

# Yongqun He

## List of Publications by Year in descending order

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173  
papers

7,001  
citations

57719

44  
h-index

76872

74  
g-index

184  
all docs

184  
docs citations

184  
times ranked

9145  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Human Phenotype Ontology in 2021. <i>Nucleic Acids Research</i> , 2021, 49, D1207-D1217.	6.5	652
2	Endoplasmic Reticulum Stress Activates the Inflammasome via NLRP3- and Caspase-2-Driven Mitochondrial Damage. <i>Immunity</i> , 2015, 43, 451-462.	6.6	328
3	COVID-19 Coronavirus Vaccine Design Using Reverse Vaccinology and Machine Learning. <i>Frontiers in Immunology</i> , 2020, 11, 1581.	2.2	301
4	Vaxign: The First Web-Based Vaccine Design Program for Reverse Vaccinology and Applications for Vaccine Development. <i>Journal of Biomedicine and Biotechnology</i> , 2010, 2010, 1-15.	3.0	260
5	The Ontology for Biomedical Investigations. <i>PLoS ONE</i> , 2016, 11, e0154556.	1.1	217
6	Modeling biomedical experimental processes with OBI. <i>Journal of Biomedical Semantics</i> , 2010, 1, S7.	0.9	207
7	The Cell Ontology 2016: enhanced content, modularization, and ontology interoperability. <i>Journal of Biomedical Semantics</i> , 2016, 7, 44.	0.9	201
8	Finding Our Way through Phenotypes. <i>PLoS Biology</i> , 2015, 13, e1002033.	2.6	178
9	OntoFox: web-based support for ontology reuse. <i>BMC Research Notes</i> , 2010, 3, 175.	0.6	145
10	Victors: a web-based knowledge base of virulence factors in human and animal pathogens. <i>Nucleic Acids Research</i> , 2019, 47, D693-D700.	6.5	120
11	Emerging Vaccine Informatics. <i>Journal of Biomedicine and Biotechnology</i> , 2010, 2010, 1-26.	3.0	114
12	Ontobee: A linked ontology data server to support ontology term dereferencing, linkage, query and integration. <i>Nucleic Acids Research</i> , 2017, 45, D347-D352.	6.5	110
13	VRprofile: gene-cluster-detection-based profiling of virulence and antibiotic resistance traits encoded within genome sequences of pathogenic bacteria. <i>Briefings in Bioinformatics</i> , 2018, 19, bbw141.	3.2	100
14	OAE: The Ontology of Adverse Events. <i>Journal of Biomedical Semantics</i> , 2014, 5, 29.	0.9	94
15	Rationale and design of the Kidney Precision Medicine Project. <i>Kidney International</i> , 2021, 99, 498-510.	2.6	94
16	Analyses of Brucella Pathogenesis, Host Immunity, and Vaccine Targets using Systems Biology and Bioinformatics. <i>Frontiers in Cellular and Infection Microbiology</i> , 2012, 2, 2.	1.8	92
17	CLO: The cell line ontology. <i>Journal of Biomedical Semantics</i> , 2014, 5, 37.	0.9	89
18	PIML: the Pathogen Information Markup Language. <i>Bioinformatics</i> , 2005, 21, 116-121.	1.8	88

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19	Brucella melitensis Triggers Time-Dependent Modulation of Apoptosis and Down-Regulation of Mitochondrion-Associated Gene Expression in Mouse Macrophages. <i>Infection and Immunity</i> , 2006, 74, 5035-5046.	1.0	85
20	Environmental Temperature Differentially Modulates C.Âelegans Longevity through a Thermosensitive TRP Channel. <i>Cell Reports</i> , 2015, 11, 1414-1424.	2.9	81
21	Vaxign-ML: supervised machine learning reverse vaccinology model for improved prediction of bacterial protective antigens. <i>Bioinformatics</i> , 2020, 36, 3185-3191.	1.8	77
22	Complementation of Brucella abortus RB51 with a Functional wboA Gene Results in O-Antigen Synthesis and Enhanced Vaccine Efficacy but No Change in Rough Phenotype and Attenuation. <i>Infection and Immunity</i> , 2000, 68, 3927-3932.	1.0	76
23	Overexpression of Protective Antigen as a Novel Approach To Enhance Vaccine Efficacy of Brucella abortus Strain RB51. <i>Infection and Immunity</i> , 2000, 68, 3286-3289.	1.0	75
24	Strong antibody responses induced by protein antigens conjugated onto the surface of lecithin-based nanoparticles. <i>Journal of Controlled Release</i> , 2010, 141, 93-100.	4.8	72
25	CIDO, a community-based ontology for coronavirus disease knowledge and data integration, sharing, and analysis. <i>Scientific Data</i> , 2020, 7, 181.	2.4	70
26	Induction of Specific Cytotoxic Lymphocytes in Mice Vaccinated with Brucella abortus RB51. <i>Infection and Immunity</i> , 2001, 69, 5502-5508.	1.0	69
27	Protegen: a web-based protective antigen database and analysis system. <i>Nucleic Acids Research</i> , 2011, 39, D1073-D1078.	6.5	69
28	Anatomical structures, cell types and biomarkers of the Human Reference Atlas. <i>Nature Cell Biology</i> , 2021, 23, 1117-1128.	4.6	68
29	A reference tissue atlas for the human kidney. <i>Science Advances</i> , 2022, 8, .	4.7	67
30	Updates on the web-based VIOLIN vaccine database and analysis system. <i>Nucleic Acids Research</i> , 2014, 42, D1124-D1132.	6.5	66
31	VIOLIN: vaccine investigation and online information network. <i>Nucleic Acids Research</i> , 2007, 36, D923-D928.	6.5	65
32	Brucella abortus Strain RB51 as a Vector for Heterologous Protein Expression and Induction of Specific Th1 Type Immune Responses. <i>Infection and Immunity</i> , 2000, 68, 3290-3296.	1.0	64
33	Safety and immunogenicity of mammalian cell derived and Modified Vaccinia Ankara vectored African swine fever subunit antigens in swine. <i>Veterinary Immunology and Immunopathology</i> , 2017, 185, 20-33.	0.5	64
34	Antibiotic Resistance Determinant-Focused Acinetobacter baumannii Vaccine Designed Using Reverse Vaccinology. <i>International Journal of Molecular Sciences</i> , 2017, 18, 458.	1.8	64
35	PHIDIAS: a pathogen-host interaction data integration and analysis system. <i>Genome Biology</i> , 2007, 8, R150.	13.9	63
36	Caspase-2 Mediated Apoptotic and Necrotic Murine Macrophage Cell Death Induced by Rough Brucella abortus. <i>PLoS ONE</i> , 2009, 4, e6830.	1.1	60

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37	A multimodal and integrated approach to interrogate human kidney biopsies with rigor and reproducibility: guidelines from the Kidney Precision Medicine Project. <i>Physiological Genomics</i> , 2021, 53, 1-11.	1.0	59
38	Genome-wide prediction of vaccine targets for human herpes simplex viruses using Vaxign reverse vaccinology. <i>BMC Bioinformatics</i> , 2013, 14, S2.	1.2	58
39	The eXtensible ontology development (XOD) principles and tool implementation to support ontology interoperability. <i>Journal of Biomedical Semantics</i> , 2018, 9, 3.	0.9	57
40	Vaxign: a web-based vaccine target design program for reverse vaccinology. <i>Procedia in Vaccinology</i> , 2009, 1, 23-29.	0.4	56
41	Mining of vaccine-associated IFN- $\gamma$ gene interaction networks using the Vaccine Ontology. <i>Journal of Biomedical Semantics</i> , 2011, 2, S8.	0.9	54
42	Presence of Putative Repeat-in-Toxin Gene <i>rtxA</i> in <i>Escherichia coli</i> Predicts Successful Colonization of the Urinary Tract. <i>MBio</i> , 2011, 2, e00066-11.	1.8	51
43	Ontology representation and analysis of vaccine formulation and administration and their effects on vaccine immune responses. <i>Journal of Biomedical Semantics</i> , 2012, 3, 17.	0.9	51
44	Ontology-Based Combinatorial Comparative Analysis of Adverse Events Associated with Killed and Live Influenza Vaccines. <i>PLoS ONE</i> , 2012, 7, e49941.	1.1	49
45	BBP: Brucella genome annotation with literature mining and curation. <i>BMC Bioinformatics</i> , 2006, 7, 347.	1.2	47
46	Bioinformatics analysis of Brucella vaccines and vaccine targets using VIOLIN. <i>Immunome Research</i> , 2010, 6, S5.	0.1	46
47	Proinflammatory Caspase-2-Mediated Macrophage Cell Death Induced by a Rough Attenuated <i>Brucella suis</i> Strain. <i>Infection and Immunity</i> , 2011, 79, 2460-2469.	1.0	46
48	Modelling kidney disease using ontology: insights from the Kidney Precision Medicine Project. <i>Nature Reviews Nephrology</i> , 2020, 16, 686-696.	4.1	45
49	Vaxjo: A Web-Based Vaccine Adjuvant Database and Its Application for Analysis of Vaccine Adjuvants and Their Uses in Vaccine Development. <i>Journal of Biomedicine and Biotechnology</i> , 2012, 2012, 1-13.	3.0	44
50	Vaxign2: the second generation of the first Web-based vaccine design program using reverse vaccinology and machine learning. <i>Nucleic Acids Research</i> , 2021, 49, W671-W678.	6.5	44
51	Molecular targets for rapid identification of <i>Brucella</i> spp. <i>BMC Microbiology</i> , 2006, 6, 13.	1.3	42
52	The Ontology of Vaccine Adverse Events (OVAE) and its usage in representing and analyzing adverse events associated with US-licensed human vaccines. <i>Journal of Biomedical Semantics</i> , 2013, 4, 40.	0.9	39
53	Ontorat: automatic generation of new ontology terms, annotations, and axioms based on ontology design patterns. <i>Journal of Biomedical Semantics</i> , 2015, 6, 4.	0.9	39
54	Literature-Based Discovery of IFN- $\gamma$ and Vaccine-Mediated Gene Interaction Networks. <i>Journal of Biomedicine and Biotechnology</i> , 2010, 2010, 1-13.	3.0	34

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55	Ontology-based Brucella vaccine literature indexing and systematic analysis of gene-vaccine association network. <i>BMC Immunology</i> , 2011, 12, 49.	0.9	34
56	Cwp22, a novel peptidoglycan cross-linking enzyme, plays pleiotropic roles in <i>Clostridioides difficile</i> . <i>Environmental Microbiology</i> , 2019, 21, 3076-3090.	1.8	34
57	Recombinant <i>Ochrobactrum anthropi</i> Expressing <i>Brucella abortus</i> Cu,Zn Superoxide Dismutase Protects Mice against <i>B. abortus</i> Infection Only after Switching of Immune Responses to Th1 Type. <i>Infection and Immunity</i> , 2002, 70, 2535-2543.	1.0	33
58	<i>Brucella abortus</i> RB51: enhancing vaccine efficacy and developing multivalent vaccines. <i>Veterinary Microbiology</i> , 2002, 90, 521-532.	0.8	32
59	A genome-wide MeSH-based literature mining system predicts implicit gene-to-gene relationships and networks. <i>BMC Systems Biology</i> , 2013, 7, S9.	3.0	32
60	Meta-analysis of variables affecting mouse protection efficacy of whole organism <i>Brucella</i> vaccines and vaccine candidates. <i>BMC Bioinformatics</i> , 2013, 14, S3.	1.2	30
61	Differential Adverse Event Profiles Associated with BCG as a Preventive Tuberculosis Vaccine or Therapeutic Bladder Cancer Vaccine Identified by Comparative Ontology-Based VAERS and Literature Meta-Analysis. <i>PLoS ONE</i> , 2016, 11, e0164792.	1.1	29
62	Systematic annotation and analysis of <i>Brucella abortus</i> virulence factors whose mutants can be used as live attenuated vaccines. <i>Vaccine</i> , 2013, 31, 797-805.	1.7	28
63	Statistical and Ontological Analysis of Adverse Events Associated with Monovalent and Combination Vaccines against Hepatitis A and B Diseases. <i>Scientific Reports</i> , 2016, 6, 34318.	1.6	28
64	Microbial modulation of host apoptosis and pyroptosis. <i>Frontiers in Cellular and Infection Microbiology</i> , 2014, 4, 83.	1.8	27
65	Linking MedDRA Coded Clinical Phenotypes to Biological Mechanisms by the Ontology of Adverse Events: A Pilot Study on Tyrosine Kinase Inhibitors. <i>Drug Safety</i> , 2016, 39, 697-707.	1.4	27
66	Using epitope predictions to evaluate efficacy and population coverage of the Mtb72f vaccine for tuberculosis. <i>BMC Immunology</i> , 2010, 11, 18.	0.9	26
67	Identification of fever and vaccine-associated gene interaction networks using ontology-based literature mining. <i>Journal of Biomedical Semantics</i> , 2012, 3, 18.	0.9	26
68	Identification of New Features from Known Bacterial Protective Vaccine Antigens Enhances Rational Vaccine Design. <i>Frontiers in Immunology</i> , 2017, 8, 1382.	2.2	25
69	Databases and In Silico Tools for Vaccine Design. <i>Methods in Molecular Biology</i> , 2013, 993, 115-127.	0.4	24
70	Caspase-2-Dependent Dendritic Cell Death, Maturation, and Priming of T Cells in Response to <i>Brucella abortus</i> Infection. <i>PLoS ONE</i> , 2012, 7, e43512.	1.1	24
71	Development and application of an interaction network ontology for literature mining of vaccine-associated gene-gene interactions. <i>Journal of Biomedical Semantics</i> , 2015, 6, 2.	0.9	23
72	Epitope promiscuity and population coverage of <i>Mycobacterium tuberculosis</i> protein antigens in current subunit vaccines under development. <i>Infection, Genetics and Evolution</i> , 2020, 80, 104186.	1.0	23

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73	Caspase-2 mediates a <i>Brucella abortus</i> RB51-induced hybrid cell death having features of apoptosis and pyroptosis. <i>Frontiers in Cellular and Infection Microbiology</i> , 2013, 3, 83.	1.8	23
74	Brucellosis Ontology (IDOBRLU) as an extension of the Infectious Disease Ontology. <i>Journal of Biomedical Semantics</i> , 2011, 2, 9.	0.9	22
75	Ontology-based collection, representation and analysis of drug-associated neuropathy adverse events. <i>Journal of Biomedical Semantics</i> , 2016, 7, 29.	0.9	22
76	Network-based analysis of vaccine-related associations reveals consistent knowledge with the vaccine ontology. <i>Journal of Biomedical Semantics</i> , 2013, 4, 33.	0.9	21
77	miniTUBA: medical inference by network integration of temporal data using Bayesian analysis. <i>Bioinformatics</i> , 2007, 23, 2423-2432.	1.8	20
78	Ontology-based time information representation of vaccine adverse events in VAERS for temporal analysis. <i>Journal of Biomedical Semantics</i> , 2012, 3, 13.	0.9	20
79	The ontology of genetic susceptibility factors (OGSF) and its application in modeling genetic susceptibility to vaccine adverse events. <i>Journal of Biomedical Semantics</i> , 2014, 5, 19.	0.9	20
80	Computational design of SARS-CoV-2 spike glycoproteins to increase immunogenicity by T cell epitope engineering. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 518-529.	1.9	19
81	Bayesian Network Expansion Identifies New ROS and Biofilm Regulators. <i>PLoS ONE</i> , 2010, 5, e9513.	1.1	19
82	RNA-seq reveals the critical role of OtpR in regulating <i>Brucella melitensis</i> metabolism and virulence under acidic stress. <i>Scientific Reports</i> , 2015, 5, 10864.	1.6	18
83	Ontology-Based Vaccine and Drug Adverse Event Representation and Theory-Guided Systematic Causal Network Analysis Toward Integrative Pharmacovigilance Research. <i>Current Pharmacology Reports</i> , 2016, 2, 113-128.	1.5	18
84	The Ontology of Biological and Clinical Statistics (OBCS) for standardized and reproducible statistical analysis. <i>Journal of Biomedical Semantics</i> , 2016, 7, 53.	0.9	18
85	DNAVaxDB: the first web-based DNA vaccine database and its data analysis. <i>BMC Bioinformatics</i> , 2014, 15, S2.	1.2	17
86	Novel Immunoprotective Proteins of <i>Streptococcus pneumoniae</i> Identified by Opsonophagocytosis Killing Screen. <i>Infection and Immunity</i> , 2018, 86, .	1.0	16
87	A statistical analysis of vaccine-adverse event data. <i>BMC Medical Informatics and Decision Making</i> , 2019, 19, 101.	1.5	16
88	Time event ontology (TEO): to support semantic representation and reasoning of complex temporal relations of clinical events. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2020, 27, 1046-1056.	2.2	16
89	COVID-19 induces lower levels of IL-8, IL-10, and MCP-1 than other acute CRS-inducing diseases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	16
90	Potential transmission chains of variant B.1.1.7 and co-mutations of SARS-CoV-2. <i>Cell Discovery</i> , 2021, 7, 44.	3.1	16

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91	Ontology-based systematical representation and drug class effect analysis of package insert-reported adverse events associated with cardiovascular drugs used in China. <i>Scientific Reports</i> , 2017, 7, 13819.	1.6	15
92	Bioinformatics analysis of bacterial protective antigens in manually curated Protegen database. <i>Procedia in Vaccinology</i> , 2012, 6, 3-9.	0.4	14
93	Architecture and usability of OntoKeeper, an ontology evaluation tool. <i>BMC Medical Informatics and Decision Making</i> , 2019, 19, 152.	1.5	14
94	Ontological modeling and analysis of experimentally or clinically verified drugs against coronavirus infection. <i>Scientific Data</i> , 2021, 8, 16.	2.4	14
95	Ontodog: a web-based ontology community view generation tool. <i>Bioinformatics</i> , 2014, 30, 1340-1342.	1.8	13
96	Ontology-based literature mining of E. coli vaccine-associated gene interaction networks. <i>Journal of Biomedical Semantics</i> , 2017, 8, 12.	0.9	13
97	Machine learning-based identification and rule-based normalization of adverse drug reactions in drug labels. <i>BMC Bioinformatics</i> , 2019, 20, 707.	1.2	13
98	Omics-Based Systems Vaccinology for Vaccine Target Identification. <i>Drug Development Research</i> , 2012, 73, 559-568.	1.4	12
99	Ontology-supported research on vaccine efficacy, safety and integrative biological networks. <i>Expert Review of Vaccines</i> , 2014, 13, 825-841.	2.0	12
100	Ontology-Based Vaccine Adverse Event Representation and Analysis. <i>Advances in Experimental Medicine and Biology</i> , 2017, 1028, 89-103.	0.8	12
101	Ontology-Based Meta-Analysis of Animal and Human Adverse Events Associated With Licensed Brucellosis Vaccines. <i>Frontiers in Pharmacology</i> , 2018, 9, 503.	1.6	12
102	VIO: ontology classification and study of vaccine responses given various experimental and analytical conditions. <i>BMC Bioinformatics</i> , 2019, 20, 704.	1.2	12
103	Profiling COVID-19 Vaccine Adverse Events by Statistical and Ontological Analysis of VAERS Case Reports. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	12
104	CRCView: a web server for analyzing and visualizing microarray gene expression data using model-based clustering. <i>Bioinformatics</i> , 2007, 23, 1843-1845.	1.8	11
105	Ontological representation, integration, and analysis of LINCS cell line cells and their cellular responses. <i>BMC Bioinformatics</i> , 2017, 18, 556.	1.2	11
106	Computational vaccinology and the ICoVax 2012 workshop. <i>BMC Bioinformatics</i> , 2013, 14, 11.	1.2	10
107	Genome Sequence of an Environmental Isolate of the Bacterial Pathogen <i>Legionella pneumophila</i> . <i>Genome Announcements</i> , 2013, 1, .	0.8	10
108	Bayesian network analysis of multi-compartmentalized immune responses in a murine model of sepsis and direct lung injury. <i>BMC Research Notes</i> , 2015, 8, 516.	0.6	10

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109	Systemic Approach to Virulence Gene Network Analysis for Gaining New Insight into Cryptococcal Virulence. <i>Frontiers in Microbiology</i> , 2016, 7, 1652.	1.5	10
110	The Non-Coding RNA Ontology (NCRO): a comprehensive resource for the unification of non-coding RNA biology. <i>Journal of Biomedical Semantics</i> , 2016, 7, 24.	0.9	10
111	Ontology-based systematic representation and analysis of traditional Chinese drugs against rheumatism. <i>BMC Systems Biology</i> , 2017, 11, 130.	3.0	10
112	ODAE: Ontology-based systematic representation and analysis of drug adverse events and its usage in study of adverse events given different patient age and disease conditions. <i>BMC Bioinformatics</i> , 2019, 20, 199.	1.2	10
113	Cwl0971, a novel peptidoglycan hydrolase, plays pleiotropic roles in <i>Clostridioides difficile</i> R20291. <i>Environmental Microbiology</i> , 2021, 23, 5222-5238.	1.8	10
114	Perform Pathway Enrichment Analysis Using ReactomeFIViz. <i>Methods in Molecular Biology</i> , 2020, 2074, 165-179.	0.4	10
115	Differential COVID-19 Symptoms Given Pandemic Locations, Time, and Comorbidities During the Early Pandemic. <i>Frontiers in Medicine</i> , 2022, 9, 770031.	1.2	10
116	Vaccine Adjuvant Informatics: From Data Integration and Analysis to Rational Vaccine Adjuvant Design. <i>Frontiers in Immunology</i> , 2014, 5, 32.	2.2	9
117	Literature Mining and Ontology based Analysis of Host-Brucella Gene-Gene Interaction Network. <i>Frontiers in Microbiology</i> , 2015, 6, 1386.	1.5	9
118	The development of non-coding RNA ontology. <i>International Journal of Data Mining and Bioinformatics</i> , 2016, 15, 214.	0.1	9
119	CIDO ontology updates and secondary analysis of host responses to COVID-19 infection based on ImmPort reports and literature. <i>Journal of Biomedical Semantics</i> , 2021, 12, 18.	0.9	9
120	A 2012 Workshop: Vaccine and Drug Ontology in the Study of Mechanism and Effect (VDOSME 2012). <i>Journal of Biomedical Semantics</i> , 2012, 3, 12.	0.9	8
121	Ontology-based representation and analysis of host-Brucella interactions. <i>Journal of Biomedical Semantics</i> , 2015, 6, 37.	0.9	8
122	VICO: Ontology-based representation and integrative analysis of Vaccination Informed Consent forms. <i>Journal of Biomedical Semantics</i> , 2016, 7, 20.	0.9	8
123	Analysis of Individual Differences in Vaccine Pharmacovigilance Using VAERS Data and MedDRA System Organ Classes: A Use Case Study With Trivalent Influenza Vaccine. <i>Biomedical Informatics Insights</i> , 2017, 9, 117822261770062.	4.6	8
124	Reverse Microbiomics: A New Reverse Dysbiosis Analysis Strategy and Its Usage in Prediction of Autoantigens and Virulent Factors in Dysbiotic Gut Microbiomes From Rheumatoid Arthritis Patients. <i>Frontiers in Microbiology</i> , 2021, 12, 633732.	1.5	8
125	Precision omics data integration and analysis with interoperable ontologies and their application for COVID-19 research. <i>Briefings in Functional Genomics</i> , 2021, 20, 235-248.	1.3	8
126	Bacterial Whole-Genome Determination and Applications. , 2015, , 357-368.		7



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127	The Interaction Network Ontology-supported modeling and mining of complex interactions represented with multiple keywords in biomedical literature. <i>BioData Mining</i> , 2016, 9, 41.	2.2	7
128	Ontology-based literature mining and class effect analysis of adverse drug reactions associated with neuropathy-inducing drugs. <i>Journal of Biomedical Semantics</i> , 2018, 9, 17.	0.9	7
129	BN+1 Bayesian network expansion for identifying molecular pathway elements. <i>Communicative and Integrative Biology</i> , 2010, 3, 549-554.	0.6	6
130	Characterization of Recombinant B. abortus Strain RB51SOD Toward Understanding the Uncorrelated Innate and Adaptive Immune Responses Induced byRB51SOD Compared to Its Parent Vaccine Strain RB51. <i>Frontiers in Cellular and Infection Microbiology</i> , 2011, 1, 10.	1.8	6
131	Vaxvec: The first web-based recombinant vaccine vector database and its data analysis. <i>Vaccine</i> , 2015, 33, 6938-6946.	1.7	6
132	Conservation in gene encoding Mycobacterium tuberculosis antigen Rv2660 and a high predicted population coverage of H56 multistage vaccine in South Africa. <i>Infection, Genetics and Evolution</i> , 2017, 55, 244-250.	1.0	6
133	OntoKeeper: Semiotic-driven Ontology Evaluation Tool For Biomedical Ontologists. , 2018, , .		6
134	OHMI: the ontology of host-microbiome interactions. <i>Journal of Biomedical Semantics</i> , 2019, 10, 25.	0.9	6
135	VaximmutorDB: A Web-Based Vaccine Immune Factor Database and Its Application for Understanding Vaccine-Induced Immune Mechanisms. <i>Frontiers in Immunology</i> , 2021, 12, 639491.	2.2	6
136	Brucella. , 2009, , 1-64.		5
137	OSCI: standardized stem cell ontology representation and use cases for stem cell investigation. <i>BMC Bioinformatics</i> , 2019, 20, 180.	1.2	5
138	Improvement in the Analysis of Vaccine Adverse Event Reporting System Database. <i>Statistics in Biopharmaceutical Research</i> , 2020, 12, 303-310.	0.6	5
139	Standardization of assay representation in the Ontology for Biomedical Investigations. <i>Database: the Journal of Biological Databases and Curation</i> , 2021, 2021, .	1.4	5
140	Ontology-based Precision Vaccinology for Deep Mechanism Understanding and Precision Vaccine Development. <i>Current Pharmaceutical Design</i> , 2021, 27, 900-910.	0.9	5
141	Cov19VaxKB: A web-based integrative COVID-19 vaccine knowledge base. <i>Vaccine: X</i> , 2022, 10, 100139.	0.9	5
142	ICEO, a biological ontology for representing and analyzing bacterial integrative and conjugative elements. <i>Scientific Data</i> , 2022, 9, 11.	2.4	5
143	Pathobiology and management of laboratory rodents administered CDC category A agents. <i>Comparative Medicine</i> , 2007, 57, 18-32.	0.4	5
144	Development of the International Classification of Diseases Ontology (ICDO) and its application for COVID-19 diagnostic data analysis. <i>BMC Bioinformatics</i> , 2021, 22, 508.	1.2	5

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145	Improvement of PubMed Literature Searching using Biomedical Ontology. Nature Precedings, 2009, , .	0.1	4
146	A 2013 workshop: vaccine and drug ontology studies (VDOS 2013). Journal of Biomedical Semantics, 2014, 5, 16.	0.9	4
147	Comparison, alignment, and synchronization of cell line information between CLO and EFO. BMC Bioinformatics, 2017, 18, 557.	1.2	4
148	The Ontology of Biological and Clinical Statistics (OBCS)-based statistical method standardization and meta-analysis of host responses to yellow fever vaccines. Quantitative Biology, 2017, 5, 291-301.	0.3	4
149	The cell line ontology-based representation, integration and analysis of cell lines used in China. BMC Bioinformatics, 2019, 20, 179.	1.2	4
150	Visual comprehension and orientation into the COVID-19 CIDO ontology. Journal of Biomedical Informatics, 2021, 120, 103861.	2.5	4
151	Towards precision informatics of pharmacovigilance: OAE-CTCAE mapping and OAE-based representation and analysis of adverse events in patients treated with cancer drugs. AMIA ... Annual Symposium proceedings, 2017, 2017, 1793-1801.	0.2	4
152	COVID-19 vaccine design using reverse and structural vaccinology, ontology-based literature mining and machine learning. Briefings in Bioinformatics, 2022, 23, .	3.2	4
153	Biomedical ontologies and their development, management, and applications in and beyond China. Journal of Bio-X Research, 2019, 2, 178-184.	0.3	3
154	Genomic population structure of <i>Helicobacter pylori</i> Shanghai isolates and identification of genomic features uniquely linked with pathogenicity. Virulence, 2021, 12, 1258-1270.	1.8	3
155	Integrative representations and analyses of vaccine-induced intended protective immunity and unintended adverse events using ontology-based and theory-guided approaches. Global Vaccines and Immunology, 2016, 1, 37-39.	0.2	3
156	Ontology-Based Classification and Analysis of Adverse Events Associated With the Usage of Chloroquine and Hydroxychloroquine. Frontiers in Pharmacology, 2022, 13, 812338.	1.6	3
157	ICoVax 2013: The 3rd ISV Pre-conference Computational Vaccinology Workshop. BMC Bioinformatics, 2014, 15, 11.	1.2	2
158	Vaccine and Drug Ontology Studies (VDOS 2014). Journal of Biomedical Semantics, 2016, 7, 6.	0.9	2
159	Integrative web-based analysis of omics data for study of drugs against SARS-CoV-2. Scientific Reports, 2021, 11, 10763.	1.6	2
160	TCDO: A Community-Based Ontology for Integrative Representation and Analysis of Traditional Chinese Drugs and Their Properties. Evidence-based Complementary and Alternative Medicine, 2021, 2021, 1-15.	0.5	2
161	Community-based Ontology Development, Annotation and Discussion with MediaWiki extension Ontokiwi and Ontokiwi-based Ontobedia. AMIA Summits on Translational Science Proceedings, 2016, 2016, 65-74.	0.4	2
162	The Ontology of Biological and Clinical Statistics (OBCS)-based statistical method standardization and meta-analysis of host responses to yellow fever vaccines. Quantitative Biology, 2017, 5, 291-301.	0.3	2

#	ARTICLE	IF	CITATIONS
163	Development and Applications of Interoperable Biomedical Ontologies for Integrative Data and Knowledge Representation and Multiscale Modeling in Systems Medicine. <i>Methods in Molecular Biology</i> , 2022, 2486, 233-244.	0.4	2
164	Prediction of Pathogenic Factors in Dysbiotic Gut Microbiomes of Colorectal Cancer Patients Using Reverse Microbiomics. <i>Frontiers in Oncology</i> , 2022, 12, 882874.	1.3	2
165	Genome-Based Computational Vaccine Discovery by Reverse Vaccinology. , 2013, , 91-104.		1
166	Cells in experimental life sciences - challenges and solution to the rapid evolution of knowledge. <i>BMC Bioinformatics</i> , 2017, 18, 560.	1.2	1
167	A 2018 workshop: vaccine and drug ontology studies (VDOS 2018). <i>BMC Bioinformatics</i> , 2019, 20, 705.	1.2	1
168	Vaxar: A Web-Based Database of Laboratory Animal Responses to Vaccinations and Its Application in the Meta-Analysis of Different Animal Responses to Tuberculosis Vaccinations. <i>Comparative Medicine</i> , 2016, 66, 119-28.	0.4	1
169	Vaccine Design by Reverse Vaccinology and Machine Learning. <i>Methods in Molecular Biology</i> , 2022, 2414, 1-16.	0.4	1
170	The Web-Based DNA Vaccine Database DNAVaxDB and Its Usage for Rational DNA Vaccine Design. <i>Methods in Molecular Biology</i> , 2016, 1404, 741-752.	0.4	0
171	Cells in Experimental Life Sciences (CELLS-2018): capturing the knowledge of normal and diseased cells with ontologies. <i>BMC Bioinformatics</i> , 2019, 20, 183.	1.2	0
172	OntoPlot: A Novel Visualisation for Non-hierarchical Associations in Large Ontologies. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2019, 26, 1-1.	2.9	0
173	Development of the International Classification of Diseases Ontology (ICDO) and its application for COVID-19 diagnostic data analysis. <i>BMC Bioinformatics</i> , 2021, 22, 508.	1.2	0