

Harm van Bakel

List of Publications by Year in descending order

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Version: 2024-02-01

140
papers

13,552
citations

41339

49
h-index

30081

103
g-index

178
all docs

178
docs citations

178
times ranked

24920
citing authors

#	ARTICLE	IF	CITATIONS
1	Determination and Inference of Eukaryotic Transcription Factor Sequence Specificity. <i>Cell</i> , 2014, 158, 1431-1443.	28.9	1,515
2	Transcriptome-wide isoform-level dysregulation in ASD, schizophrenia, and bipolar disorder. <i>Science</i> , 2018, 362, .	12.6	805
3	Comprehensive functional genomic resource and integrative model for the human brain. <i>Science</i> , 2018, 362, .	12.6	618
4	Integrative functional genomic analysis of human brain development and neuropsychiatric risks. <i>Science</i> , 2018, 362, .	12.6	516
5	The draft genome and transcriptome of <i>Cannabis sativa</i> . <i>Genome Biology</i> , 2011, 12, R102.	9.6	479
6	SARS-CoV-2 Omicron virus causes attenuated disease in mice and hamsters. <i>Nature</i> , 2022, 603, 687-692.	27.8	475
7	Reconstruction of a Functional Human Gene Network, with an Application for Prioritizing Positional Candidate Genes. <i>American Journal of Human Genetics</i> , 2006, 78, 1011-1025.	6.2	456
8	A Library of Yeast Transcription Factor Motifs Reveals a Widespread Function for Rsc3 in Targeting Nucleosome Exclusion at Promoters. <i>Molecular Cell</i> , 2008, 32, 878-887.	9.7	415
9	Activity of convalescent and vaccine serum against SARS-CoV-2 Omicron. <i>Nature</i> , 2022, 602, 682-688.	27.8	395
10	Most "Dark Matter" Transcripts Are Associated With Known Genes. <i>PLoS Biology</i> , 2010, 8, e1000371.	5.6	377
11	The PsychENCODE project. <i>Nature Neuroscience</i> , 2015, 18, 1707-1712.	14.8	371
12	Shedding of Viable SARS-CoV-2 after Immunosuppressive Therapy for Cancer. <i>New England Journal of Medicine</i> , 2020, 383, 2586-2588.	27.0	356
13	Introductions and early spread of SARS-CoV-2 in the New York City area. <i>Science</i> , 2020, 369, 297-301.	12.6	356
14	Characterization of the human ESC transcriptome by hybrid sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E4821-30.	7.1	316
15	Large-Scale Genetic Perturbations Reveal Regulatory Networks and an Abundance of Gene-Specific Repressors. <i>Cell</i> , 2014, 157, 740-752.	28.9	248
16	SARS-CoV-2 mRNA vaccination induces functionally diverse antibodies to NTD, RBD, and S2. <i>Cell</i> , 2021, 184, 3936-3948.e10.	28.9	241
17	Origins of the 2009 H1N1 influenza pandemic in swine in Mexico. <i>ELife</i> , 2016, 5, .	6.0	237
18	Transcriptome and epigenome landscape of human cortical development modeled in organoids. <i>Science</i> , 2018, 362, .	12.6	220

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19	Mediator Expression Profiling Epistasis Reveals a Signal Transduction Pathway with Antagonistic Submodules and Highly Specific Downstream Targets. <i>Molecular Cell</i> , 2005, 19, 511-522.	9.7	192
20	Lsr2 is a nucleoid-associated protein that targets AT-rich sequences and virulence genes in <i>Mycobacterium tuberculosis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 5154-5159.	7.1	192
21	A physical and genetic map of <i>Cannabis sativa</i> identifies extensive rearrangements at the THC/CBD acid synthase loci. <i>Genome Research</i> , 2019, 29, 146-156.	5.5	160
22	Monitoring global messenger RNA changes in externally controlled microarray experiments. <i>EMBO Reports</i> , 2003, 4, 387-393.	4.5	150
23	Mutations in SARS-CoV-2 variants of concern link to increased spike cleavage and virus transmission. <i>Cell Host and Microbe</i> , 2022, 30, 373-387.e7.	11.0	138
24	Topoisomerase 1 inhibition suppresses inflammatory genes and protects from death by inflammation. <i>Science</i> , 2016, 352, aad7993.	12.6	132
25	Repeated cross-sectional sero-monitoring of SARS-CoV-2 in New York City. <i>Nature</i> , 2021, 590, 146-150.	27.8	128
26	A Compendium of Nucleosome and Transcript Profiles Reveals Determinants of Chromatin Architecture and Transcription. <i>PLoS Genetics</i> , 2013, 9, e1003479.	3.5	125
27	Intestinal Host Response to SARS-CoV-2 Infection and COVID-19 Outcomes in Patients With Gastrointestinal Symptoms. <i>Gastroenterology</i> , 2021, 160, 2435-2450.e34.	1.3	118
28	Defining the risk of SARS-CoV-2 variants on immune protection. <i>Nature</i> , 2022, 605, 640-652.	27.8	117
29	Analysis of Escherichia coli RNase E and RNase III activity in vivo using tiling microarrays. <i>Nucleic Acids Research</i> , 2011, 39, 3188-3203.	14.5	112
30	Targeting Viral Proteostasis Limits Influenza Virus, HIV, and Dengue Virus Infection. <i>Immunity</i> , 2016, 44, 46-58.	14.3	110
31	Influenza A variants with reduced susceptibility to baloxavir isolated from Japanese patients are fit and transmit through respiratory droplets. <i>Nature Microbiology</i> , 2020, 5, 27-33.	13.3	102
32	Contribution of SARS-CoV-2 Accessory Proteins to Viral Pathogenicity in K18 Human ACE2 Transgenic Mice. <i>Journal of Virology</i> , 2021, 95, e0040221.	3.4	97
33	SARS-CoV-2 Transmission among Marine Recruits during Quarantine. <i>New England Journal of Medicine</i> , 2020, 383, 2407-2416.	27.0	94
34	Two-Color Cell Array Screen Reveals Interdependent Roles for Histone Chaperones and a Chromatin Boundary Regulator in Histone Gene Repression. <i>Molecular Cell</i> , 2009, 35, 340-351.	9.7	88
35	Multi-platform α Omics Analysis of Human Ebola Virus Disease Pathogenesis. <i>Cell Host and Microbe</i> , 2017, 22, 817-829.e8.	11.0	88
36	Avian Influenza Viruses in Wild Birds: Virus Evolution in a Multihost Ecosystem. <i>Journal of Virology</i> , 2018, 92, .	3.4	83

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37	Sequence specificity is obtained from the majority of modular C2H2 zinc-finger arrays. <i>Nucleic Acids Research</i> , 2011, 39, 4680-4690.	14.5	82
38	Epigenomic characterization of <i>Clostridioides difficile</i> finds a conserved DNA methyltransferase that mediates sporulation and pathogenesis. <i>Nature Microbiology</i> , 2020, 5, 166-180.	13.3	75
39	A household case evidences shorter shedding of SARS-CoV-2 in naturally infected cats compared to their human owners. <i>Emerging Microbes and Infections</i> , 2021, 10, 376-383.	6.5	74
40	A humanized MDCK cell line for the efficient isolation and propagation of human influenza viruses. <i>Nature Microbiology</i> , 2019, 4, 1268-1273.	13.3	73
41	Gene expression profiling of liver cells after copper overload in vivo and in vitro reveals new copper-regulated genes. <i>Journal of Biological Inorganic Chemistry</i> , 2007, 12, 495-507.	2.6	72
42	Interplay of host microbiota, genetic perturbations, and inflammation promotes local development of intestinal neoplasms in mice. <i>Journal of Experimental Medicine</i> , 2014, 211, 457-472.	8.5	71
43	Gene expression profiling and phenotype analyses of <i>S. cerevisiae</i> in response to changing copper reveals six genes with new roles in copper and iron metabolism. <i>Physiological Genomics</i> , 2005, 22, 356-367.	2.3	69
44	A Gene-Specific Requirement of RNA Polymerase II CTD Phosphorylation for Sexual Differentiation in <i>S. pombe</i> . <i>Current Biology</i> , 2010, 20, 1053-1064.	3.9	67
45	Cooperative action of NC2 and Mot1p to regulate TATA-binding protein function across the genome. <i>Genes and Development</i> , 2008, 22, 2359-2369.	5.9	66
46	In control: systematic assessment of microarray performance. <i>EMBO Reports</i> , 2004, 5, 964-969.	4.5	62
47	Establishing legitimacy and function in the new transcriptome. <i>Briefings in Functional Genomics & Proteomics</i> , 2009, 8, 424-436.	3.8	62
48	The FaceBase Consortium: A comprehensive resource for craniofacial researchers. <i>Development (Cambridge)</i> , 2016, 143, 2677-88.	2.5	62
49	Sequential evolution of virulence and resistance during clonal spread of community-acquired methicillin-resistant <i>Staphylococcus aureus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 1745-1754.	7.1	59
50	Global analysis of SUMO chain function reveals multiple roles in chromatin regulation. <i>Journal of Cell Biology</i> , 2013, 201, 145-163.	5.2	58
51	Activity of convalescent and vaccine serum against SARS-CoV-2 Omicron. <i>Nature</i> , 0, , .	27.8	56
52	Global transcriptional responses of fission and budding yeast to changes in copper and iron levels: a comparative study. <i>Genome Biology</i> , 2007, 8, R73.	9.6	54
53	Senataxin suppresses the antiviral transcriptional response and controls viral biogenesis. <i>Nature Immunology</i> , 2015, 16, 485-494.	14.5	50
54	Application of Genome Wide Association and Genomic Prediction for Improvement of Cacao Productivity and Resistance to Black and Frosty Pod Diseases. <i>Frontiers in Plant Science</i> , 2017, 8, 1905.	3.6	50

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55	Genome Plasticity of <i>agr</i> -Defective <i>Staphylococcus aureus</i> during Clinical Infection. <i>Infection and Immunity</i> , 2018, 86, .	2.2	50
56	Limited intestinal inflammation despite diarrhea, fecal viral RNA and SARS-CoV-2-specific IgA in patients with acute COVID-19. <i>Scientific Reports</i> , 2021, 11, 13308.	3.3	50
57	The RNA Exosome Syncs IAV-RNAPII Transcription to Promote Viral Ribogenesis and Infectivity. <i>Cell</i> , 2017, 169, 679-692.e14.	28.9	48
58	Influenza virus infection causes global RNAPII termination defects. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 885-893.	8.2	48
59	Neuronal and glial 3D chromatin architecture informs the cellular etiology of brain disorders. <i>Nature Communications</i> , 2021, 12, 3968.	12.8	48
60	Neutrophil Recruitment and Barrier Impairment in Celiac Disease: A Genomic Study. <i>Clinical Gastroenterology and Hepatology</i> , 2007, 5, 574-581.e5.	4.4	46
61	The purine biosynthesis regulator PurR moonlights as a virulence regulator in <i>Staphylococcus aureus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 13563-13572.	7.1	46
62	Cdk11-CyclinL Controls the Assembly of the RNA Polymerase II Mediator Complex. <i>Cell Reports</i> , 2012, 2, 1068-1076.	6.4	44
63	Evidence for retained spike-binding and neutralizing activity against emerging SARS-CoV-2 variants in serum of COVID-19 mRNA vaccine recipients. <i>EBioMedicine</i> , 2021, 73, 103626.	6.1	43
64	Integrated Transcriptome and Network Analysis Reveals Spatiotemporal Dynamics of Calvarial Suturogenesis. <i>Cell Reports</i> , 2020, 32, 107871.	6.4	42
65	Transmission of Methicillin-Resistant <i>Staphylococcus aureus</i> via Deceased Donor Liver Transplantation Confirmed by Whole Genome Sequencing. <i>American Journal of Transplantation</i> , 2014, 14, 2640-2644.	4.7	41
66	Restriction of histone gene transcription to S phase by phosphorylation of a chromatin boundary protein. <i>Genes and Development</i> , 2011, 25, 2489-2501.	5.9	40
67	Improved genome-wide localization by ChIP-chip using double-round T7 RNA polymerase-based amplification. <i>Nucleic Acids Research</i> , 2008, 36, e21-e21.	14.5	35
68	A systematic characterization of Cwc21, the yeast ortholog of the human spliceosomal protein SRm300. <i>Rna</i> , 2009, 15, 2174-2185.	3.5	34
69	Hybrid Gene Origination Creates Human-Virus Chimeric Proteins during Infection. <i>Cell</i> , 2020, 181, 1502-1517.e23.	28.9	33
70	The arrival and spread of SARS-CoV-2 in Colombia. <i>Journal of Medical Virology</i> , 2021, 93, 1158-1163.	5.0	33
71	A novel germline mutation of PTEN associated with brain tumours of multiple lineages. <i>British Journal of Cancer</i> , 2002, 86, 1586-1591.	6.4	30
72	Response to "The Reality of Pervasive Transcription". <i>PLoS Biology</i> , 2011, 9, e1001102.	5.6	30

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73	Multiple Incursions and Recurrent Epidemic Fade-Out of H3N2 Canine Influenza A Virus in the United States. <i>Journal of Virology</i> , 2018, 92, .	3.4	30
74	Timing of Transcriptional Quiescence during Gametogenesis Is Controlled by Global Histone H3K4 Demethylation. <i>Developmental Cell</i> , 2012, 23, 1059-1071.	7.0	29
75	High Capsidâ€“Genome Correlation Facilitates Creation of AAV Libraries for Directed Evolution. <i>Molecular Therapy</i> , 2015, 23, 675-682.	8.2	25
76	FaceBase 3: analytical tools and FAIR resources for craniofacial and dental research. <i>Development (Cambridge)</i> , 2020, 147, .	2.5	25
77	Whole-Genome Sequencing Identifies Emergence of a Quinolone Resistance Mutation in a Case of <i>Stenotrophomonas maltophilia</i> Bacteremia. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 7117-7120.	3.2	24
78	TEAM: a tool for the integration of expression, and linkage and association maps. <i>European Journal of Human Genetics</i> , 2004, 12, 633-638.	2.8	22
79	Midface and upper airway dysgenesis in FGFR2-craniosynostosis involves multiple tissue-specific and cell cycle effects. <i>Development (Cambridge)</i> , 2018, 145, .	2.5	22
80	Genetic Basis of Emerging Vancomycin, Linezolid, and Daptomycin Heteroresistance in a Case of Persistent <i>Enterococcus faecium</i> Bacteremia. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	3.2	21
81	A unified model for yeast transcript definition. <i>Genome Research</i> , 2014, 24, 154-166.	5.5	20
82	Avian Influenza Virus H5 Strain with North American and Eurasian Lineage Genes in an Antarctic Penguin. <i>Emerging Infectious Diseases</i> , 2016, 22, 2221-2223.	4.3	20
83	Mandibular dysmorphology due to abnormal embryonic osteogenesis in FGFR2-related craniosynostosis mice. <i>DMM Disease Models and Mechanisms</i> , 2019, 12, .	2.4	19
84	Mutations in the Hemagglutinin Stalk Domain Do Not Permit Escape from a Protective, Stalk-Based Vaccine-Induced Immune Response in the Mouse Model. <i>MBio</i> , 2021, 12, .	4.1	19
85	Circulation of low pathogenic avian influenza (LPAI) viruses in wild birds and poultry in the Netherlands, 2006â€“2016. <i>Scientific Reports</i> , 2019, 9, 13681.	3.3	18
86	Molecular evidence of SARS-CoV-2 in New York before the first pandemic wave. <i>Nature Communications</i> , 2021, 12, 3463.	12.8	18
87	Genomic confirmation of vancomycin-resistant <i>Enterococcus</i> transmission from deceased donor to liver transplant recipient. <i>PLoS ONE</i> , 2017, 12, e0170449.	2.5	16
88	A Complete Genome Screening Program of Clinical Methicillin-Resistant <i>Staphylococcus aureus</i> Isolates Identifies the Origin and Progression of a Neonatal Intensive Care Unit Outbreak. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	3.9	16
89	SARS-CoV-2 spread across the Colombian-Venezuelan border. <i>Infection, Genetics and Evolution</i> , 2020, 86, 104616.	2.3	16
90	Evidence of a fixed internal gene constellation in influenza A viruses isolated from wild birds in Argentina (2006â€“2016). <i>Emerging Microbes and Infections</i> , 2018, 7, 1-13.	6.5	15

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91	Identification and Characterization of Novel Antibody Epitopes on the N2 Neuraminidase. MSphere, 2021, 6, .	2.9	15
92	Effect of Structured Group Education on Glycemic Control and Hypoglycemia in Insulin-Treated Patients. Diabetes Care, 2003, 26, 251-251.	8.6	14
93	Single-cell analysis identifies a key role for Hhip in murine coronal suture development. Nature Communications, 2021, 12, 7132.	12.8	14
94	BCL11B expression in intramembranous osteogenesis during murine craniofacial suture development. Gene Expression Patterns, 2015, 17, 16-25.	0.8	13
95	Fission Yeast Cdk7 Controls Gene Expression through both Its CAK and C-Terminal Domain Kinase Activities. Molecular and Cellular Biology, 2015, 35, 1480-1490.	2.3	13
96	Prothymosin $\hat{\pm}$ Variants Isolated From CD8+ T Cells and Cervicovaginal Fluid Suppress HIV-1 Replication Through Type I Interferon Induction. Journal of Infectious Diseases, 2015, 211, 1467-1475.	4.0	13
97	PathoSPOT genomic epidemiology reveals under-the-radar nosocomial outbreaks. Genome Medicine, 2020, 12, 96.	8.2	13
98	Real-Time Investigation of a Large Nosocomial Influenza A Outbreak Informed by Genomic Epidemiology. Clinical Infectious Diseases, 2021, 73, e4375-e4383.	5.8	13
99	Prokaryotic diversity of the Saccharomyces cerevisiae Atx1p-mediated copper pathway. Bioinformatics, 2004, 20, 2644-2655.	4.1	12
100	Mce3R Stress-Resistance Pathway Is Vulnerable to Small-Molecule Targeting That Improves Tuberculosis Drug Activities. ACS Infectious Diseases, 2019, 5, 1239-1251.	3.8	12
101	Reemergence of H3N8 Equine Influenza A virus in Chile, 2018. Transboundary and Emerging Diseases, 2018, 65, 1408-1415.	3.0	11
102	Blurred Molecular Epidemiological Lines Between the Two Dominant Methicillin-Resistant Staphylococcus aureus Clones. Open Forum Infectious Diseases, 2019, 6, ofz302.	0.9	11
103	Viable virus shedding during SARS-CoV-2 reinfection. Lancet Respiratory Medicine, the, 2021, 9, e56-e57.	10.7	11
104	Robust clinical detection of SARS-CoV-2 variants by RT-PCR/MALDI-TOF multitarget approach. Journal of Medical Virology, 2022, 94, 1606-1616.	5.0	9
105	Evidence of Intercontinental Spread and Uncommon Variants of Low-Pathogenicity Avian Influenza Viruses in Ducks Overwintering in Guatemala. MSphere, 2017, 2, .	2.9	8
106	Novel Epitopes of the Influenza Virus N1 Neuraminidase Targeted by Human Monoclonal Antibodies. Journal of Virology, 2022, , e0033222.	3.4	8
107	Estimating Local Costs Associated With <i>Clostridium difficile</i> Infection Using Machine Learning and Electronic Medical Records. Infection Control and Hospital Epidemiology, 2017, 38, 1478-1486.	1.8	7
108	A Heterogeneous Swine Show Circuit Drives Zoonotic Transmission of Influenza A Viruses in the United States. Journal of Virology, 2020, 94, .	3.4	7

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109	Family matters: gene regulation by metal-dependent transcription factors. Topics in Current Genetics, 2005, , 341-394.	0.7	6
110	Community-Acquired Cavitory <i>Pseudomonas</i> Pneumonia Linked to Use of a Home Humidifier. Case Reports in Infectious Diseases, 2017, 2017, 1-4.	0.5	6
111	Deciphering the introduction and transmission of SARS-CoV-2 in the Colombian Amazon Basin. PLoS Neglected Tropical Diseases, 2021, 15, e0009327.	3.0	6
112	Respiratory Tract Explant Infection Dynamics of Influenza A Virus in California Sea Lions, Northern Elephant Seals, and Rhesus Macaques. Journal of Virology, 2021, 95, e0040321.	3.4	6
113	Hotspots for SARS-CoV-2 Omicron variant spread: Lessons from New York City. Journal of Medical Virology, 2022, 94, 2911-2914.	5.0	6
114	Isolation of Highly Pathogenic H5N1 Influenza Viruses in 2009-2013 in Vietnam. Frontiers in Microbiology, 2019, 10, 1411.	3.5	5
115	Influenza Virus Polymerase Mutation Stabilizes a Foreign Gene Inserted into the Virus Genome by Enhancing the Transcription/Replication Efficiency of the Modified Segment. MBio, 2019, 10, .	4.1	5
116	SARS-CoV-2 in Transit: Characterization of SARS-CoV-2 Genomes From Venezuelan Migrants in Colombia. International Journal of Infectious Diseases, 2021, 110, 410-416.	3.3	5
117	Relationship of β 2-Adrenergic Receptor Polymorphism With Obesity in Type 2 Diabetes. Diabetes Care, 2003, 26, 251-252.	8.6	4
118	Interactions of Transcription Factors with Chromatin. Sub-Cellular Biochemistry, 2011, 52, 223-259.	2.4	4
119	Positive, again! What to make of α -positive SARS-CoV-2 molecular test results. EBioMedicine, 2020, 60, 103011.	6.1	4
120	Characterization of Novel Cross-Reactive Influenza B Virus Hemagglutinin Head Specific Antibodies That Lack Hemagglutination Inhibition Activity. Journal of Virology, 2020, 94, .	3.4	3
121	Lemierre's syndrome associated with hypervirulent <i>Klebsiella pneumoniae</i> : A case report and genomic characterization of the isolate. IDCases, 2021, 25, e01173.	0.9	3
122	RT-PCR and Matrix-Assisted Laser Desorption-Ionization Time-of-Flight Mass Spectrometry Diagnostic Target Performance Reflects Circulating Severe Acute Respiratory Syndrome Coronavirus 2 Variant Diversity in New York City. Journal of Molecular Diagnostics, 2022, , .	2.8	3
123	Longitudinal Whole-Genome Analysis Identifies Variants Associated with Vancomycin and Linezolid Resistance Changes in <i>Enterococcus faecium</i> in Response to Treatment. Open Forum Infectious Diseases, 2016, 3, .	0.9	2
124	Continuous Surveillance by Whole-Genome Sequencing to Identify and Manage Methicillin-Resistant <i>Staphylococcus aureus</i> Outbreaks. Open Forum Infectious Diseases, 2016, 3, .	0.9	2
125	Laser Capture Microdissection of Mouse Embryonic Cartilage and Bone for Gene Expression Analysis. Journal of Visualized Experiments, 2019, , .	0.3	2
126	Modified methicillin-resistant <i>Staphylococcus aureus</i> detected in neonatal intensive care patients. Journal of Antimicrobial Chemotherapy, 2021, 76, 2774-2777.	3.0	2

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127	Evolution of Influenza A Virus in Intensive and Free-Range Swine Farms in Spain. <i>Virus Evolution</i> , 2022, 7, veab099.	4.9	2
128	Everybody nose: molecular and clinical characteristics of nasal colonization during active methicillin-resistant <i>Staphylococcus aureus</i> bloodstream infection. <i>BMC Infectious Diseases</i> , 2022, 22, 400.	2.9	2
129	Phylogenetic analysis and comparative genomics of SARS-CoV-2 from survivor and non-survivor COVID-19 patients in Cordoba, Argentina. <i>BMC Genomics</i> , 2022, 23, .	2.8	2
130	Skeletal Stem Cells in Craniofacial Bone. , 2020, , 141-149.		1
131	Chromatiblock: scalable whole-genome visualization of structural differences in prokaryotes. <i>Journal of Open Source Software</i> , 2020, 5, 2451.	4.6	1
132	PathogenDB: A Modular Software Suite Integrating Genomic Clinical Microbiology and Epidemiology. <i>Open Forum Infectious Diseases</i> , 2016, 3, .	0.9	0
133	Estimating Local Attributable Cost of <i>Clostridium difficile</i> Infection Using Electronic Medical Record Data. <i>Open Forum Infectious Diseases</i> , 2016, 3, .	0.9	0
134	Genetic Variation and Altered Virulence Associated With Loss of Agr Quorum-Sensing Functionality in Patients With <i>Staphylococcus aureus</i> Bacteremia. <i>Open Forum Infectious Diseases</i> , 2016, 3, .	0.9	0
135	Epigenomic Landscape of <i>Clostridium difficile</i> : Largely Neglected Complexity and Opportunity Learned from 45 Hospital Isolates. <i>Open Forum Infectious Diseases</i> , 2016, 3, .	0.9	0
136	Comparative Genomics and Assessment of Strain Diversity, Pathogenicity and Transmission of <i>Clostridium difficile</i> Isolates From a Hospital Setting. <i>Open Forum Infectious Diseases</i> , 2016, 3, .	0.9	0
137	2561. Using Whole Genome Sequencing to Assess the Emergence of Antibiotic Resistance During Treatment of <i>Enterococcus faecium</i> and <i>Enterococcus faecalis</i> Bacteremia at Mount Sinai Hospital. <i>Open Forum Infectious Diseases</i> , 2018, 5, S71-S71.	0.9	0
138	A30â€fAvian influenza viruses in wild birds: Virus evolution in a multi-host ecosystem. <i>Virus Evolution</i> , 2019, 5, .	4.9	0
139	552. Within-Host Evaluation of Colonization During Active Methicillin-Resistant <i>S. aureus</i> Bacteremia. <i>Open Forum Infectious Diseases</i> , 2019, 6, S262-S263.	0.9	0
140	261. A Single-Center Case Series of Methicillin-Resistant <i>S. aureus</i> Bacteremia with Elevated Minimal Inhibitory Concentrations to Vancomycin. <i>Open Forum Infectious Diseases</i> , 2020, 7, S130-S130.	0.9	0