Yongqun He

List of Publications by Year
in descending order

173 papers	7,001 citations	57758 44 h-index	76900 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. Nucleic Acids Research, 2021, 49, D1207-D1217.	14.5	652
2	Endoplasmic Reticulum Stress Activates the Inflammasome via NLRP3- and Caspase-2-Driven Mitochondrial Damage. Immunity, 2015, 43, 451-462.	14.3	328
3	COVID-19 Coronavirus Vaccine Design Using Reverse Vaccinology and Machine Learning. Frontiers in Immunology, 2020, 11, 1581.	4.8	301
4	Vaxign: The First Web-Based Vaccine Design Program for Reverse Vaccinology and Applications for Vaccine Development. Journal of Biomedicine and Biotechnology, 2010, 2010, 1-15.	3.0	260
5	The Ontology for Biomedical Investigations. PLoS ONE, 2016, 11, e0154556.	2.5	217
6	Modeling biomedical experimental processes with OBI. Journal of Biomedical Semantics, 2010, 1, S7.	1.6	207
7	The Cell Ontology 2016: enhanced content, modularization, and ontology interoperability. Journal of Biomedical Semantics, 2016, 7, 44.	1.6	201
8	Finding Our Way through Phenotypes. PLoS Biology, 2015, 13, e1002033.	5.6	178
9	OntoFox: web-based support for ontology reuse. BMC Research Notes, 2010, 3, 175.	1.4	145
10	Victors: a web-based knowledge base of virulence factors in human and animal pathogens. Nucleic Acids Research, 2019, 47, D693-D700.	14.5	120
11	Emerging Vaccine Informatics. Journal of Biomedicine and Biotechnology, 2010, 2010, 1-26.	3.0	114
12	Ontobee: A linked ontology data server to support ontology term dereferencing, linkage, query and integration. Nucleic Acids Research, 2017, 45, D347-D352.	14.5	110
13	VRprofile: gene-cluster-detection-based profiling of virulence and antibiotic resistance traits encoded within genome sequences of pathogenic bacteria. Briefings in Bioinformatics, 2018, 19, bbw141.	6.5	100
14	OAE: The Ontology of Adverse Events. Journal of Biomedical Semantics, 2014, 5, 29.	1.6	94
15	Rationale and design of the Kidney Precision Medicine Project. Kidney International, 2021, 99, 498-510.	5.2	94
16	Analyses of Brucella Pathogenesis, Host Immunity, and Vaccine Targets using Systems Biology and Bioinformatics. Frontiers in Cellular and Infection Microbiology, 2012, 2, 2.	3.9	92
17	CLO: The cell line ontology. Journal of Biomedical Semantics, 2014, 5, 37.	1.6	89
18	PIML: the Pathogen Information Markup Language. Bioinformatics, 2005, 21, 116-121.	4.1	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. Infection and Immunity, 2006, 74, 5035-5046.	2.2	85
20	Environmental Temperature Differentially Modulates C.Âelegans Longevity through a Thermosensitive TRP Channel. Cell Reports, 2015, 11, 1414-1424.	6.4	81
21	Vaxign-ML: supervised machine learning reverse vaccinology model for improved prediction of bacterial protective antigens. Bioinformatics, 2020, 36, 3185-3191.	4.1	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. Infection and Immunity, 2000, 68, 3927-3932.	2.2	76
23	Overexpression of Protective Antigen as a Novel Approach To Enhance Vaccine Efficacy of Brucella abortus Strain RB51. Infection and Immunity, 2000, 68, 3286-3289.	2.2	75
24	Strong antibody responses induced by protein antigens conjugated onto the surface of lecithin-based nanoparticles. Journal of Controlled Release, 2010, 141, 93-100.	9.9	72
25	CIDO, a community-based ontology for coronavirus disease knowledge and data integration, sharing, and analysis. Scientific Data, 2020, 7, 181.	5.3	70
26	Induction of Specific Cytotoxic Lymphocytes in Mice Vaccinated with Brucella abortus RB51. Infection and Immunity, 2001, 69, 5502-5508.	2.2	69
27	Protegen: a web-based protective antigen database and analysis system. Nucleic Acids Research, 2011, 39, D1073-D1078.	14.5	69
28	Anatomical structures, cell types and biomarkers of the Human Reference Atlas. Nature Cell Biology, 2021, 23, 1117-1128.	10.3	68
29	A reference tissue atlas for the human kidney. Science Advances, 2022, 8, .	10.3	67
30	Updates on the web-based VIOLIN vaccine database and analysis system. Nucleic Acids Research, 2014, 42, D1124-D1132.	14.5	66
31	VIOLIN: vaccine investigation and online information network. Nucleic Acids Research, 2007, 36, D923-D928.	14.5	65
32	Brucella abortus Strain RB51 as a Vector for Heterologous Protein Expression and Induction of Specific Th1 Type Immune Responses. Infection and Immunity, 2000, 68, 3290-3296.	2.2	64
33	Safety and immunogenicity of mammalian cell derived and Modified Vaccinia Ankara vectored African swine fever subunit antigens in swine. Veterinary Immunology and Immunopathology, 2017, 185, 20-33.	1.2	64
34	Antibiotic Resistance Determinant-Focused Acinetobacter baumannii Vaccine Designed Using Reverse Vaccinology. International Journal of Molecular Sciences, 2017, 18, 458.	4.1	64
35	PHIDIAS: a pathogen-host interaction data integration and analysis system. Genome Biology, 2007, 8, R150.	9.6	63
36	Caspase-2 Mediated Apoptotic and Necrotic Murine Macrophage Cell Death Induced by Rough Brucella abortus. PLoS ONE, 2009, 4, e6830.	2.5	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. Physiological Genomics, 2021, 53, 1-11.	2.3	59
38	Genome-wide prediction of vaccine targets for human herpes simplex viruses using Vaxign reverse vaccinology. BMC Bioinformatics, 2013, 14, S2.	2.6	58
39	The eXtensible ontology development (XOD) principles and tool implementation to support ontology interoperability. Journal of Biomedical Semantics, 2018, 9, 3.	1.6	57
40	Vaxign: a web-based vaccine target design program for reverse vaccinology. Procedia in Vaccinology, 2009, 1, 23-29.	0.4	56
41	Mining of vaccine-associated IFN-Î³ gene interaction networks using the Vaccine Ontology. Journal of Biomedical Semantics, 2011, 2, S8.	1.6	54
42	Presence of Putative Repeat-in-Toxin Gene tosA in Escherichia coli Predicts Successful Colonization of the Urinary Tract. MBio, 2011, 2, e00066-11.	4.1	51
43	Ontology representation and analysis of vaccine formulation and administration and their effects on vaccine immune responses. Journal of Biomedical Semantics, 2012, 3, 17.	1.6	51
44	Ontology-Based Combinatorial Comparative Analysis of Adverse Events Associated with Killed and Live Influenza Vaccines. PLoS ONE, 2012, 7, e49941.	2.5	49
45	BBP: Brucella genome annotation with literature mining and curation. BMC Bioinformatics, 2006, 7, 347.	2.6	47
46	Bioinformatics analysis of Brucella vaccines and vaccine targets using VIOLIN. Immunome Research, 2010, 6, S5.	0.1	46
47	Proinflammatory Caspase-2-Mediated Macrophage Cell Death Induced by a Rough Attenuated Brucella suis Strain. Infection and Immunity, 2011, 79, 2460-2469.	2.2	46
48	Modelling kidney disease using ontology: insights from the Kidney Precision Medicine Project. Nature Reviews Nephrology, 2020, 16, 686-696.	9.6	45
49	Vaxjo: A Web-Based Vaccine Adjuvant Database and Its Application for Analysis of Vaccine Adjuvants and Their Uses in Vaccine Development. Journal of Biomedicine and Biotechnology, 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. Nucleic Acids Research, 2021, 49, W671-W678.	14.5	44
51	Molecular targets for rapid identification of Brucella spp. BMC Microbiology, 2006, 6, 13.	3.3	42
52	The Ontology of Vaccine Adverse Events (OVAE) and its usage in representing and analyzing adverse events associated with US-licensed human vaccines. Journal of Biomedical Semantics, 2013, 4, 40.	1.6	39
53	Ontorat: automatic generation of new ontology terms, annotations, and axioms based on ontology design patterns. Journal of Biomedical Semantics, 2015, 6, 4.	1.6	39
54	Literature-Based Discovery of IFN-<mml:math xmlns:mml="http://www.w3.org/1998/Math/MathML"><mml:mi>Î³</mml:mi></mml:math>and Vaccine-Mediated Gene Interaction Networks. Journal of Biomedicine and Biotechnology, 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. BMC Immunology, 2011, 12, 49.	2.2	34
56	Cwp22, a novel peptidoglycan crossâ€linking enzyme, plays pleiotropic roles in Clostridioides difficile. Environmental Microbiology, 2019, 21, 3076-3090.	3.8	34
57	Recombinant Ochrobactrum anthropi Expressing Brucella abortus Cu,Zn Superoxide Dismutase Protects Mice against B. abortus Infection Only after Switching of Immune Responses to Th1 Type. Infection and Immunity, 2002, 70, 2535-2543.	2.2	33
58	Brucella abortus RB51: enhancing vaccine efficacy and developing multivalent vaccines. Veterinary Microbiology, 2002, 90, 521-532.	1.9	32
59	A genome-wide MeSH-based literature mining system predicts implicit gene-to-gene relationships and networks. BMC Systems Biology, 2013, 7, S9.	3.0	32
60	Meta-analysis of variables affecting mouse protection efficacy of whole organism Brucella vaccines and vaccine candidates. BMC Bioinformatics, 2013, 14, S3.	2.6	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. PLoS ONE, 2016, 11, e0164792.	2.5	29
62	Systematic annotation and analysis of â€œvirmugensâ€â€"Virulence factors whose mutants can be used as live attenuated vaccines. Vaccine, 2013, 31, 797-805.	3.8	28
63	Statistical and Ontological Analysis of Adverse Events Associated with Monovalent and Combination Vaccines against Hepatitis A and B Diseases. Scientific Reports, 2016, 6, 34318.	3.3	28
64	Microbial modulation of host apoptosis and pyroptosis. Frontiers in Cellular and Infection Microbiology, 2014, 4, 83.	3.9	27
65	Linking MedDRAÂ®-Coded Clinical Phenotypes to Biological Mechanisms by the Ontology of Adverse Events: A Pilot Study on Tyrosine Kinase Inhibitors. Drug Safety, 2016, 39, 697-707.	3.2	27
66	Using epitope predictions to evaluate efficacy and population coverage of the Mtb72f vaccine for tuberculosis. BMC Immunology, 2010, 11, 18.	2.2	26
67	Identification of fever and vaccine-associated gene interaction networks using ontology-based literature mining. Journal of Biomedical Semantics, 2012, 3, 18.	1.6	26
68	Identification of New Features from Known Bacterial Protective Vaccine Antigens Enhances Rational Vaccine Design. Frontiers in Immunology, 2017, 8, 1382.	4.8	25
69	Databases and In Silico Tools for Vaccine Design. Methods in Molecular Biology, 2013, 993, 115-127.	0.9	24
70	Caspase-2-Dependent Dendritic Cell Death, Maturation, and Priming of T Cells in Response to Brucella abortus Infection. PLoS ONE, 2012, 7, e43512.	2.5	24
71	Development and application of an interaction network ontology for literature mining of vaccine-associated gene-gene interactions. Journal of Biomedical Semantics, 2015, 6, 2.	1.6	23
72	Epitope promiscuity and population coverage of Mycobacterium tuberculosis protein antigens in current subunit vaccines under development. Infection, Genetics and Evolution, 2020, 80, 104186.	2.3	23

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73	Caspase-2 mediates a Brucella abortus RB51-induced hybrid cell death having features of apoptosis and pyroptosis. Frontiers in Cellular and Infection Microbiology, 2013, 3, 83.	3.9	23
74	Brucellosis Ontology (IDOBRU) as an extension of the Infectious Disease Ontology. Journal of Biomedical Semantics, 2011, 2, 9.	1.6	22
75	Ontology-based collection, representation and analysis of drug-associated neuropathy adverse events. Journal of Biomedical Semantics, 2016, 7, 29.	1.6	22
76	Network-based analysis of vaccine-related associations reveals consistent knowledge with the vaccine ontology. Journal of Biomedical Semantics, 2013, 4, 33.	1.6	21
77	miniTUBA: medical inference by network integration of temporal data using Bayesian analysis. Bioinformatics, 2007, 23, 2423-2432.	4.1	20
78	Ontology-based time information representation of vaccine adverse events in VAERS for temporal analysis. Journal of Biomedical Semantics, 2012, 3, 13.	1.6	20
79	The ontology of genetic susceptibility factors (OGSF) and its application in modeling genetic susceptibility to vaccine adverse events. Journal of Biomedical Semantics, 2014, 5, 19.	1.6	20
80	Computational design of SARS-CoV-2 spike glycoproteins to increase immunogenicity by T cell epitope engineering. Computational and Structural Biotechnology Journal, 2021, 19, 518-529.	4.1	19
81	Bayesian Network Expansion Identifies New ROS and Biofilm Regulators. PLoS ONE, 2010, 5, e9513.	2.5	19
82	RNA-seq reveals the critical role of OtpR in regulating Brucella melitensis metabolism and virulence under acidic stress. Scientific Reports, 2015, 5, 10864.	3.3	18
83	Ontology-Based Vaccine and Drug Adverse Event Representation and Theory-Guided Systematic Causal Network Analysis Toward Integrative Pharmacovigilance Research. Current Pharmacology Reports, 2016, 2, 113-128.	3.0	18
84	The Ontology of Biological and Clinical Statistics (OBCS) for standardized and reproducible statistical analysis. Journal of Biomedical Semantics, 2016, 7, 53.	1.6	18
85	DNAVaxDB: the first web-based DNA vaccine database and its data analysis. BMC Bioinformatics, 2014, 15, S2.	2.6	17
86	Novel Immunoprotective Proteins of Streptococcus pneumoniae Identified by Opsonophagocytosis Killing Screen. Infection and Immunity, 2018, 86, .	2.2	16
87	A statistical analysis of vaccine-adverse event data. BMC Medical Informatics and Decision Making, 2019, 19, 101.	3.0	16
88	Time event ontology (TEO): to support semantic representation and reasoning of complex temporal relations of clinical events. Journal of the American Medical Informatics Association: JAMIA, 2020, 27, 1046-1056.	4.4	16
89	COVID-19 induces lower levels of IL-8, IL-10, and MCP-1 than other acute CRS-inducing diseases. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	16
90	Potential transmission chains of variant B.1.1.7 and co-mutations of SARS-CoV-2. Cell Discovery, 2021, 7, 44.	6.7	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. Scientific Reports, 2017, 7, 13819.	3.3	15
92	Bioinformatics analysis of bacterial protective antigens in manually curated Protegen database. Procedia in Vaccinology, 2012, 6, 3-9.	0.4	14
93	Architecture and usability of OntoKeeper, an ontology evaluation tool. BMC Medical Informatics and Decision Making, 2019, 19, 152.	3.0	14
94	Ontological modeling and analysis of experimentally or clinically verified drugs against coronavirus infection. Scientific Data, 2021, 8, 16.	5.3	14
95	Ontodog: a web-based ontology community view generation tool. Bioinformatics, 2014, 30, 1340-1342.	4.1	13
96	Ontology-based literature mining of E. coli vaccine-associated gene interaction networks. Journal of Biomedical Semantics, 2017, 8, 12.	1.6	13
97	Machine learning-based identification and rule-based normalization of adverse drug reactions in drug labels. BMC Bioinformatics, 2019, 20, 707.	2.6	13
98	Omicsâ€Based Systems Vaccinology for Vaccine Target Identification. Drug Development Research, 2012, 73, 559-568.	2.9	12
99	Ontology-supported research on vaccine efficacy, safety and integrative biological networks. Expert Review of Vaccines, 2014, 13, 825-841.	4.4	12
100	Ontology-Based Vaccine Adverse Event Representation and Analysis. Advances in Experimental Medicine and Biology, 2017, 1028, 89-103.	1.6	12
101	Ontology-Based Meta-Analysis of Animal and Human Adverse Events Associated With Licensed Brucellosis Vaccines. Frontiers in Pharmacology, 2018, 9, 503.	3.5	12
102	VIO: ontology classification and study of vaccine responses given various experimental and analytical conditions. BMC Bioinformatics, 2019, 20, 704.	2.6	12
103	Profiling COVID-19 Vaccine Adverse Events by Statistical and Ontological Analysis of VAERS Case Reports. Frontiers in Pharmacology, 0, 13, .	3.5	12
104	CRCView: a web server for analyzing and visualizing microarray gene expression data using model-based clustering. Bioinformatics, 2007, 23, 1843-1845.	4.1	11
105	Ontological representation, integration, and analysis of LINCS cell line cells and their cellular responses. BMC Bioinformatics, 2017, 18, 556.	2.6	11
106	Computational vaccinology and the ICoVax 2012 workshop. BMC Bioinformatics, 2013, 14, I1.	2.6	10
107	Genome Sequence of an Environmental Isolate of the Bacterial Pathogen Legionella pneumophila. Genome Announcements, 2013, 1, .	0.8	10
108	Bayesian network analysis of multi-compartmentalized immune responses in a murine model of sepsis and direct lung injury. BMC Research Notes, 2015, 8, 516.	1.4	10

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109	Systemic Approach to Virulence Gene Network Analysis for Gaining New Insight into Cryptococcal Virulence. Frontiers in Microbiology, 2016, 7, 1652.	3.5	10
110	The Non-Coding RNA Ontology (NCRO): a comprehensive resource for the unification of non-coding RNA biology. Journal of Biomedical Semantics, 2016, 7, 24.	1.6	10
111	Ontology-based systematic representation and analysis of traditional Chinese drugs against rheumatism. BMC Systems Biology, 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. BMC Bioinformatics, 2019, 20, 199.	2.6	10
113	Cwl0971, a novel peptidoglycan hydrolase, plays pleiotropic roles in Clostridioides difficile R20291. Environmental Microbiology, 2021, 23, 5222-5238.	3.8	10
114	Perform Pathway Enrichment Analysis Using ReactomeFIViz. Methods in Molecular Biology, 2020, 2074, 165-179.	0.9	10
115	Differential COVID-19 Symptoms Given Pandemic Locations, Time, and Comorbidities During the Early Pandemic. Frontiers in Medicine, 2022, 9, 770031.	2.6	10
116	Vaccine Adjuvant Informatics: From Data Integration and Analysis to Rational Vaccine Adjuvant Design. Frontiers in Immunology, 2014, 5, 32.	4.8	9
117	Literature Mining and Ontology based Analysis of Host-Brucella Geneâ€"Gene Interaction Network. Frontiers in Microbiology, 2015, 6, 1386.	3.5	9
118	The development of non-coding RNA ontology. International Journal of Data Mining and Bioinformatics, 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. Journal of Biomedical Semantics, 2021, 12, 18.	1.6	9
120	A 2012 Workshop: Vaccine and Drug Ontology in the Study of Mechanism and Effect (VDOSME 2012). Journal of Biomedical Semantics, 2012, 3, 12.	1.6	8
121	Ontology-based representation and analysis of host-Brucella interactions. Journal of Biomedical Semantics, 2015, 6, 37.	1.6	8
122	VICO: Ontology-based representation and integrative analysis of Vaccination Informed Consent forms. Journal of Biomedical Semantics, 2016, 7, 20.	1.6	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. Biomedical Informatics Insights, 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. Frontiers in Microbiology, 2021, 12, 633732.	3.5	8
125	Precision omics data integration and analysis with interoperable ontologies and their application for COVID-19 research. Briefings in Functional Genomics, 2021, 20, 235-248.	2.7	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. BioData Mining, 2016, 9, 41.	4.0	7
128	Ontology-based literature mining and class effect analysis of adverse drug reactions associated with neuropathy-inducing drugs. Journal of Biomedical Semantics, 2018, 9, 17.	1.6	7
129	BN+1 Bayesian network expansion for identifying molecular pathway elements. Communicative and Integrative Biology, 2010, 3, 549-554.	1.4	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. Frontiers in Cellular and Infection Microbiology, 2011, 1, 10.	3.9	6
131	Vaxvec: The first web-based recombinant vaccine vector database and its data analysis. Vaccine, 2015, 33, 6938-6946.	3.8	6
132	Conservation in gene encoding Mycobacterium tuberculosis antigen Rv2660 and a high predicted population coverage of H56 multistage vaccine in South Africa. Infection, Genetics and Evolution, 2017, 55, 244-250.	2.3	6
133	OntoKeeper: Semiotic-driven Ontology Evaluation Tool For Biomedical Ontologists. , 2018, , .		6
134	OHMI: the ontology of host-microbiome interactions. Journal of Biomedical Semantics, 2019, 10, 25.	1.6	6
135	VaximmutorDB: A Web-Based Vaccine Immune Factor Database and Its Application for Understanding Vaccine-Induced Immune Mechanisms. Frontiers in Immunology, 2021, 12, 639491.	4.8	6
136	Brucella. , 2009, , 1-64.		5
137	OSCI: standardized stem cell ontology representation and use cases for stem cell investigation. BMC Bioinformatics, 2019, 20, 180.	2.6	5
138	Improvement in the Analysis of Vaccine Adverse Event Reporting System Database. Statistics in Biopharmaceutical Research, 2020, 12, 303-310.	0.8	5
139	Standardization of assay representation in the Ontology for Biomedical Investigations. Database: the Journal of Biological Databases and Curation, 2021, 2021, .	3.0	5
140	Ontology-based Precision Vaccinology for Deep Mechanism Understanding and Precision Vaccine Development. Current Pharmaceutical Design, 2021, 27, 900-910.	1.9	5
141	Cov19VaxKB: A web-based integrative COVID-19 vaccine knowledge base. Vaccine: X, 2022, 10, 100139.	2.1	5
142	ICEO, a biological ontology for representing and analyzing bacterial integrative and conjugative elements. Scientific Data, 2022, 9, 11.	5.3	5
143	Pathobiology and management of laboratory rodents administered CDC category A agents. Comparative Medicine, 2007, 57, 18-32.	1.0	5
144	Development of the International Classification of Diseases Ontology (ICDO) and its application for COVID-19 diagnostic data analysis. BMC Bioinformatics, 2021, 22, 508.	2.6	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.	1.6	4
147	Comparison, alignment, and synchronization of cell line information between CLO and EFO. BMC Bioinformatics, 2017, 18, 557.	2.6	4
148	The Ontology of Biological and Clinical Statistics (OBCS)â€based statistical method standardization and metaâ€analysis of host responses to yellow fever vaccines. Quantitative Biology, 2017, 5, 291-301.	0.5	4
149	The cell line ontology-based representation, integration and analysis of cell lines used in China. BMC Bioinformatics, 2019, 20, 179.	2.6	4
150	Visual comprehension and orientation into the COVID-19 CIDO ontology. Journal of Biomedical Informatics, 2021, 120, 103861.	4.3	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, .	6.5	4
153	Biomedical ontologies and their development, management, and applications in and beyond China. Journal of Bio-X Research, 2019, 2, 178-184.	0.2	3
154	Genomic population structure of Helicobacter pylori Shanghai isolates and identification of genomic features uniquely linked with pathogenicity. Virulence, 2021, 12, 1258-1270.	4.4	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.	3.5	3
157	ICoVax 2013: The 3rd ISV Pre-conference Computational Vaccinology Workshop. BMC Bioinformatics, 2014, 15, I1.	2.6	2
158	Vaccine and Drug Ontology Studies (VDOS 2014). Journal of Biomedical Semantics, 2016, 7, 6.	1.6	2
159	Integrative web-based analysis of omics data for study of drugs against SARS-CoV-2. Scientific Reports, 2021, 11, 10763.	3.3	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.	1.2	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.	0.5	2

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163	Development and Applications of Interoperable Biomedical Ontologies for Integrative Data and Knowledge Representation and Multiscale Modeling in Systems Medicine. Methods in Molecular Biology, 2022, 2486, 233-244.	0.9	2
164	Prediction of Pathogenic Factors in Dysbiotic Gut Microbiomes of Colorectal Cancer Patients Using Reverse Microbiomics. Frontiers in Oncology, 2022, 12, 882874.	2.8	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. BMC Bioinformatics, 2017, 18, 560.	2.6	1
167	A 2018 workshop: vaccine and drug ontology studies (VDOS 2018). BMC Bioinformatics, 2019, 20, 705.	2.6	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. Comparative Medicine, 2016, 66, 119-28.	1.0	1
169	Vaccine Design by Reverse Vaccinology and Machine Learning. Methods in Molecular Biology, 2022, 2414, 1-16.	0.9	1
170	The Web-Based DNA Vaccine Database DNAVaxDB and Its Usage for Rational DNA Vaccine Design. Methods in Molecular Biology, 2016, 1404, 741-752.	0.9	0
171	Cells in ExperimentaL Life Sciences (CELLS-2018): capturing the knowledge of normal and diseased cells with ontologies. BMC Bioinformatics, 2019, 20, 183.	2.6	0
172	OntoPlot: A Novel Visualisation for Non-hierarchical Associations in Large Ontologies. IEEE Transactions on Visualization and Computer Graphics, 2019, 26, 1-1.	4.4	0
173	Development of the International Classification of Diseases Ontology (ICDO) and its application for COVID-19 diagnostic data analysis. BMC Bioinformatics, 2021, 22, 508.	2.6	0