

Zigui Chen

List of Publications by Year in Descending Order

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Version: 2024-04-27

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

157
papers

7,863
citations

43
h-index

86
g-index

174
ext. papers

10,172
ext. citations

7
avg. IF

6.02
L-index

#	Paper	IF	Citations
157	Case series of HIV SARS-CoV-2 co-infection in Chinese adults.. <i>Journal of Clinical Virology Plus</i> , 2022 , 2, 100062		
156	Determinants and Interactions of Oral Bacterial and Fungal Microbiota in Healthy Chinese Adults.. <i>Microbiology Spectrum</i> , 2022 , e0241021	8.9	4
155	Quantifying the effect of government interventions and virus mutations on transmission advantage during COVID-19 pandemic.. <i>Journal of Infection and Public Health</i> , 2022 , 15, 338-342	7.4	0
154	Profiling of SARS-CoV-2 Subgenomic RNAs in Clinical Specimens.. <i>Microbiology Spectrum</i> , 2022 , e0018222	8.9	1
153	Non-human primate papillomavirus E6-mediated p53 degradation reveals ancient evolutionary adaptation of carcinogenic phenotype to host niche.. <i>PLoS Pathogens</i> , 2022 , 18, e1010444	7.6	1
152	Seroprevalence of Unidentified SARS-CoV-2 Infection in Hong Kong During 3 Pandemic Waves. <i>JAMA Network Open</i> , 2021 , 4, e2132923	10.4	1
151	Oesophageal carcinoma: The prevalence of DNA tumour viruses and therapy.. <i>Tumour Virus Research</i> , 2021 , 13, 200231		0
150	Restoration of the Oral Microbiota After Surgery for Head and Neck Squamous Cell Carcinoma Is Associated With Patient Outcomes. <i>Frontiers in Oncology</i> , 2021 , 11, 737843	5.3	0
149	Real-time quantification of the transmission advantage associated with a single mutation in pathogen genomes: a case study on the D614G substitution of SARS-CoV-2. <i>BMC Infectious Diseases</i> , 2021 , 21, 1039	4	0
148	Temporal-Geographical Dispersion of SARS-CoV-2 Spike Glycoprotein Variant Lineages and Their Functional Prediction Using Approach. <i>MBio</i> , 2021 , 12, e0268721	7.8	3
147	Depicting SARS-CoV-2 faecal viral activity in association with gut microbiota composition in patients with COVID-19. <i>Gut</i> , 2021 , 70, 276-284	19.2	180
146	Modelling the association between COVID-19 transmissibility and D614G substitution in SARS-CoV-2 spike protein: using the surveillance data in California as an example. <i>Theoretical Biology and Medical Modelling</i> , 2021 , 18, 10	2.3	6
145	Differential Influence of Age on the Relationship between Genetic Mismatch and A(H1N1)pdm09 Vaccine Effectiveness. <i>Viruses</i> , 2021 , 13,	6.2	2
144	Temporal landscape of human gut RNA and DNA virome in SARS-CoV-2 infection and severity. <i>Microbiome</i> , 2021 , 9, 91	16.6	13
143	Inferring the Association between the Risk of COVID-19 Case Fatality and N501Y Substitution in SARS-CoV-2. <i>Viruses</i> , 2021 , 13,	6.2	17
142	Current Updates on Cancer-Causing Types of Human Papillomaviruses (HPVs) in East, Southeast, and South Asia. <i>Cancers</i> , 2021 , 13,	6.6	4
141	A global analysis of replacement of genetic variants of SARS-CoV-2 in association with containment capacity and changes in disease severity. <i>Clinical Microbiology and Infection</i> , 2021 ,	9.5	8

140	An early assessment of a case fatality risk associated with P.1 SARS-CoV-2 lineage in Brazil: an ecological study. <i>Journal of Travel Medicine</i> , 2021 , 28,	12.9	3
139	Genomic and evolutionary comparison between SARS-CoV-2 and other human coronaviruses. <i>Journal of Virological Methods</i> , 2021 , 289, 114032	2.6	18
138	Genetic signatures for lineage/sublineage classification of HPV16, 18, 52 and 58 variants. <i>Virology</i> , 2021 , 553, 62-69	3.6	4
137	Quantifying the transmission advantage associated with N501Y substitution of SARS-CoV-2 in the UK: an early data-driven analysis. <i>Journal of Travel Medicine</i> , 2021 , 28,	12.9	51
136	Acceptance of the COVID-19 vaccine based on the health belief model: A population-based survey in Hong Kong. <i>Vaccine</i> , 2021 , 39, 1148-1156	4.1	149
135	A Bayesian method for synthesizing multiple diagnostic outcomes of COVID-19 tests. <i>Royal Society Open Science</i> , 2021 , 8, 201867	3.3	2
134	Mer Analyses Reveal Different Evolutionary Histories of Alpha, Beta, and Gamma Papillomaviruses. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	2
133	Genomic Epidemiology of Multidrug-Resistant Nontyphoidal Salmonella in Young Children Hospitalized for Gastroenteritis. <i>Microbiology Spectrum</i> , 2021 , 9, e0024821	8.9	2
132	Comparison of self-collected mouth gargle with deep-throat saliva samples for the diagnosis of COVID-19: Mouth gargle for diagnosis of COVID-19. <i>Journal of Infection</i> , 2021 , 83, 496-522	18.9	1
131	Longitudinal Cytokine Profile in Patients With Mild to Critical COVID-19.. <i>Frontiers in Immunology</i> , 2021 , 12, 763292	8.4	5
130	Micro-/Nanorobots in Antimicrobial Applications: Recent Progress, Challenges, and Opportunities.. <i>Advanced Healthcare Materials</i> , 2021 , e2101991	10.1	5
129	Human Papillomavirus 58 E7 T20I/G63S Variant Isolated from an East Asian Population Possesses High Oncogenicity. <i>Journal of Virology</i> , 2020 , 94,	6.6	4
128	Alterations in Gut Microbiota of Patients With COVID-19 During Time of Hospitalization. <i>Gastroenterology</i> , 2020 , 159, 944-955.e8	13.3	555
127	Persistence and clearance of oral human papillomavirus infections: A prospective population-based cohort study. <i>Journal of Medical Virology</i> , 2020 , 92, 3807	19.7	2
126	Quantifying the importance of the key sites on haemagglutinin in determining the selection advantage of influenza virus: Using A/H3N2 as an example. <i>Journal of Infection</i> , 2020 , 81, 452-482	18.9	7
125	Association of HPV35 with cervical carcinogenesis among women of African ancestry: Evidence of viral-host interaction with implications for disease intervention. <i>International Journal of Cancer</i> , 2020 , 147, 2677-2686	7.5	24
124	Epidemiological characteristics of the first 100 cases of coronavirus disease 2019 (COVID-19) in Hong Kong Special Administrative Region, China, a city with a stringent containment policy. <i>International Journal of Epidemiology</i> , 2020 , 49, 1096-1105	7.8	18
123	Southern Chinese populations harbour non-nucleatum Fusobacteria possessing homologues of the colorectal cancer-associated FadA virulence factor. <i>Gut</i> , 2020 , 69, 1998-2007	19.2	16

122	Systematic review of human gut resistome studies revealed variable definitions and approaches. <i>Gut Microbes</i> , 2020 , 12, 1700755	8.8	7
121	Stringent containment measures without complete city lockdown to achieve low incidence and mortality across two waves of COVID-19 in Hong Kong. <i>BMJ Global Health</i> , 2020 , 5,	6.6	17
120	Bacteria pathogens drive host colonic epithelial cell promoter hypermethylation of tumor suppressor genes in colorectal cancer. <i>Microbiome</i> , 2020 , 8, 108	16.6	14
119	The Intersection between Oral Microbiota, Host Gene Methylation and Patient Outcomes in Head and Neck Squamous Cell Carcinoma. <i>Cancers</i> , 2020 , 12,	6.6	11
118	Serologic Responses in Healthy Adult with SARS-CoV-2 Reinfection, Hong Kong, August 2020. <i>Emerging Infectious Diseases</i> , 2020 , 26, 3076-3078	10.2	29
117	Prospective Study Comparing Deep Throat Saliva With Other Respiratory Tract Specimens in the Diagnosis of Novel Coronavirus Disease 2019. <i>Journal of Infectious Diseases</i> , 2020 , 222, 1612-1619	7	27
116	Seasonal dynamics and starvation impact on the gut microbiome of urochordate ascidian <i>Halocynthia roretzi</i> . <i>Animal Microbiome</i> , 2020 , 2, 30	4.1	2
115	SARS-CoV-2 RNA Detection on Disposable Wooden Chopsticks, Hong Kong. <i>Emerging Infectious Diseases</i> , 2020 , 26,	10.2	6
114	Characterization and Diversity of 243 Complete Human Papillomavirus Genomes in Cervical Swabs Using Next Generation Sequencing. <i>Viruses</i> , 2020 , 12,	6.2	1
113	Viral dynamics of SARS-CoV-2 across a spectrum of disease severity in COVID-19. <i>Journal of Infection</i> , 2020 , 81, 318-356	18.9	44
112	Non-human Primate Papillomaviruses Share Similar Evolutionary Histories and Niche Adaptation as the Human Counterparts. <i>Frontiers in Microbiology</i> , 2019 , 10, 2093	5.7	8
111	Liquid biopsy of HPV DNA in cervical cancer. <i>Journal of Clinical Virology</i> , 2019 , 114, 32-36	14.5	22
110	Role of polycyclic aromatic hydrocarbons as a co-factor in human papillomavirus-mediated carcinogenesis. <i>BMC Cancer</i> , 2019 , 19, 138	4.8	13
109	Evaluation of Oral Cavity DNA Extraction Methods on Bacterial and Fungal Microbiota. <i>Scientific Reports</i> , 2019 , 9, 1531	4.9	20
108	Impact of Preservation Method and 16S rRNA Hypervariable Region on Gut Microbiota Profiling. <i>MSystems</i> , 2019 , 4,	7.6	59
107	Molecular epidemiological study of enterovirus D68 in hospitalised children in Hong Kong in 2014-2015 and their complete coding sequences. <i>BMJ Open Respiratory Research</i> , 2019 , 6, e000437	5.6	1
106	Impact of inter- and intra-individual variation, sample storage and sampling fraction on human stool microbial community profiles. <i>PeerJ</i> , 2019 , 7, e6172	3.1	14
105	Oncogenicity Comparison of Human Papillomavirus Type 52 E6 Variants. <i>Journal of General Virology</i> , 2019 , 100, 484-496	4.9	5

104	Human papillomavirus 16 sub-lineage dispersal and cervical cancer risk worldwide: Whole viral genome sequences from 7116 HPV16-positive women. <i>Papillomavirus Research (Amsterdam, Netherlands)</i> , 2019 , 7, 67-74	4.6	20
103	Human papillomavirus type 18 oncoproteins exert their oncogenicity in esophageal and tongue squamous cell carcinoma cell lines distinctly. <i>BMC Cancer</i> , 2019 , 19, 1211	4.8	5
102	The human oral cavity microbiota composition during acute tonsillitis: a cross-sectional survey. <i>BMC Oral Health</i> , 2019 , 19, 275	3.7	11
101	Oncogenic comparison of human papillomavirus type 58 E7 variants. <i>Journal of Cellular and Molecular Medicine</i> , 2019 , 23, 1517-1527	5.6	4
100	The role of human papillomavirus in laryngeal cancer in Southern China. <i>Journal of Medical Virology</i> , 2018 , 90, 1150-1159	19.7	6
99	Classification and evolution of human papillomavirus genome variants: Alpha-5 (HPV26, 51, 69, 82), Alpha-6 (HPV30, 53, 56, 66), Alpha-11 (HPV34, 73), Alpha-13 (HPV54) and Alpha-3 (HPV61). <i>Virology</i> , 2018 , 516, 86-101	3.6	17
98	Complete Genome Sequences of Three Novel Papillomavirus Types Isolated from the Cervicovaginal Region of Squirrel Monkeys. <i>Genome Announcements</i> , 2018 , 6,		3
97	Age-specific seroprevalence of dengue infection in Hong Kong. <i>Journal of Medical Virology</i> , 2018 , 90, 1427-1430	19.7	3
96	Alterations in Enteric Virome Are Associated With Colorectal Cancer and Survival Outcomes. <i>Gastroenterology</i> , 2018 , 155, 529-541.e5	13.3	132
95	Lower airway microbiota and mycobiota in children with severe asthma. <i>Journal of Allergy and Clinical Immunology</i> , 2018 , 141, 808-811.e7	11.5	26
94	Prevalence and Epidemiologic Profile of Oral Infection with Alpha, Beta, and Gamma Papillomaviruses in an Asian Chinese Population. <i>Journal of Infectious Diseases</i> , 2018 , 218, 388-397	7	19
93	Multi-cohort analysis of colorectal cancer metagenome identified altered bacteria across populations and universal bacterial markers. <i>Microbiome</i> , 2018 , 6, 70	16.6	165
92	Oral Alpha, Beta, and Gamma HPV Types and Risk of Incident Esophageal Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2018 , 27, 1168-1175	4	9
91	Mucosal microbiome dysbiosis in gastric carcinogenesis. <i>Gut</i> , 2018 , 67, 1024-1032	19.2	249
90	ICTV Virus Taxonomy Profile: Papillomaviridae. <i>Journal of General Virology</i> , 2018 , 99, 989-990	4.9	76
89	Complete Genome Sequences of Six Novel Macaca mulatta Papillomavirus Types Isolated from Genital Sites of Rhesus Monkeys in Hong Kong SAR, China. <i>Microbiology Resource Announcements</i> , 2018 , 7,	1.3	3
88	Niche adaptation and viral transmission of human papillomaviruses from archaic hominins to modern humans. <i>PLoS Pathogens</i> , 2018 , 14, e1007352	7.6	32
87	Diversity of macaque microbiota compared to the human counterparts. <i>Scientific Reports</i> , 2018 , 8, 155734.9	34.9	24

86	Frequent Genetic Mismatch between Vaccine Strains and Circulating Seasonal Influenza Viruses, Hong Kong, China, 1996-2012. <i>Emerging Infectious Diseases</i> , 2018 , 24, 1825-1834	10.2	5
85	Oncogenes expand during evolution to withstand somatic amplification. <i>Annals of Oncology</i> , 2018 , 29, 2254-2260	10.3	1
84	Integrated genomic and molecular characterization of cervical cancer. <i>Nature</i> , 2017 , 543, 378-384	50.4	755
83	Clinical features and seasonality of parechovirus infection in an Asian subtropical city, Hong Kong. <i>PLoS ONE</i> , 2017 , 12, e0184533	3.7	16
82	HPV16 E7 Genetic Conservation Is Critical to Carcinogenesis. <i>Cell</i> , 2017 , 170, 1164-1174.e6	56.2	138
81	Ancient Evolution and Dispersion of Human Papillomavirus 58 Variants. <i>Journal of Virology</i> , 2017 , 91,	6.6	19
80	Complete Genome Sequence of a Novel Human Papillomavirus Isolated from Oral Rinse. <i>Genome Announcements</i> , 2017 , 5,		2
79	Detection and Genotyping of Human Papillomaviruses from Archival Formalin-Fixed Tissue Samples. <i>Current Protocols in Microbiology</i> , 2016 , 43, 14B.9.1-14B.9.20	7.1	2
78	Associations of Oral β and γ Human Papillomavirus Types With Risk of Incident Head and Neck Cancer. <i>JAMA Oncology</i> , 2016 , 2, 599-606	13.4	92
77	Cross-protection of the Bivalent Human Papillomavirus (HPV) Vaccine Against Variants of Genetically Related High-Risk HPV Infections. <i>Journal of Infectious Diseases</i> , 2016 , 213, 939-47	7	14
76	Distinct Ecological Niche of Anal, Oral, and Cervical Mucosal Microbiomes in Adolescent Women. <i>Yale Journal of Biology and Medicine</i> , 2016 , 89, 277-284	2.4	9
75	Comparison of three human papillomavirus DNA detection methods: Next generation sequencing, multiplex-PCR and nested-PCR followed by Sanger based sequencing. <i>Journal of Medical Virology</i> , 2016 , 88, 888-94	19.7	17
74	Global Genomic Diversity of Human Papillomavirus 11 Based on 433 Isolates and 78 Complete Genome Sequences. <i>Journal of Virology</i> , 2016 , 90, 5503-5513	6.6	15
73	Evidence for a distinct gut microbiome in kidney stone formers compared to non-stone formers. <i>Urolithiasis</i> , 2016 , 44, 399-407	3.2	81
72	HPV16 Sublineage Associations With Histology-Specific Cancer Risk Using HPV Whole-Genome Sequences in 3200 Women. <i>Journal of the National Cancer Institute</i> , 2016 , 108,	9.7	93
71	In vitro inhibition of human papillomavirus following use of a carrageenan-containing vaginal gel. <i>Gynecologic Oncology</i> , 2016 , 143, 313-318	4.9	15
70	Deep sequencing of HPV16 genomes: A new high-throughput tool for exploring the carcinogenicity and natural history of HPV16 infection. <i>Papillomavirus Research (Amsterdam, Netherlands)</i> , 2015 , 1, 3-11	4.6	47
69	HPV16 CpG methyl-haplotypes are associated with cervix precancer and cancer in the Guanacaste natural history study. <i>Gynecologic Oncology</i> , 2015 , 138, 94-100	4.9	7

68	HPV16 methyl-haplotypes determined by a novel next-generation sequencing method are associated with cervical precancer. <i>International Journal of Cancer</i> , 2015 , 136, E146-53	7.5	25
67	HPV Infection and Cervical Screening in Socially Isolated Indigenous Women Inhabitants of the Amazonian Rainforest. <i>PLoS ONE</i> , 2015 , 10, e0133635	3.7	29
66	Evolution and classification of oncogenic human papillomavirus types and variants associated with cervical cancer. <i>Methods in Molecular Biology</i> , 2015 , 1249, 3-26	1.4	17
65	Human papillomavirus 33 worldwide genetic variation and associated risk of cervical cancer. <i>Virology</i> , 2014 , 448, 356-62	3.6	19
64	Geographical distribution and risk association of human papillomavirus genotype 52-variant lineages. <i>Journal of Infectious Diseases</i> , 2014 , 210, 1600-4	7	30
63	Three-gene based phylogeny of the Urostyloidea (Protista, Ciliophora, Hypotricha), with notes on classification of some core taxa. <i>Molecular Phylogenetics and Evolution</i> , 2014 , 70, 337-47	4.1	77
62	Characterization of the North American beaver (<i>Castor canadensis</i>) papillomavirus genome. <i>Veterinary Microbiology</i> , 2014 , 168, 214-20	3.3	3
61	Global genomic diversity of human papillomavirus 6 based on 724 isolates and 190 complete genome sequences. <i>Journal of Virology</i> , 2014 , 88, 7307-16	6.6	26
60	Human papillomavirus genomics: past, present and future. <i>Current Problems in Dermatology</i> , 2014 , 45, 1-18		30
59	Characterization of HPV DNA methylation of contiguous CpG sites by bisulfite treatment and massively parallel sequencing-the FRAGMENT approach. <i>Frontiers in Genetics</i> , 2014 , 5, 150	4.5	8
58	<i>Lactobacillus crispatus</i> dominant vaginal microbiome is associated with inhibitory activity of female genital tract secretions against <i>Escherichia coli</i> . <i>PLoS ONE</i> , 2014 , 9, e96659	3.7	65
57	Human papillomavirus 16 non-European variants are preferentially associated with high-grade cervical lesions. <i>PLoS ONE</i> , 2014 , 9, e100746	3.7	52
56	Human papillomavirus genome variants. <i>Virology</i> , 2013 , 445, 232-43	3.6	249
55	Morphology, ontogeny, and molecular phylogeny of two novel bakuellid-like hypotrichs (Ciliophora: Hypotrichia), with establishment of two new genera. <i>European Journal of Protistology</i> , 2013 , 49, 78-92	3.6	46
54	Geographical distribution and oncogenic risk association of human papillomavirus type 58 E6 and E7 sequence variations. <i>International Journal of Cancer</i> , 2013 , 132, 2528-36	7.5	46
53	Oral human papillomavirus detection in older adults who have human immunodeficiency virus infection. <i>Oral Surgery, Oral Medicine, Oral Pathology and Oral Radiology</i> , 2013 , 115, 505-14	2	22
52	Condylomatous genital lesions in cynomolgus macaques from Mauritius. <i>Toxicologic Pathology</i> , 2013 , 41, 893-901	2.1	7
51	Novel genital alphapapillomaviruses in baboons (<i>Papio hamadryas anubis</i>) with cervical dysplasia. <i>Veterinary Pathology</i> , 2013 , 50, 200-8	2.8	22

50	Evolution and taxonomic classification of alphapapillomavirus 7 complete genomes: HPV18, HPV39, HPV45, HPV59, HPV68 and HPV70. <i>PLoS ONE</i> , 2013 , 8, e72565	3.7	39
49	Characterization of human papillomavirus type 120: a novel betapapillomavirus with tropism for multiple anatomical niches. <i>Journal of General Virology</i> , 2012 , 93, 1774-1779	4.9	23
48	A novel papillomavirus isolated from proliferative skin lesions of a wild American beaver (<i>Castor canadensis</i>). <i>Journal of Veterinary Diagnostic Investigation</i> , 2012 , 24, 750-4	1.5	6
47	The cervical microbiome over 7 years and a comparison of methodologies for its characterization. <i>PLoS ONE</i> , 2012 , 7, e40425	3.7	81
46	Papillomaviruses: evolution, Linnaean taxonomy and current nomenclature. <i>Trends in Microbiology</i> , 2011 , 19, 49-50; author reply 50-1	12.4	29
45	Novel betapapillomavirus associated with hand and foot papillomas in a cynomolgus macaque. <i>Veterinary Pathology</i> , 2011 , 48, 731-6	2.8	13
44	Evolution and taxonomic classification of human papillomavirus 16 (HPV16)-related variant genomes: HPV31, HPV33, HPV35, HPV52, HPV58 and HPV67. <i>PLoS ONE</i> , 2011 , 6, e20183	3.7	113
43	The oral cavity contains abundant known and novel human papillomaviruses from the Betapapillomavirus and Gammapapillomavirus genera. <i>Journal of Infectious Diseases</i> , 2011 , 204, 787-92	7	135
42	Sequence imputation of HPV16 genomes for genetic association studies. <i>PLoS ONE</i> , 2011 , 6, e21375	3.7	59
41	Classification and nomenclature system for human Alphapapillomavirus variants: general features, nucleotide landmarks and assignment of HPV6 and HPV11 isolates to variant lineages. <i>Acta Dermatovenerologica Alpina, Panonica Et Adriatica</i> , 2011 , 20, 113-23	0.7	29
40	Degradation of p53 by human Alphapapillomavirus E6 proteins shows a stronger correlation with phylogeny than oncogenicity. <i>PLoS ONE</i> , 2010 , 5, e12816	3.7	46
39	A population-based prospective study of carcinogenic human papillomavirus variant lineages, viral persistence, and cervical neoplasia. <i>Cancer Research</i> , 2010 , 70, 3159-69	10.1	190
38	Lack of heterogeneity of HPV16 E7 sequence compared with HPV31 and HPV73 may be related to its unique carcinogenic properties. <i>Archives of Virology</i> , 2010 , 155, 367-70	2.6	8
37	On four closely related hypotrichous ciliates (Protozoa, Ciliophora, Spirotrichea): molecular characters, interspecific relationships and phylogeny defined with multigene sequence information. <i>Acta Oceanologica Sinica</i> , 2010 , 29, 90-96	1	6
36	Classification of papillomaviruses (PVs) based on 189 PV types and proposal of taxonomic amendments. <i>Virology</i> , 2010 , 401, 70-9	3.6	1118
35	Human papillomaviruses: genetic basis of carcinogenicity. <i>Public Health Genomics</i> , 2009 , 12, 281-90	1.9	88
34	Evolutionary dynamics of variant genomes of human papillomavirus types 18, 45, and 97. <i>Journal of Virology</i> , 2009 , 83, 1443-55	6.6	76
33	Does Kiiitricha (Protista, Ciliophora, Spirotrichea) belong to Euplotida or represent a primordial spirotrichous taxon? With suggestion to establish a new subclass Protohypotrichia. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2009 , 59, 439-46	2.2	18

32	Evolutionary relationship and species separation of four morphologically similar stichotrichous ciliates (Protozoa, Ciliophora). <i>Progress in Natural Science: Materials International</i> , 2009 , 19, 581-586	3.6	8
31	Genomic characterization of two novel reptilian papillomaviruses, <i>Chelonia mydas</i> papillomavirus 1 and <i>Caretta caretta</i> papillomavirus 1. <i>Virology</i> , 2009 , 383, 131-5	3.6	60
30	Genomic diversity and interspecies host infection of alpha12 <i>Macaca fascicularis</i> papillomaviruses (MfPVs). <i>Virology</i> , 2009 , 393, 304-10	3.6	45
29	Phylogenetic analyses suggest that <i>Psammomitra</i> (Ciliophora, Urostylida) should represent an urostylid family, based on small subunit rRNA and alpha-tubulin gene sequence information. <i>Zoological Journal of the Linnean Society</i> , 2009 , 157, 227-236	2.4	29
28	Reconsideration of systematic relationships within the order Euplotida (Protista, Ciliophora) using new sequences of the gene coding for small-subunit rRNA and testing the use of combined data sets to construct phylogenies of the Diophrys-complex. <i>Molecular Phylogenetics and Evolution</i> , 2009 , 50, 599-607	4.1	54
27	Evolutionary and biophysical relationships among the papillomavirus E2 proteins. <i>Frontiers in Bioscience - Landmark</i> , 2009 , 14, 900-17	2.8	16
26	Molecular phylogeny of <i>Pseudokeronopsis</i> (Protozoa, Ciliophora, Urostylida), with reconsideration of three closely related species at inter- and intra-specific levels inferred from the small subunit ribosomal RNA gene and the ITS1-5.8S-ITS2 region sequences. <i>Journal of Zoology</i> , 2008 , 275, 268-275	2	27
25	A molecular phylogenetic investigation of <i>Pseudoamphisiella</i> and <i>Parabirojimia</i> (Protozoa, Ciliophora, Spirotrichea), two genera with ambiguous systematic positions. <i>European Journal of Protistology</i> , 2008 , 44, 45-53	3.6	44
24	Phylogeny of some systematically uncertain urostylids-- <i>Apokeronopsis</i> , <i>Metaurostylopsis</i> , <i>Thigmokeronopsis</i> (Ciliophora, Stichotrichia) estimated with small subunit rRNA gene sequence information: discrepancies and agreements with morphological data. <i>European Journal of Protistology</i> , 2008 , 44, 254-62	3.6	40
23	HPV16 transmission between a couple with HPV-related head and neck cancer. <i>Oral Oncology</i> , 2008 , 44, 812-5	4.4	29
22	Phylogenetic position of three <i>Condylostoma</i> species (Protozoa, Ciliophora, Heterotrichea) inferred from the small subunit rRNA gene sequence. <i>Progress in Natural Science: Materials International</i> , 2008 , 18, 1089-1093	3.6	5
21	Analysis of the internal transcribed spacer 2 (ITS2) region of scuticociliates and related taxa (Ciliophora, Oligohymenophorea) to infer their evolution and phylogeny. <i>Protist</i> , 2008 , 159, 519-33	2.5	58
20	Reconsideration of the phylogenetic positions of five peritrich genera, <i>Vorticella</i> , <i>Pseudovorticella</i> , <i>Zoothamnopsis</i> , <i>Zoothamnium</i> , and <i>Epicarchesium</i> (Ciliophora, Peritrichia, Sessilida), based on small subunit rRNA gene sequences. <i>Journal of Eukaryotic Microbiology</i> , 2008 , 55, 448-56	3.6	36
19	Phylogeny of six genera of the subclass Haptoria (Ciliophora, Litostomatea) inferred from sequences of the gene coding for small subunit ribosomal RNA. <i>Journal of Eukaryotic Microbiology</i> , 2008 , 55, 562-6	3.6	28
18	Identification of a novel human papillomavirus (HPV97) related to HPV18 and HPV45. <i>International Journal of Cancer</i> , 2007 , 121, 193-8	7.5	14
17	A unique euplotid ciliate, <i>Gastrocirrhus</i> (Protozoa, Ciliophora): assessment of its phylogenetic position inferred from the small subunit rRNA gene sequence. <i>Journal of Eukaryotic Microbiology</i> , 2007 , 54, 371-8	3.6	17
16	Human papillomavirus (HPV) types 101 and 103 isolated from cervicovaginal cells lack an E6 open reading frame (ORF) and are related to gamma-papillomaviruses. <i>Virology</i> , 2007 , 360, 447-53	3.6	55
15	Characterization and experimental transmission of an oncogenic papillomavirus in female macaques. <i>Journal of Virology</i> , 2007 , 81, 6339-45	6.6	54

14	Identification and characterization of two novel human papillomaviruses (HPVs) by overlapping PCR: HPV102 and HPV106. <i>Journal of General Virology</i> , 2007 , 88, 2952-2955	4.9	20
13	A new investigation of the marine ciliate, <i>Trachelostyla pediculiformis</i> (Cohn, 1866) Borrer, 1972 (Ciliophora, Hypotrichida), with establishment of a new genus, <i>Spirotrachelostyla</i> nov. gen. <i>European Journal of Protistology</i> , 2006 , 42, 63-73	3.6	15
12	Phylogenetic position of the marine ciliate, <i>Cardiostomatella vermiforme</i> (Kahl, 1928) Corliss, 1960 inferred from the complete SSrRNA gene sequence, with establishment of a new order Loxocephalida n. ord. (Ciliophora, Oligohymenophorea). <i>European Journal of Protistology</i> , 2006 , 42, 107-14	3.6	22
11	Phylogenetic position of two marine ciliates, <i>Metanophrys similis</i> and <i>Pseudocohnilembus hargisi</i> (Protozoa, Ciliophora Scuticociliatia), inferred from complete small subunit rRNA gene sequence *. <i>Progress in Natural Science: Materials International</i> , 2006 , 16, 373-378	3.6	9
10	The carcinogenicity of human papillomavirus types reflects viral evolution. <i>Virology</i> , 2005 , 337, 76-84	3.6	421
9	Phylogenetic incongruence among oncogenic genital alpha human papillomaviruses. <i>Journal of Virology</i> , 2005 , 79, 15503-10	6.6	86
8	Diversifying selection in human papillomavirus type 16 lineages based on complete genome analyses. <i>Journal of Virology</i> , 2005 , 79, 7014-23	6.6	132
7	Variants of human papillomaviruses 16 and 18 and their natural history in human immunodeficiency virus-positive women. <i>Journal of General Virology</i> , 2005 , 86, 2709-2720	4.9	44
6	Lack of the canonical pRB-binding domain in the E7 ORF of artiodactyl papillomaviruses is associated with the development of fibropapillomas. <i>Journal of General Virology</i> , 2004 , 85, 1243-1250	4.9	51
5	Comparison of some closely-related <i>Metanophrys</i> -taxa with description of a new species <i>Metanophrys similis</i> nov. spec. (Ciliophora, Scuticociliatida). <i>European Journal of Protistology</i> , 2002 , 38, 45-53	3.6	9
4	Characterization and identification of the <i>Diophrys</i> species (Protozoa, Ciliophora, Hypotrichida) based on RAPD fingerprinting and ARDRA riboprinting. <i>European Journal of Protistology</i> , 2002 , 38, 383-391	3.6	14
3	Species separation among seven <i>Euplotes</i> spp. (Protozoa: Ciliophora: Hypotrichida) using PCR/RFLP analysis of nuclear ribosomal DNA. <i>Journal of Zoology</i> , 2002 , 258, 375-379	2	5
2	Phylogenetic positions of <i>Uronychia transfuga</i> and <i>Diophrys appendiculata</i> (Euplotida, Hypotrichia, Ciliophora) within hypotrichous ciliates inferred from the small subunit ribosomal RNA gene sequences. <i>European Journal of Protistology</i> , 2001 , 37, 291-301	3.6	19
1	Genetic mismatch explains sizable variation of COVID-19 vaccine efficacy in clinical trials		1