Antibody-Free SARS-CoV-2 Detection. <i>Analytical Chemistry</i> , 2022, 94, 7278-7285.	6.5	25
45	Recurrent somatic loss of <i>TNFRSF14</i> in classical Hodgkin lymphoma. <i>Genes Chromosomes and Cancer</i> , 2016, 55, 278-287.	2.8	23
46	Molecular Diagnosis of Subcutaneous <i>Pythium insidiosum</i> Infection by Use of PCR Screening and DNA Sequencing. <i>Journal of Clinical Microbiology</i> , 2012, 50, 1480-1483.	3.9	22
47	Characterization of a Multidrug-Resistant, Novel <i>Bacteroides</i> Genomespecies. <i>Emerging Infectious Diseases</i> , 2015, 21, 95-98.	4.3	22
48	International Spread of Multidrug-Resistant <i>Campylobacter coli</i> in Men Who Have Sex With Men in Washington State and Québec, 2015–2018. <i>Clinical Infectious Diseases</i> , 2020, 71, 1896-1904.	5.8	20
49	Dalbavancin exposure <i>in vitro</i> selects for dalbavancin-non-susceptible and vancomycin-intermediate strains of methicillin-resistant <i>Staphylococcus aureus</i> . <i>Clinical Microbiology and Infection</i> , 2021, 27, 910.e1-910.e8.	6.0	20
50	Comprehensive evaluation of complex polymicrobial specimens using next generation sequencing and standard microbiological culture. <i>Scientific Reports</i> , 2020, 10, 5446.	3.3	19
51	High Clinical Impact of Broad-Range Fungal PCR in Suspected Fungal Sinusitis. <i>Journal of Clinical Microbiology</i> , 2021, 59, e0095521.	3.9	17
52	Molecular Diagnosis of <i>Actinomyces madurae</i> Infection by 16S rRNA Deep Sequencing. <i>Journal of Clinical Microbiology</i> , 2013, 51, 4262-4265.	3.9	16
53	Improved Species-Level Clinical Identification of Enterobacteriaceae through Broad-Range <i>dnaJ</i> PCR and Sequencing. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	3.9	16
54	Targeting Ligands Deliver Model Drug Cargo into the Central Nervous System along Autonomic Neurons. <i>ACS Nano</i> , 2019, 13, 10961-10971.	14.6	15

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55	Sensitive Identification of Bacterial DNA in Clinical Specimens by Broad-Range 16S rRNA Gene Enrichment. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	3.9	15
56	Identifying Optimal Loci for the Molecular Diagnosis of Microsatellite Instability. <i>Clinical Chemistry</i> , 2020, 66, 1310-1318.	3.2	15
57	Cell free DNA from respiratory pathogens is detectable in the blood plasma of Cystic Fibrosis patients. <i>Scientific Reports</i> , 2020, 10, 6903.	3.3	15
58	Discovery and Characterization of Spike N-Terminal Domain-Binding Aptamers for Rapid SARS-CoV-2 Detection. <i>Angewandte Chemie</i> , 2021, 133, 21381-21385.	2.0	14
59	Deep sequencing with intronic capture enables identification of an APC exon 10 inversion in a patient with polyposis. <i>Genetics in Medicine</i> , 2014, 16, 783-786.	2.4	13
60	Identification of a DNA Aptamer That Binds to Human Monocytes and Macrophages. <i>Bioconjugate Chemistry</i> , 2020, 31, 1899-1907.	3.6	13
61	Emergence of Dalbavancin, Vancomycin, and Daptomycin Nonsusceptible <i>Staphylococcus aureus</i> in a Patient Treated With Dalbavancin: Case Report and Isolate Characterization. <i>Clinical Infectious Diseases</i> , 2022, 75, 1641-1644.	5.8	12
62	Genome-wide protein-DNA interaction site mapping in bacteria using a double-stranded DNA-specific cytosine deaminase. <i>Nature Microbiology</i> , 2022, 7, 844-855.	13.3	12
63	Genomic Analysis Identifies Novel <i>Pseudomonas aeruginosa</i> Resistance Genes under Selection during Inhaled Aztreonam Therapy <i>In Vivo</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	11
64	Whole Genome Sequencing of Peruvian <i>Klebsiella pneumoniae</i> Identifies Novel Plasmid Vectors Bearing Carbapenem Resistance Gene NDM-1. <i>Open Forum Infectious Diseases</i> , 2020, 7, ofaa266.	0.9	11
65	Whole genome sequencing indicates <i>Corynebacterium jeikeium</i> comprises 4 separate genomospecies and identifies a dominant genomospecies among clinical isolates. <i>International Journal of Medical Microbiology</i> , 2014, 304, 1001-1010.	3.6	10
66	Artificial Selection for Pathogenicity Mutations in <i>Staphylococcus aureus</i> Identifies Novel Factors Relevant to Chronic Infection. <i>Infection and Immunity</i> , 2019, 87, .	2.2	10
67	Applying Ancestry and Sex Computation as a Quality Control Tool in Targeted Next-Generation Sequencing. <i>American Journal of Clinical Pathology</i> , 2016, 145, 308-315.	0.7	9
68	Identification of a novel tedizolid resistance mutation in <i>rpoB</i> of MRSA after <i>in vitro</i> serial passage. <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 292-296.	3.0	8
69	Case Report: Comparison of Plasma Metagenomics to Bacterial PCR in a Case of Prosthetic Valve Endocarditis. <i>Frontiers in Pediatrics</i> , 2020, 8, 575674.	1.9	8
70	Evolution of cefiderocol resistance in <i>Stenotrophomonas maltophilia</i> using <i>in vitro</i> serial passage techniques. <i>JAC-Antimicrobial Resistance</i> , 2022, 4, dlac011.	2.1	8
71	High-resolution profiling of human cytomegalovirus cell-free DNA in human plasma highlights its exceptionally fragmented nature. <i>Scientific Reports</i> , 2020, 10, 3734.	3.3	7
72	Synergy Between Beta-Lactams and Lipo-, Glyco-, and Lipoglycopeptides, Is Independent of the Seesaw Effect in Methicillin-Resistant <i>Staphylococcus aureus</i> . <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 688357.	3.5	7

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73	Genome Editing in <i>Staphylococcus aureus</i> by Conditional Recombineering and CRISPR/Cas9-Mediated Counterselection. <i>Methods in Molecular Biology</i> , 2020, 2050, 127-143.	0.9	7
74	Open-Sourced CIViC Annotation Pipeline to Identify and Annotate Clinically Relevant Variants Using Single-Molecule Molecular Inversion Probes. <i>JCO Clinical Cancer Informatics</i> , 2019, 3, 1-12.	2.1	6
75	Discovery of coordinately regulated pathways that provide innate protection against interbacterial antagonism. <i>ELife</i> , 2022, 11, .	6.0	6
76	Letter to the Editor regarding Qui etÂal: â€œCutibacterium acnes and the shoulder microbiomeâ€• <i>Journal of Shoulder and Elbow Surgery</i> , 2019, 28, e275-e276.	2.6	5
77	Whole-genome sequencing of clinical <i>Clostridioides difficile</i> isolates reveals molecular epidemiology and discrepancies with conventional laboratory diagnostic testing. <i>Journal of Hospital Infection</i> , 2021, 108, 64-71.	2.9	5
78	Repeated isolation of an antibiotic-dependent and temperature-sensitive mutant of <i>Pseudomonas aeruginosa</i> from a cystic fibrosis patient. <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 616-625.	3.0	5
79	Incidental identification of <i>Strongyloides stercoralis</i> infection by broad-range 28S rDNA gene sequencing in a patient with a hemolymphoid malignancy. <i>Diagnostic Microbiology and Infectious Disease</i> , 2016, 86, 362-364.	1.8	3
80	Ultrasensitive Detection of Chimerism by Single-Molecule Molecular Inversion Probe Capture and High-Throughput Sequencing of Copy Number Deletion Polymorphisms. <i>Clinical Chemistry</i> , 2018, 64, 938-949.	3.2	3
81	Characterizing the molecular composition and diagnostic potential of <i>Mycobacterium tuberculosis</i> urinary cell-free DNA using next-generation sequencing. <i>International Journal of Infectious Diseases</i> , 2021, 112, 330-337.	3.3	3
82	Neutrophilic inflammation in gallbladder carcinoma correlates with patient survival: A case-control study. <i>Annals of Diagnostic Pathology</i> , 2022, 56, 151845.	1.3	3
83	Ultrasensitive Quantitation of Genomic Chimerism by Single-Molecule Molecular Inversion Probe Capture and High-Throughput Sequencing of Copy Number Deletion Polymorphisms. <i>Journal of Molecular Diagnostics</i> , 2021, , .	2.8	3
84	16S rRNA deep sequencing identifies <i>Actinotignum schaalii</i> as the major component of a polymicrobial intra-abdominal infection and implicates a urinary source. <i>JMM Case Reports</i> , 2017, 4, e005091.	1.3	2
85	Identification of <i>Leptotrichia goodfellowii</i> infective endocarditis by next-generation sequencing of 16S rDNA amplicons. <i>Journal of Physical Education and Sports Management</i> , 2021, 7, a005876.	1.2	2
86	A population-level strain genotyping method to study pathogen strain dynamics in human infections. <i>JCI Insight</i> , 2021, 6, .	5.0	2
87	Contaminated Incubators: Source of a Multispecies <i>Enterobacter</i> Outbreak of Neonatal Sepsis. <i>Microbiology Spectrum</i> , 2022, 10, .	3.0	2
88	Recombineering in <i>Staphylococcus aureus</i> . <i>Methods in Molecular Biology</i> , 2022, 2479, 135-157.	0.9	0