

Susanna Kar-Pui Lau

List of Publications by Year in descending order

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381
papers

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citations

8732

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383
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383
docs citations

383
times ranked

24635
citing authors

#	ARTICLE	IF	CITATIONS
1	Severe acute respiratory syndrome coronavirus-like virus in Chinese horseshoe bats. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 14040-14045.	3.3	1,322
2	Characterization and Complete Genome Sequence of a Novel Coronavirus, Coronavirus HKU1, from Patients with Pneumonia. Journal of Virology, 2005, 79, 884-895.	1.5	1,269
3	Discovery of Seven Novel Mammalian and Avian Coronaviruses in the Genus Deltacoronavirus Supports Bat Coronaviruses as the Gene Source of Alphacoronavirus and Betacoronavirus and Avian Coronaviruses as the Gene Source of Gammacoronavirus and Deltacoronavirus. Journal of Virology, 2012, 86, 3995-4008.	1.5	1,244
4	Severe Acute Respiratory Syndrome Coronavirus as an Agent of Emerging and Reemerging Infection. Clinical Microbiology Reviews, 2007, 20, 660-694.	5.7	886
5	Middle East Respiratory Syndrome Coronavirus: Another Zoonotic Betacoronavirus Causing SARS-Like Disease. Clinical Microbiology Reviews, 2015, 28, 465-522.	5.7	703
6	Coronavirus Genomics and Bioinformatics Analysis. Viruses, 2010, 2, 1804-1820.	1.5	650
7	Coronavirus Diversity, Phylogeny and Interspecies Jumping. Experimental Biology and Medicine, 2009, 234, 1117-1127.	1.1	548
8	Coronavirus HKU1 and Other Coronavirus Infections in Hong Kong. Journal of Clinical Microbiology, 2006, 44, 2063-2071.	1.8	370
9	Delayed induction of proinflammatory cytokines and suppression of innate antiviral response by the novel Middle East respiratory syndrome coronavirus: implications for pathogenesis and treatment. Journal of General Virology, 2013, 94, 2679-2690.	1.3	347
10	Clinical Features and Complete Genome Characterization of a Distinct Human Rhinovirus (HRV) Genetic Cluster, Probably Representing a Previously Undetected HRV Species, HRV-C, Associated with Acute Respiratory Illness in Children. Journal of Clinical Microbiology, 2007, 45, 3655-3664.	1.8	313
11	Delayed antiviral plus immunomodulator treatment still reduces mortality in mice infected by high inoculum of influenza A/H5N1 virus. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 8091-8096.	3.3	280
12	Global Epidemiology of Bat Coronaviruses. Viruses, 2019, 11, 174.	1.5	261
13	Molecular diversity of coronaviruses in bats. Virology, 2006, 351, 180-187.	1.1	256
14	Ecoepidemiology and Complete Genome Comparison of Different Strains of Severe Acute Respiratory Syndrome-Related <i>Rhinolophus</i> Bat Coronavirus in China Reveal Bats as a Reservoir for Acute, Self-Limiting Infection That Allows Recombination Events. Journal of Virology, 2010, 84, 2808-2819.	1.5	242
15	Comparative Analysis of Twelve Genomes of Three Novel Group 2c and Group 2d Coronaviruses Reveals Unique Group and Subgroup Features. Journal of Virology, 2007, 81, 1574-1585.	1.5	233
16	Genetic Characterization of Betacoronavirus Lineage C Viruses in Bats Reveals Marked Sequence Divergence in the Spike Protein of Pipistrellus Bat Coronavirus HKU5 in Japanese Pipistrelle: Implications for the Origin of the Novel Middle East Respiratory Syndrome Coronavirus. Journal of Virology, 2013, 87, 8638-8650.	1.5	225
17	Clinical and Molecular Epidemiological Features of Coronavirus HKU1-Associated Community-Acquired Pneumonia. Journal of Infectious Diseases, 2005, 192, 1898-1907.	1.9	221
18	Possible Bat Origin of Severe Acute Respiratory Syndrome Coronavirus 2. Emerging Infectious Diseases, 2020, 26, 1542-1547.	2.0	221

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19	Molecular Epidemiology of Human Coronavirus OC43 Reveals Evolution of Different Genotypes over Time and Recent Emergence of a Novel Genotype due to Natural Recombination. <i>Journal of Virology</i> , 2011, 85, 11325-11337.	1.5	218
20	Soluble ACE2-mediated cell entry of SARS-CoV-2 via interaction with proteins related to the renin-angiotensin system. <i>Cell</i> , 2021, 184, 2212-2228.e12.	13.5	216
21	Molecular epidemiology, evolution and phylogeny of SARS coronavirus. <i>Infection, Genetics and Evolution</i> , 2019, 71, 21-30.	1.0	215
22	New Hepatitis E Virus Genotype in Camels, the Middle East. <i>Emerging Infectious Diseases</i> , 2014, 20, 1044-1048.	2.0	213
23	Comparative Analysis of 22 Coronavirus HKU1 Genomes Reveals a Novel Genotype and Evidence of Natural Recombination in Coronavirus HKU1. <i>Journal of Virology</i> , 2006, 80, 7136-7145.	1.5	205
24	<i>Talaromyces (Penicillium) marneffeii</i> infection in non-HIV-infected patients. <i>Emerging Microbes and Infections</i> , 2016, 5, 1-9.	3.0	201
25	Comparative Analysis of Complete Genome Sequences of Three Avian Coronaviruses Reveals a Novel Group 3c Coronavirus. <i>Journal of Virology</i> , 2009, 83, 908-917.	1.5	196
26	Differential Cell Line Susceptibility to the Emerging Novel Human Betacoronavirus 2c EMC/2012: Implications for Disease Pathogenesis and Clinical Manifestation. <i>Journal of Infectious Diseases</i> , 2013, 207, 1743-1752.	1.9	195
27	Clinical and Molecular Epidemiology of Human Bocavirus in Respiratory and Fecal Samples from Children in Hong Kong. <i>Journal of Infectious Diseases</i> , 2007, 196, 986-993.	1.9	172
28	Severe Acute Respiratory Syndrome (SARS) Coronavirus ORF8 Protein Is Acquired from SARS-Related Coronavirus from Greater Horseshoe Bats through Recombination. <i>Journal of Virology</i> , 2015, 89, 10532-10547.	1.5	172
29	Rat Hepatitis E Virus as Cause of Persistent Hepatitis after Liver Transplant. <i>Emerging Infectious Diseases</i> , 2018, 24, 2241-2250.	2.0	167
30	Hepatitis E Virus Genotypes and Evolution: Emergence of Camel Hepatitis E Variants. <i>International Journal of Molecular Sciences</i> , 2017, 18, 869.	1.8	163
31	Usefulness of the MicroSeq 500 16S Ribosomal DNA-Based Bacterial Identification System for Identification of Clinically Significant Bacterial Isolates with Ambiguous Biochemical Profiles. <i>Journal of Clinical Microbiology</i> , 2003, 41, 1996-2001.	1.8	162
32	Complete genome sequence of bat coronavirus HKU2 from Chinese horseshoe bats revealed a much smaller spike gene with a different evolutionary lineage from the rest of the genome. <i>Virology</i> , 2007, 367, 428-439.	1.1	162
33	Comparative genomic analysis of pre-epidemic and epidemic Zika virus strains for virological factors potentially associated with the rapidly expanding epidemic. <i>Emerging Microbes and Infections</i> , 2016, 5, 1-12.	3.0	162
34	Longitudinal Profile of Immunoglobulin G (IgG), IgM, and IgA Antibodies against the Severe Acute Respiratory Syndrome (SARS) Coronavirus Nucleocapsid Protein in Patients with Pneumonia Due to the SARS Coronavirus. <i>Vaccine Journal</i> , 2004, 11, 665-668.	2.6	158
35	Cross-reactive antibodies in convalescent SARS patients' sera against the emerging novel human coronavirus EMC (2012) by both immunofluorescent and neutralizing antibody tests. <i>Journal of Infection</i> , 2013, 67, 130-140.	1.7	158
36	New Hepatitis E Virus Genotype in Bactrian Camels, Xinjiang, China, 2013. <i>Emerging Infectious Diseases</i> , 2016, 22, 2219-2221.	2.0	153

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37	Feline morbillivirus, a previously undescribed paramyxovirus associated with tubulointerstitial nephritis in domestic cats. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 5435-5440.	3.3	150
38	Identification of novel porcine and bovine parvoviruses closely related to human parvovirus 4. Journal of General Virology, 2008, 89, 1840-1848.	1.3	148
39	Discovery of a Novel Coronavirus, China Rattus Coronavirus HKU24, from Norway Rats Supports the Murine Origin of Betacoronavirus 1 and Has Implications for the Ancestor of Betacoronavirus Lineage A. Journal of Virology, 2015, 89, 3076-3092.	1.5	147
40	Elizabethkingia anophelis bacteremia is associated with clinically significant infections and high mortality. Scientific Reports, 2016, 6, 26045.	1.6	146
41	Human enterovirus 71 epidemics: what's next?. Emerging Health Threats Journal, 2013, 6, 19780.	3.0	141
42	MERS coronavirus induces apoptosis in kidney and lung by upregulating Smad7 and FGF2. Nature Microbiology, 2016, 1, 16004.	5.9	140
43	Relative rates of non-pneumonic SARS coronavirus infection and SARS coronavirus pneumonia. Lancet, The, 2004, 363, 841-845.	6.3	134
44	Invasive Streptococcus iniae Infections Outside North America. Journal of Clinical Microbiology, 2003, 41, 1004-1009.	1.8	126
45	Discovery of a Novel Bottlenose Dolphin Coronavirus Reveals a Distinct Species of Marine Mammal Coronavirus in Gammacoronavirus. Journal of Virology, 2014, 88, 1318-1331.	1.5	126
46	Clinical and Molecular Epidemiology of Human Rhinovirus C in Children and Adults in Hong Kong Reveals a Possible Distinct Human Rhinovirus C Subgroup. Journal of Infectious Diseases, 2009, 200, 1096-1103.	1.9	125
47	Cytokine Profiles Induced by the Novel Swine Origin Influenza A/H1N1 Virus: Implications for Treatment Strategies. Journal of Infectious Diseases, 2010, 201, 346-353.	1.9	125
48	Identification of MicroRNA-Like RNAs in Mycelial and Yeast Phases of the Thermal Dimorphic Fungus Penicillium marneffei. PLoS Neglected Tropical Diseases, 2013, 7, e2398.	1.3	121
49	Transmission of Rat Hepatitis E Virus Infection to Humans in Hong Kong: A Clinical and Epidemiological Analysis. Hepatology, 2021, 73, 10-22.	3.6	121
50	Laribacter hongkongensis gen. nov., sp. nov., a Novel Gram-Negative Bacterium Isolated from a Cirrhotic Patient with Bacteremia and Empyema. Journal of Clinical Microbiology, 2001, 39, 4227-4232.	1.8	119
51	Differential Sensitivities of Severe Acute Respiratory Syndrome (SARS) Coronavirus Spike Polypeptide Enzyme-Linked Immunosorbent Assay (ELISA) and SARS Coronavirus Nucleocapsid Protein ELISA for Serodiagnosis of SARS Coronavirus Pneumonia. Journal of Clinical Microbiology, 2005, 43, 3054-3058.	1.8	118
52	Eggerthella hongkongensis sp. nov. and eggerthella sinensis sp. nov., two novel Eggerthella species, account for half of the cases of Eggerthella bacteremia. Diagnostic Microbiology and Infectious Disease, 2004, 49, 255-263.	0.8	116
53	The emerging novel Middle East respiratory syndrome coronavirus: The 'knowns' and 'unknowns'. Journal of the Formosan Medical Association, 2013, 112, 372-381.	0.8	115
54	Detection of Specific Antibodies to Severe Acute Respiratory Syndrome (SARS) Coronavirus Nucleocapsid Protein for Serodiagnosis of SARS Coronavirus Pneumonia. Journal of Clinical Microbiology, 2004, 42, 2306-2309.	1.8	114

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55	Isolation and Characterization of a Novel Betacoronavirus Subgroup A Coronavirus, Rabbit Coronavirus HKU14, from Domestic Rabbits. <i>Journal of Virology</i> , 2012, 86, 5481-5496.	1.5	114
56	Detection of Severe Acute Respiratory Syndrome (SARS) Coronavirus Nucleocapsid Protein in SARS Patients by Enzyme-Linked Immunosorbent Assay. <i>Journal of Clinical Microbiology</i> , 2004, 42, 2884-2889.	1.8	113
57	Outbreak of Intestinal Infection Due to <i>Rhizopus microsporus</i> . <i>Journal of Clinical Microbiology</i> , 2009, 47, 2834-2843.	1.8	110
58	Group G Beta-Hemolytic Streptococcal Bacteremia Characterized by 16S Ribosomal RNA Gene Sequencing. <i>Journal of Clinical Microbiology</i> , 2001, 39, 3147-3155.	1.8	105
59	High diversity of polyketide synthase genes and the melanin biosynthesis gene cluster in <i>Penicillium marneffeii</i> . <i>FEBS Journal</i> , 2010, 277, 3750-3758.	2.2	105
60	Coexistence of Different Genotypes in the Same Bat and Serological Characterization of <i>Rousettus</i> Bat Coronavirus HKU9 Belonging to a Novel Betacoronavirus Subgroup. <i>Journal of Virology</i> , 2010, 84, 11385-11394.	1.5	102
61	Arginine Metabolism in Bacterial Pathogenesis and Cancer Therapy. <i>International Journal of Molecular Sciences</i> , 2016, 17, 363.	1.8	100
62	Comparative Host Gene Transcription by Microarray Analysis Early after Infection of the Huh7 Cell Line by Severe Acute Respiratory Syndrome Coronavirus and Human Coronavirus 229E. <i>Journal of Virology</i> , 2005, 79, 6180-6193.	1.5	97
63	Novel Betacoronavirus in Dromedaries of the Middle East, 2013. <i>Emerging Infectious Diseases</i> , 2014, 20, 560-572.	2.0	94
64	<i>Streptococcus sinensis</i> sp. nov., a Novel Species Isolated from a Patient with Infective Endocarditis. <i>Journal of Clinical Microbiology</i> , 2002, 40, 805-810.	1.8	92
65	Human Parainfluenza Virus 4 Outbreak and the Role of Diagnostic Tests. <i>Journal of Clinical Microbiology</i> , 2005, 43, 4515-4521.	1.8	92
66	Recent Transmission of a Novel Alphacoronavirus, Bat Coronavirus HKU10, from Leschenault's Rousettus to Pomona Leaf-Nosed Bats: First Evidence of Interspecies Transmission of Coronavirus between Bats of Different Suborders. <i>Journal of Virology</i> , 2012, 86, 11906-11918.	1.5	87
67	<i>Granulicatella adiacens</i> and <i>Abiotrophia defectiva</i> bacteraemia characterized by 16S rRNA gene sequencing. <i>Journal of Medical Microbiology</i> , 2003, 52, 137-140.	0.7	86
68	A Rapid, Simple, Inexpensive, and Mobile Colorimetric Assay COVID-19-LAMP for Mass On-Site Screening of COVID-19. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5380.	1.8	85
69	Association of <i>Laribacter hongkongensis</i> in community-acquired gastroenteritis with travel and eating fish: a multicentre case-control study. <i>Lancet, The</i> , 2004, 363, 1941-1947.	6.3	83
70	Emergence of enterovirus 71 double-recombinant strains belonging to a novel genotype D originating from southern China: first evidence for combination of intratypic and intertypic recombination events in EV71. <i>Archives of Virology</i> , 2010, 155, 1413-1424.	0.9	83
71	Identification and characterization of bocaviruses in cats and dogs reveals a novel feline bocavirus and a novel genetic group of canine bocavirus. <i>Journal of General Virology</i> , 2012, 93, 1573-1582.	1.3	83
72	Acute Middle East Respiratory Syndrome Coronavirus Infection in Livestock Dromedaries, Dubai, 2014. <i>Emerging Infectious Diseases</i> , 2015, 21, 1019-1022.	2.0	81

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73	Evidence for <i>Elizabethkingia anophelis</i> Transmission from Mother to Infant, Hong Kong. <i>Emerging Infectious Diseases</i> , 2015, 21, 232-241.	2.0	81
74	Cytosine deamination and selection of CpG suppressed clones are the two major independent biological forces that shape codon usage bias in coronaviruses. <i>Virology</i> , 2007, 369, 431-442.	1.1	80
75	Receptor Usage of a Novel Bat Lineage C Betacoronavirus Reveals Evolution of Middle East Respiratory Syndrome-Related Coronavirus Spike Proteins for Human Dipeptidyl Peptidase 4 Binding. <i>Journal of Infectious Diseases</i> , 2018, 218, 197-207.	1.9	80
76	Complete Genome Analysis of Three Novel Picornaviruses from Diverse Bat Species. <i>Journal of Virology</i> , 2011, 85, 8819-8828.	1.5	79
77	Laboratory diagnosis of melioidosis: Past, present and future. <i>Experimental Biology and Medicine</i> , 2015, 240, 742-751.	1.1	79
78	False-Positive Results in a Recombinant Severe Acute Respiratory Syndrome-Associated Coronavirus (SARS-CoV) Nucleocapsid Enzyme-Linked Immunosorbent Assay Due to HCoV-OC43 and HCoV-229E Rectified by Western Blotting with Recombinant SARS-CoV Spike Polypeptide. <i>Journal of Clinical Microbiology</i> , 2004, 42, 5885-5888.	1.8	78
79	Rediscovery and genomic characterization of bovine astroviruses. <i>Journal of General Virology</i> , 2011, 92, 1888-1898.	1.3	77
80	Identification by 16S rRNA Gene Sequencing of <i>Lactobacillus salivarius</i> Bacteremic Cholecystitis. <i>Journal of Clinical Microbiology</i> , 2002, 40, 265-267.	1.8	76
81	A sensitive and specific antigen detection assay for Middle East respiratory syndrome coronavirus. <i>Emerging Microbes and Infections</i> , 2015, 4, 1-5.	3.0	74
82	Development and Evaluation of Novel Real-Time Reverse Transcription-PCR Assays with Locked Nucleic Acid Probes Targeting Leader Sequences of Human-Pathogenic Coronaviruses. <i>Journal of Clinical Microbiology</i> , 2015, 53, 2722-2726.	1.8	73
83	The biosynthetic pathway for a thousand-year-old natural food colorant and citrinin in <i>Penicillium marneffei</i> . <i>Scientific Reports</i> , 2014, 4, 6728.	1.6	73
84	Misidentification of <i>Aspergillus nomius</i> and <i>Aspergillus tamarii</i> as <i>Aspergillus flavus</i> : Characterization by Internal Transcribed Spacer, β -Tubulin, and Calmodulin Gene Sequencing, Metabolic Fingerprinting, and Matrix-Assisted Laser Desorption Ionization–Time of Flight Mass Spectrometry. <i>Journal of Clinical Microbiology</i> , 2014, 52, 1153-1160.	1.8	71
85	Clinical Spectrum of <i>Exophiala</i> Infections and a Novel <i>Exophiala</i> Species, <i>Exophiala hongkongensis</i> . <i>Journal of Clinical Microbiology</i> , 2013, 51, 260-267.	1.8	68
86	Clinical isolates of <i>Streptococcus iniae</i> from Asia are more mucoid and β -hemolytic than those from North America. <i>Diagnostic Microbiology and Infectious Disease</i> , 2006, 54, 177-181.	0.8	67
87	Geographical difference of disease association in <i>Streptococcus bovis</i> bacteraemia. <i>Journal of Medical Microbiology</i> , 2003, 52, 903-908.	0.7	66
88	SARS Coronavirus Detection Methods. <i>Emerging Infectious Diseases</i> , 2005, 11, 1108-1111.	2.0	66
89	Catheter-Related Microbacterium Bacteremia Identified by 16S rRNA Gene Sequencing. <i>Journal of Clinical Microbiology</i> , 2002, 40, 2681-2685.	1.8	65
90	Natural Occurrence and Characterization of Two Internal Ribosome Entry Site Elements in a Novel Virus, Canine Picodicistrovirus, in the Picornavirus-Like Superfamily. <i>Journal of Virology</i> , 2012, 86, 2797-2808.	1.5	65

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91	Metagenomic analysis of viromes of dromedary camel fecal samples reveals large number and high diversity of circoviruses and picobirnaviruses. <i>Virology</i> , 2014, 471-473, 117-125.	1.1	65
92	Streptococcus milleri endocarditis caused by S. streptococcus anginosus. <i>Diagnostic Microbiology and Infectious Disease</i> , 2004, 48, 81-88.	0.8	64
93	Coronaviruses: emerging and re-emerging pathogens in humans and animals. <i>Virology Journal</i> , 2015, 12, 209.	1.4	64
94	Complete Genome Sequence of <i>Staphylococcus lugdunensis</i> Strain HKU09-01. <i>Journal of Bacteriology</i> , 2010, 192, 1471-1472.	1.0	62
95	Disseminated Infections with <i>Talaromyces marneffei</i> in Non-AIDS Patients Given Monoclonal Antibodies against CD20 and Kinase Inhibitors. <i>Emerging Infectious Diseases</i> , 2015, 21, 1101-1106.	2.0	62
96	Discovery and Sequence Analysis of Four Deltacoronaviruses from Birds in the Middle East Reveal Interspecies Jumping with Recombination as a Potential Mechanism for Avian-to-Avian and Avian-to-Mammalian Transmission. <i>Journal of Virology</i> , 2018, 92, .	1.5	62
97	Genomic and experimental evidence for a potential sexual cycle in the pathogenic thermal dimorphic fungus <i>Penicillium marneffei</i> . <i>FEBS Letters</i> , 2006, 580, 3409-3416.	1.3	60
98	<i>Catabacter hongkongensis</i> gen. nov., sp. nov., Isolated from Blood Cultures of Patients from Hong Kong and Canada. <i>Journal of Clinical Microbiology</i> , 2007, 45, 395-401.	1.8	60
99	Taxonomy and evolution of <i>Aspergillus</i> , <i>Penicillium</i> and <i>Talaromyces</i> in the omics era – Past, present and future. <i>Computational and Structural Biotechnology Journal</i> , 2018, 16, 197-210.	1.9	59
100	Transmission of a Novel Genotype of Hepatitis E Virus from Bactrian Camels to <i>Cynomolgus</i> Macaques. <i>Journal of Virology</i> , 2019, 93, .	1.5	59
101	Co-existence of multiple strains of two novel porcine bocaviruses in the same pig, a previously undescribed phenomenon in members of the family Parvoviridae, and evidence for inter- and intra-host genetic diversity and recombination. <i>Journal of General Virology</i> , 2011, 92, 2047-2059.	1.3	59
102	Detection of Antibodies Specific to an Antigenic Cell Wall Galactomannoprotein for Serodiagnosis of <i>Aspergillus fumigatus</i> Aspergillosis. <i>Journal of Clinical Microbiology</i> , 2002, 40, 2041-2045.	1.8	57
103	Identification and complete genome analysis of three novel paramyxoviruses, Tuhoko virus 1, 2 and 3, in fruit bats from China. <i>Virology</i> , 2010, 404, 106-116.	1.1	57
104	The mitochondrial genome of the thermal dimorphic fungus <i>Penicillium marneffei</i> is more closely related to those of molds than yeasts. <i>FEBS Letters</i> , 2003, 555, 469-477.	1.3	56
105	Hepatitis E: A disease of reemerging importance. <i>Journal of the Formosan Medical Association</i> , 2015, 114, 681-690.	0.8	56
106	Identification of specific metabolites in culture supernatant of <i>Mycobacterium tuberculosis</i> using metabolomics: exploration of potential biomarkers. <i>Emerging Microbes and Infections</i> , 2015, 4, 1-10.	3.0	55
107	<i>Lasiodiplodia theobromae</i> Pneumonia in a Liver Transplant Recipient. <i>Journal of Clinical Microbiology</i> , 2008, 46, 380-384.	1.8	54
108	Comparative analysis of six genome sequences of three novel picornaviruses, turdiviruses 1, 2 and 3, in dead wild birds, and proposal of two novel genera, Orthoturdivirus and Paraturdivirus, in the family Picornaviridae. <i>Journal of General Virology</i> , 2010, 91, 2433-2448.	1.3	54

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109	First Discovery of Two Polyketide Synthase Genes for Mitorubrinic Acid and Mitorubrinol Yellow Pigment Biosynthesis and Implications in Virulence of <i>Penicillium marneffeii</i> . <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1871.	1.3	54
110	Novel Partitivirus Enhances Virulence of and Causes Aberrant Gene Expression in <i>Talaromyces marneffeii</i> . <i>MBio</i> , 2018, 9, .	1.8	54
111	<i>Tsukamurella</i> Conjunctivitis: a Novel Clinical Syndrome. <i>Journal of Clinical Microbiology</i> , 2003, 41, 3368-3371.	1.8	53
112	SARS coronavirus spike polypeptide DNA vaccine priming with recombinant spike polypeptide from <i>Escherichia coli</i> as booster induces high titer of neutralizing antibody against SARS coronavirus. <i>Vaccine</i> , 2005, 23, 4959-4968.	1.7	53
113	<i>Laribacter hongkongensis</i> : a potential cause of infectious diarrhea. <i>Diagnostic Microbiology and Infectious Disease</i> , 2003, 47, 551-556.	0.8	52
114	The Complete Genome and Proteome of <i>Laribacter hongkongensis</i> Reveal Potential Mechanisms for Adaptations to Different Temperatures and Habitats. <i>PLoS Genetics</i> , 2009, 5, e1000416.	1.5	52
115	More and More Coronaviruses: Human Coronavirus HKU1. <i>Viruses</i> , 2009, 1, 57-71.	1.5	51
116	Internal Transcribed Spacer Region Sequence Heterogeneity in <i>Rhizopus microsporus</i> : Implications for Molecular Diagnosis in Clinical Microbiology Laboratories. <i>Journal of Clinical Microbiology</i> , 2010, 48, 208-214.	1.8	51
117	Epidemiology of human parechovirus, Aichi virus and salivirus in fecal samples from hospitalized children with gastroenteritis in Hong Kong. <i>Virology Journal</i> , 2014, 11, 182.	1.4	51
118	Bacteremia Due to <i>Clostridium hathewayi</i> in a Patient with Acute Appendicitis. <i>Journal of Clinical Microbiology</i> , 2004, 42, 5947-5949.	1.8	50
119	Ecoepidemiology of <i>Laribacter hongkongensis</i> , a Novel Bacterium Associated with Gastroenteritis. <i>Journal of Clinical Microbiology</i> , 2005, 43, 919-922.	1.8	50
120	Matrix-Assisted Laser Desorption Ionization–Time of Flight Mass Spectrometry for Rapid Identification of <i>Burkholderia pseudomallei</i> : Importance of Expanding Databases with Pathogens Endemic to Different Localities. <i>Journal of Clinical Microbiology</i> , 2012, 50, 3142-3143.	1.8	50
121	Two-dimensional gel electrophoresis in bacterial proteomics. <i>Protein and Cell</i> , 2012, 3, 346-363.	4.8	49
122	Complete Genome Sequence of a Novel Paramyxovirus, Tailam Virus, Discovered in Sikkim Rats. <i>Journal of Virology</i> , 2011, 85, 13473-13474.	1.5	48
123	A Novel Psittacine Adenovirus Identified During an Outbreak of Avian Chlamydiosis and Human Psittacosis: Zoonosis Associated with Virus-Bacterium Coinfection in Birds. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e3318.	1.3	48
124	Guidelines for interpretation of 16S rRNA gene sequence-based results for identification of medically important aerobic Gram-positive bacteria. <i>Journal of Medical Microbiology</i> , 2009, 58, 1030-1036.	0.7	47
125	Proteome profiling of the dimorphic fungus <i>Penicillium marneffeii</i> extracellular proteins and identification of glyceraldehyde-3-phosphate dehydrogenase as an important adhesion factor for conidial attachment. <i>FEBS Journal</i> , 2013, 280, 6613-6626.	2.2	47
126	Lipid metabolites as potential diagnostic and prognostic biomarkers for acute community acquired pneumonia. <i>Diagnostic Microbiology and Infectious Disease</i> , 2016, 85, 249-254.	0.8	46

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127	Single gene target bacterial identification. <i>Diagnostic Microbiology and Infectious Disease</i> , 2002, 44, 143-149.	0.8	45
128	Clinical and Molecular Epidemiology of Human Parainfluenza Virus 4 Infections in Hong Kong: Subtype 4B as Common as Subtype 4A. <i>Journal of Clinical Microbiology</i> , 2009, 47, 1549-1552.	1.8	45
129	Novel Pan-Genomic Analysis Approach in Target Selection for Multiplex PCR Identification and Detection of <i>Burkholderia pseudomallei</i> , <i>Burkholderia thailandensis</i> , and <i>Burkholderia cepacia</i> Complex Species: a Proof-of-Concept Study. <i>Journal of Clinical Microbiology</i> , 2011, 49, 814-821.	1.8	45
130	Diagnosis of pelvic actinomycosis by 16S ribosomal RNA gene sequencing and its clinical significance. <i>Diagnostic Microbiology and Infectious Disease</i> , 2002, 43, 113-118.	0.8	44
131	Automated Identification of Medically Important Bacteria by 16S rRNA Gene Sequencing Using a Novel Comprehensive Database, 16SpathDB. <i>Journal of Clinical Microbiology</i> , 2011, 49, 1799-1809.	1.8	44
132	Identification of a Novel Feline Picornavirus from the Domestic Cat. <i>Journal of Virology</i> , 2012, 86, 395-405.	1.5	44
133	Complete Genome Sequences of Novel Canine Noroviruses in Hong Kong. <i>Journal of Virology</i> , 2012, 86, 9531-9532.	1.5	44
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