

# Xiu-Feng Wan

## List of Publications by Year in descending order

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129  
papers

3,811  
citations

159585

30  
h-index

161849

54  
g-index

139  
all docs

139  
docs citations

139  
times ranked

4714  
citing authors

#	ARTICLE	IF	CITATIONS
1	Defining biological and biophysical properties of SARS-CoV-2 genetic material in wastewater. <i>Science of the Total Environment</i> , 2022, 807, 150786.	8.0	36
2	Time-Dependent Proinflammatory Responses Shape Virus Interference during Coinfections of Influenza A Virus and Influenza D Virus. <i>Viruses</i> , 2022, 14, 224.	3.3	4
3	Intrauterine Fetal Demise in the Third Trimester of Pregnancy Associated With Mild Infection With the SARS-CoV-2 Delta Variant Without Protection From Vaccination. <i>Journal of Infectious Diseases</i> , 2022, 225, 748-753.	4.0	18
4	Highly pathogenic avian influenza is an emerging disease threat to wild birds in North America. <i>Journal of Wildlife Management</i> , 2022, 86, .	1.8	43
5	Antigenic characterization of influenza and SARS-CoV-2 viruses. <i>Analytical and Bioanalytical Chemistry</i> , 2022, 414, 2841-2881.	3.7	11
6	Systematic synthesis of bisected <i>N</i> -glycans and unique recognitions by glycan-binding proteins. <i>Chemical Science</i> , 2022, 13, 7644-7656.	7.4	7
7	Influenza Virus Infections in Polarized Cells. <i>Viruses</i> , 2022, 14, 1307.	3.3	0
8	Exposure of white-tailed deer in North America to influenza D virus. <i>Virology</i> , 2022, 573, 111-117.	2.4	6
9	Placental SARS-CoV-2 in a pregnant woman with mild COVID-19 disease. <i>Journal of Medical Virology</i> , 2021, 93, 1038-1044.	5.0	76
10	Reduced Influenza B-Specific Postvaccination Antibody Cross-reactivity in the B/Victoria Lineage-Predominant 2019/20 Season. <i>Clinical Infectious Diseases</i> , 2021, 72, e776-e783.	5.8	4
11	A review on medical management of inflammatory bowel disease during the coronavirus disease 2019 pandemic. <i>Journal of Gastroenterology and Hepatology (Australia)</i> , 2021, 36, 918-926.	2.8	6
12	Terminal Epitope-Dependent Branch Preference of Siglecs Toward N-Glycans. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 645999.	3.5	8
13	SARS-CoV-2 show no infectivity at later stages in a prolonged COVID-19 patient despite positivity in RNA testing. <i>Journal of Medical Virology</i> , 2021, 93, 4570-4575.	5.0	7
14	Rapid High-Throughput Whole-Genome Sequencing of SARS-CoV-2 by Using One-Step Reverse Transcription-PCR Amplification with an Integrated Microfluidic System and Next-Generation Sequencing. <i>Journal of Clinical Microbiology</i> , 2021, 59, .	3.9	15
15	Site-Specific N- and O-Glycosylation Analysis of Human Plasma Fibronectin. <i>Frontiers in Chemistry</i> , 2021, 9, 691217.	3.6	8
16	Reinfection with two genetically distinct SARS-CoV-2 viruses within 19 days. <i>Journal of Medical Virology</i> , 2021, 93, 5700-5703.	5.0	12
17	Variations outside the conserved motifs of PB1 catalytic active site may affect replication efficiency of the RNP complex of influenza A virus. <i>Virology</i> , 2021, 559, 145-155.	2.4	4
18	Characterization of Subtype H6 Avian Influenza A Viruses Isolated From Wild Birds in Poyang Lake, China. <i>Frontiers in Veterinary Science</i> , 2021, 8, 685399.	2.2	6

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19	Cell-Adapted Mutations and Antigenic Diversity of Influenza B Viruses in Missouri, 2019â€“2020 Season. <i>Viruses</i> , 2021, 13, 1896.	3.3	3
20	Triple reassortment increases compatibility among viral ribonucleoprotein genes of contemporary avian and human influenza A viruses. <i>PLoS Pathogens</i> , 2021, 17, e1009962.	4.7	3
21	Inferring seasonal infection risk at population and regional scales from serology samples. <i>Ecology</i> , 2020, 101, e02882.	3.2	6
22	Cross-Protection by Inactivated H5 Prepandemic Vaccine Seed Strains against Diverse Goose/Guangdong Lineage H5N1 Highly Pathogenic Avian Influenza Viruses. <i>Journal of Virology</i> , 2020, 94, .	3.4	11
23	Antibody Responses to SARS-CoV-2 Antigens in Humans and Animals. <i>Vaccines</i> , 2020, 8, 684.	4.4	11
24	Tissue Tropisms of Avian Influenza A Viruses Affect Their Spillovers from Wild Birds to Pigs. <i>Journal of Virology</i> , 2020, 94, .	3.4	7
25	Transport and fate of human expiratory dropletsâ€”A modeling approach. <i>Physics of Fluids</i> , 2020, 32, 083307.	4.0	101
26	Multi-task learning sparse group lasso: a method for quantifying antigenicity of influenza A(H1N1) virus using mutations and variations in glycosylation of Hemagglutinin. <i>BMC Bioinformatics</i> , 2020, 21, 182.	2.6	10
27	Are pangolins the intermediate host of the 2019 novel coronavirus (SARS-CoV-2)?. <i>PLoS Pathogens</i> , 2020, 16, e1008421.	4.7	318
28	Measuring Site-specific Glycosylation Similarity between Influenza A Virus Variants with Statistical Certainty. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1533-1545.	3.8	16
29	Limited Cross-Protection Provided by Prior Infection Contributes to High Prevalence of Influenza D Viruses in Cattle. <i>Journal of Virology</i> , 2020, 94, .	3.4	8
30	Comprehensive Nâ€• and Oâ€• Glycosylation mapping of human coagulation factor V. <i>Journal of Thrombosis and Haemostasis</i> , 2020, 18, 1884-1892.	3.8	9
31	HA stabilization promotes replication and transmission of swine H1N1 gamma influenza viruses in ferrets. <i>ELife</i> , 2020, 9, .	6.0	19
32	H7N1 Low Pathogenicity Avian Influenza Viruses in Poultry in the United States During 2018. <i>Avian Diseases</i> , 2020, 65, 59-62.	1.0	1
33	Graph-guided multi-task sparse learning model: a method for identifying antigenic variants of influenza A(H3N2) virus. <i>Bioinformatics</i> , 2019, 35, 77-87.	4.1	14
34	The neuraminidase of A(H3N2) influenza viruses circulating since 2016 is antigenically distinct from the A/Hong Kong/4801/2014 vaccine strain. <i>Nature Microbiology</i> , 2019, 4, 2216-2225.	13.3	59
35	Individual-Level Antibody Dynamics Reveal Potential Drivers of Influenza A Seasonality in Wild Pig Populations. <i>Integrative and Comparative Biology</i> , 2019, 59, 1231-1242.	2.0	8
36	Pathogenesis of co-infections of influenza D virus and <i>Mannheimia haemolytica</i> in cattle. <i>Veterinary Microbiology</i> , 2019, 231, 246-253.	1.9	24

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37	Aerosol Transmission of Gull-Origin Iceland Subtype H10N7 Influenza A Virus in Ferrets. <i>Journal of Virology</i> , 2019, 93, .	3.4	17
38	Influenza Neuraminidase: Underrated Role in Receptor Binding. <i>Trends in Microbiology</i> , 2019, 27, 477-479.	7.7	33
39	Prediction of DNA-binding proteins by interaction fusion feature representation and selective ensemble. <i>Knowledge-Based Systems</i> , 2019, 163, 598-610.	7.1	10
40	SURVEY OF ARCTIC ALASKAN WILDLIFE FOR INFLUENZA A ANTIBODIES: LIMITED EVIDENCE FOR EXPOSURE OF MAMMALS. <i>Journal of Wildlife Diseases</i> , 2019, 55, 387.	0.8	28
41	Serologic Evidence for Influenza a Virus Exposure in Three Loon Species Breeding in Alaska, USA. <i>Journal of Wildlife Diseases</i> , 2019, 55, 862.	0.8	2
42	Serologic Evidence for Influenza A Virus Exposure in Three Loon Species Breeding in Alaska, USA. <i>Journal of Wildlife Diseases</i> , 2019, 55, 862-867.	0.8	0
43	Imprinting of Repeated Influenza A/H3 Exposures on Antibody Quantity and Antibody Quality: Implications for Seasonal Vaccine Strain Selection and Vaccine Performance. <i>Clinical Infectious Diseases</i> , 2018, 67, 1523-1532.	5.8	49
44	A Y161F Hemagglutinin Substitution Increases Thermostability and Improves Yields of 2009 H1N1 Influenza A Virus in Cells. <i>Journal of Virology</i> , 2018, 92, .	3.4	21
45	Tissue tropisms opt for transmissible reassortants during avian and swine influenza A virus co-infection in swine. <i>PLoS Pathogens</i> , 2018, 14, e1007417.	4.7	21
46	Evolutionary pathway for the 2017 emergence of a novel highly pathogenic avian influenza A(H7N9) virus among domestic poultry in Tennessee, United States. <i>Virology</i> , 2018, 525, 32-39.	2.4	6
47	Genetic Evidence Supports Sporadic and Independent Introductions of Subtype H5 Low-Pathogenic Avian Influenza A Viruses from Wild Birds to Domestic Poultry in North America. <i>Journal of Virology</i> , 2018, 92, .	3.4	23
48	Mutation W222L at the Receptor Binding Site of Hemagglutinin Could Facilitate Viral Adaption from Equine Influenza A(H3N8) Virus to Dogs. <i>Journal of Virology</i> , 2018, 92, .	3.4	27
49	Influenza D Virus Infection in Feral Swine Populations, United States. <i>Emerging Infectious Diseases</i> , 2018, 24, 1020-1028.	4.3	48
50	Detection of Antigenic Variants of Subtype H3 Swine Influenza A Viruses from Clinical Samples. <i>Journal of Clinical Microbiology</i> , 2017, 55, 1037-1045.	3.9	3
51	Low-Pathogenic Influenza A Viruses in North American Diving Ducks Contribute to the Emergence of a Novel Highly Pathogenic Influenza A(H7N8) Virus. <i>Journal of Virology</i> , 2017, 91, .	3.4	27
52	Pathogenicity and transmission of a swine influenza A(H6N6) virus. <i>Emerging Microbes and Infections</i> , 2017, 6, 1-13.	6.5	19
53	Differential Effects of Prior Influenza Exposures on H3N2 Cross-reactivity of Human Postvaccination Sera. <i>Clinical Infectious Diseases</i> , 2017, 65, 259-267.	5.8	22
54	Feral Swine in the United States Have Been Exposed to both Avian and Swine Influenza A Viruses. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	22

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55	Zoonotic Risk, Pathogenesis, and Transmission of Avian-Origin H3N2 Canine Influenza Virus. <i>Journal of Virology</i> , 2017, 91, .	3.4	15
56	Serological evidence for high prevalence of Influenza D Viruses in Cattle, Nebraska, United States, 2003â€“2004. <i>Virology</i> , 2017, 501, 88-91.	2.4	52
57	HA Triggers the Switch from MEK1 SUMOylation to Phosphorylation of the ERK Pathway in Influenza A Virus-Infected Cells and Facilitates Its Infection. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 27.	3.9	12
58	Generalized Hierarchical Sparse Model for Arbitrary-Order Interactive Antigenic Sites Identification in Flu Virus Data. , 2016, 2016, 865-874.		6
59	Pathogenesis of Influenza D Virus in Cattle. <i>Journal of Virology</i> , 2016, 90, 5636-5642.	3.4	125
60	A quantitative RT-PCR assay for rapid detection of Eurasian-lineage H10 subtype influenza A virus. <i>Virologica Sinica</i> , 2016, 31, 444-447.	3.0	3
61	Limited Antigenic Diversity in Contemporary H7 Avian-Origin Influenza A Viruses from North America. <i>Scientific Reports</i> , 2016, 6, 20688.	3.3	22
62	Antigenic Characterization of H3 Subtypes of Avian Influenza A Viruses from North America. <i>Avian Diseases</i> , 2016, 60, 346.	1.0	11
63	Association analyses of large-scale glycan microarray data reveal novel host-specific substructures in influenza A virus binding glycans. <i>Scientific Reports</i> , 2015, 5, 15778.	3.3	18
64	Detection of Avian H7N9 Influenza A Viruses in the Yangtze Delta Region of China During Early H7N9 Outbreaks. <i>Avian Diseases</i> , 2015, 60, 118.	1.0	4
65	H3N2 Mismatch of 2014â€“15 Northern Hemisphere Influenza Vaccines and Head-to-head Comparison between Human and Ferret Antisera derived Antigenic Maps. <i>Scientific Reports</i> , 2015, 5, 15279.	3.3	118
66	Identification of the source of A (H10N8) virus causing human infection. <i>Infection, Genetics and Evolution</i> , 2015, 30, 159-163.	2.3	18
67	Detection of influenza antigenic variants directly from clinical samples using polyclonal antibody based proximity ligation assays. <i>Virology</i> , 2015, 476, 151-158.	2.4	5
68	Error-prone pcr-based mutagenesis strategy for rapidly generating high-yield influenza vaccine candidates. <i>Virology</i> , 2015, 482, 234-243.	2.4	17
69	Testing the Effect of Internal Genes Derived from a Wild-Bird-Origin H9N2 Influenza A Virus on the Pathogenicity of an A/H7N9 Virus. <i>Cell Reports</i> , 2015, 12, 1831-1841.	6.4	13
70	Influenza D virus infection in Mississippi beef cattle. <i>Virology</i> , 2015, 486, 28-34.	2.4	115
71	Dynamics of virus shedding and antibody responses in influenza A virus-infected feral swine. <i>Journal of General Virology</i> , 2015, 96, 2569-2578.	2.9	14
72	Sequence-Based Antigenic Change Prediction by a Sparse Learning Method Incorporating Co-Evolutionary Information. <i>PLoS ONE</i> , 2014, 9, e106660.	2.5	21

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73	Influenza A Subtype H3 Viruses in Feral Swine, United States, 2011â€“2012. <i>Emerging Infectious Diseases</i> , 2014, 20, 839-842.	4.3	25
74	Potency, Efficacy, and Antigenic Mapping of H7 Avian Influenza Virus Vaccines Against the 2012 H7N3 Highly Pathogenic Avian Influenza Virus from Mexico. <i>Avian Diseases</i> , 2014, 58, 359-366.	1.0	10
75	Variation in protection of four divergent avian influenza virus vaccine seed strains against eight clade 2.2.1 and 2.2.1.1. Egyptian H5N1 high pathogenicity variants in poultry. <i>Influenza and Other Respiratory Viruses</i> , 2014, 8, 654-662.	3.4	16
76	Use of serological and mucosal immune responses to <i>Mycoplasma hyopneumoniae</i> antigens P97R1, P46 and P36 in the diagnosis of infection. <i>Veterinary Journal</i> , 2014, 202, 128-133.	1.7	14
77	Antigenic and Genetic Evolution of Low-Pathogenicity Avian Influenza Viruses of Subtype H7N3 following Heterologous Vaccination. <i>Vaccine Journal</i> , 2014, 21, 603-612.	3.1	21
78	Quartet-based methods to reconstruct phylogenetic networks. <i>BMC Systems Biology</i> , 2014, 8, 21.	3.0	17
79	Detection of African swine fever virus-like sequences in ponds in the Mississippi Delta through metagenomic sequencing. <i>Virus Genes</i> , 2013, 46, 441-446.	1.6	21
80	Mutation tryptophan to leucine at position 222 of haemagglutinin could facilitate H3N2 influenza A virus infection in dogs. <i>Journal of General Virology</i> , 2013, 94, 2599-2608.	2.9	38
81	Antigenic characterization of recent H5N1 highly pathogenic avian influenza viruses circulating in Egyptian poultry. <i>Virology</i> , 2013, 435, 350-356.	2.4	21
82	Mutation from arginine to lysine at the position 189 of hemagglutinin contributes to the antigenic drift in H3N2 swine influenza viruses. <i>Virology</i> , 2013, 446, 225-229.	2.4	15
83	Perspective on emergence and re-emergence of amantadine resistant influenza A viruses in domestic animals in China. <i>Infection, Genetics and Evolution</i> , 2013, 20, 298-303.	2.3	16
84	Using Sequence Data To Infer the Antigenicity of Influenza Virus. <i>MBio</i> , 2013, 4, .	4.1	85
85	Molecular Basis for Broad Neuraminidase Immunity: Conserved Epitopes in Seasonal and Pandemic H1N1 as Well as H5N1 Influenza Viruses. <i>Journal of Virology</i> , 2013, 87, 9290-9300.	3.4	141
86	Antigenic Characterization of H3N2 Influenza A Viruses from Ohio Agricultural Fairs. <i>Journal of Virology</i> , 2013, 87, 7655-7667.	3.4	33
87	Quartet-Net: A Quartet-Based Method to Reconstruct Phylogenetic Networks. <i>Molecular Biology and Evolution</i> , 2013, 30, 1206-1217.	8.9	24
88	A Perspective on Multiple Waves of Influenza Pandemics. <i>PLoS ONE</i> , 2013, 8, e60343.	2.5	42
89	A Joint Matrix Completion and Filtering Model for Influenza Serological Data Integration. <i>PLoS ONE</i> , 2013, 8, e69842.	2.5	3
90	A quantitative structureâ€“activity relationship (QSAR) study on glycan array data to determine the specificities of glycan-binding proteins. <i>Glycobiology</i> , 2012, 22, 552-560.	2.5	22

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91	A Triclude DNA Vaccine Designed on the Basis of a Comprehensive Serologic Study Elicits Neutralizing Antibody Responses against All Clades and Subclades of Highly Pathogenic Avian Influenza H5N1 Viruses. <i>Journal of Virology</i> , 2012, 86, 6970-6978.	3.4	45
92	Antigenic distance measurements for seasonal influenza vaccine selection. <i>Vaccine</i> , 2012, 30, 448-453.	3.8	28
93	Identifying Antigenicity-Associated Sites in Highly Pathogenic H5N1 Influenza Virus Hemagglutinin by Using Sparse Learning. <i>Journal of Molecular Biology</i> , 2012, 422, 145-155.	4.2	43
94	Population-environment drivers of H5N1 avian influenza molecular change in Vietnam. <i>Health and Place</i> , 2012, 18, 1122-1131.	3.3	10
95	AntigenMap 3D: an online antigenic cartography resource. <i>Bioinformatics</i> , 2012, 28, 1292-1293.	4.1	44
96	Highly Pathogenic H5N1 Avian Influenza Viruses Exhibit Few Barriers to Gene Flow in Vietnam. <i>EcoHealth</i> , 2012, 9, 60-69.	2.0	5
97	SO2426 is a positive regulator of siderophore expression in <i>Shewanella oneidensis</i> MR-1. <i>BMC Microbiology</i> , 2011, 11, 125.	3.3	0
98	Identification of an H6N6 swine influenza virus in southern China. <i>Infection, Genetics and Evolution</i> , 2011, 11, 1174-1177.	2.3	71
99	Extent of Antigenic Cross-Reactivity among Highly Pathogenic H5N1 Influenza Viruses. <i>Journal of Clinical Microbiology</i> , 2011, 49, 3531-3536.	3.9	28
100	Genetic Variation of Highly Pathogenic H5N1 Avian Influenza Viruses in Vietnam Shows Both Species-Specific and Spatiotemporal Associations. <i>Avian Diseases</i> , 2011, 55, 659-666.	1.0	8
101	Indications that Live Poultry Markets Are a Major Source of Human H5N1 Influenza Virus Infection in China. <i>Journal of Virology</i> , 2011, 85, 13432-13438.	3.4	128
102	IPMiner: a progenitor gene identifier for influenza A virus. <i>Influenza and Other Respiratory Viruses</i> , 2011, 5, 413-5.	3.4	1
103	Concepts and applications for influenza antigenic cartography. <i>Influenza and Other Respiratory Viruses</i> , 2011, 5, 204-7.	3.4	21
104	Mixture model analysis reflecting dynamics of the population diversity of 2009 pandemic H1N1 influenza virus. <i>In Silico Biology</i> , 2011, 11, 225-36.	0.9	1
105	Proteomics inference of genes involved in host adaptation of <i>Mycoplasma gallinarum</i> . <i>Veterinary Microbiology</i> , 2010, 145, 177-184.	1.9	3
106	Avian-origin H3N2 canine influenza A viruses in Southern China. <i>Infection, Genetics and Evolution</i> , 2010, 10, 1286-1288.	2.3	150
107	A Computational Framework for Influenza Antigenic Cartography. <i>PLoS Computational Biology</i> , 2010, 6, e1000949.	3.2	119
108	Spatiotemporal Structure of Molecular Evolution of H5N1 Highly Pathogenic Avian Influenza Viruses in Vietnam. <i>PLoS ONE</i> , 2010, 5, e8631.	2.5	22

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109	Characterization of a highly pathogenic avian influenza H5N1 virus sublineage in poultry seized at ports of entry into Vietnam. <i>Virology</i> , 2009, 387, 250-256.	2.4	42
110	Identifying a few foot-and-mouth disease virus signature nucleotide strings for computational genotyping. <i>BMC Bioinformatics</i> , 2008, 9, 279.	2.6	8
111	Transcriptome analysis reveals response regulator SO2426-mediated gene expression in <i>Shewanella oneidensis</i> MR-1 under chromate challenge. <i>BMC Genomics</i> , 2008, 9, 395.	2.8	24
112	UBIQUITOUS REASSORTMENTS IN INFLUENZA A VIRUSES. <i>Journal of Bioinformatics and Computational Biology</i> , 2008, 06, 981-999.	0.8	9
113	Genotypic diversity of H5N1 highly pathogenic avian influenza viruses. <i>Journal of General Virology</i> , 2008, 89, 2182-2193.	2.9	37
114	Exploring Core/Periphery Structures in Protein Interaction Networks Provides Structure-Property Relation Insights. , 2008, , .		0
115	Evolution of Highly Pathogenic H5N1 Avian Influenza Viruses in Vietnam between 2001 and 2007. <i>PLoS ONE</i> , 2008, 3, e3462.	2.5	112
116	Nucleotide composition string selection in HIV-1 subtyping using whole genomes. <i>Bioinformatics</i> , 2007, 23, 1744-1752.	4.1	47
117	A quantitative genotype algorithm reflecting H5N1 Avian influenza niches. <i>Bioinformatics</i> , 2007, 23, 2368-2375.	4.1	23
118	Computational Identification of Reassortments in Avian Influenza Viruses. <i>Avian Diseases</i> , 2007, 51, 434-439.	1.0	19
119	Ascovirus and its evolution. <i>Virologica Sinica</i> , 2007, 22, 137-147.	3.0	7
120	Phylogenetic analysis using complete signature information of whole genomes and clustered Neighbour-Joining method. <i>International Journal of Bioinformatics Research and Applications</i> , 2006, 2, 219.	0.2	45
121	WHOLE GENOME COMPOSITION DISTANCE FOR HIV-1 GENOTYPING. , 2006, , .		1
122	Transcriptome Profiling of <i>Shewanella oneidensis</i> Gene Expression following Exposure to Acidic and Alkaline pH. <i>Journal of Bacteriology</i> , 2006, 188, 1633-1642.	2.2	62
123	The Ribosomal Shunt Translation Strategy of Cauliflower Mosaic Virus Has Evolved from Ancient Long Terminal Repeats. <i>Journal of Virology</i> , 2006, 80, 3811-3822.	3.4	8
124	RNALL: AN EFFICIENT ALGORITHM FOR PREDICTING RNA LOCAL SECONDARY STRUCTURAL LANDSCAPE IN GENOMES. <i>Journal of Bioinformatics and Computational Biology</i> , 2006, 04, 1015-1031.	0.8	12
125	Intrinsic Terminator Prediction and Its Application in <i>Synechococcus</i> sp. WH8102. <i>Journal of Computer Science and Technology</i> , 2005, 20, 465-482.	1.5	11
126	Computational Methods for Remote Homolog Identification. <i>Current Protein and Peptide Science</i> , 2005, 6, 527-546.	1.4	24



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127	Transcriptomic and Proteomic Characterization of the Fur Modulon in the Metal-Reducing Bacterium <i>Shewanella oneidensis</i> . <i>Journal of Bacteriology</i> , 2004, 186, 8385-8400.	2.2	134
128	Revealing gene transcription and translation initiation patterns in archaea, using an interactive clustering model. <i>Extremophiles</i> , 2004, 8, 291-299.	2.3	13
129	Identification and Initial Characterization of a Putative <i>Mycoplasma gallinarum</i> Leucine Aminopeptidase Gene. <i>Current Microbiology</i> , 2004, 48, 32-38.	2.2	4