

Jake Y Chen

List of Publications by Year in descending order

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170
papers

6,606
citations

87888

38
h-index

69250

77
g-index

179
all docs

179
docs citations

179
times ranked

9394
citing authors

#	ARTICLE	IF	CITATIONS
1	DisProt: the Database of Disordered Proteins. <i>Nucleic Acids Research</i> , 2007, 35, D786-D793.	14.5	711
2	Silk implants for the healing of critical size bone defects. <i>Bone</i> , 2005, 37, 688-698.	2.9	416
3	Disorder and Sequence Repeats in Hub Proteins and Their Implications for Network Evolution. <i>Journal of Proteome Research</i> , 2006, 5, 2985-2995.	3.7	312
4	Decoding SARS-CoV-2 hijacking of host mitochondria in COVID-19 pathogenesis. <i>American Journal of Physiology - Cell Physiology</i> , 2020, 319, C258-C267.	4.6	258
5	Effects of miR-335-5p in modulating osteogenic differentiation by specifically downregulating Wnt antagonist DKK1. <i>Journal of Bone and Mineral Research</i> , 2011, 26, 1953-1963.	2.8	257
6	The use of injectable sonication-induced silk hydrogel for VEGF165 and BMP-2 delivery for elevation of the maxillary sinus floor. <i>Biomaterials</i> , 2011, 32, 9415-9424.	11.4	255
7	Porous silk fibroin 3-D scaffolds for delivery of bone morphogenetic protein-2 in vitro and in vivo. <i>Journal of Biomedical Materials Research - Part A</i> , 2006, 78A, 324-334.	4.0	201
8	Mandibular repair in rats with premineralized silk scaffolds and BMP-2-modified bMSCs. <i>Biomaterials</i> , 2009, 30, 4522-4532.	11.4	194
9	Regenerative Potential of Neonatal Porcine Hearts. <i>Circulation</i> , 2018, 138, 2809-2816.	1.6	179
10	Application of induced pluripotent stem (iPS) cells in periodontal tissue regeneration. <i>Journal of Cellular Physiology</i> , 2011, 226, 150-157.	4.1	175
11	Building Disease-Specific Drug-Protein Connectivity Maps from Molecular Interaction Networks and PubMed Abstracts. <i>PLoS Computational Biology</i> , 2009, 5, e1000450.	3.2	158
12	Critical-size calvarial bone defects healing in a mouse model with silk scaffolds and SATB2-modified iPSCs. <i>Biomaterials</i> , 2011, 32, 5065-5076.	11.4	148
13	HAPPI: an online database of comprehensive human annotated and predicted protein interactions. <i>BMC Genomics</i> , 2009, 10, S16.	2.8	133
14	Exercise-induced irisin in bone and systemic irisin administration reveal new regulatory mechanisms of bone metabolism. <i>Bone Research</i> , 2017, 5, 16056.	11.4	126
15	Osterix enhances proliferation and osteogenic potential of bone marrow stromal cells. <i>Biochemical and Biophysical Research Communications</i> , 2006, 341, 1257-1265.	2.1	121
16	Apatite-coated silk fibroin scaffolds to healing mandibular border defects in canines. <i>Bone</i> , 2009, 45, 517-527.	2.9	109
17	Predicting adverse side effects of drugs. <i>BMC Genomics</i> , 2011, 12, S11.	2.8	105
18	Adiponectin Inhibits Osteoclastogenesis and Bone Resorption via APPL1-mediated Suppression of Akt1. <i>Journal of Biological Chemistry</i> , 2011, 286, 12542-12553.	3.4	100

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19	Osterix Overexpression in Mesenchymal Stem Cells Stimulates Healing of Critical-Sized Defects in Murine Calvarial Bone. <i>Tissue Engineering</i> , 2007, 13, 2431-2440.	4.6	99
20	Pathway and network analysis in proteomics. <i>Journal of Theoretical Biology</i> , 2014, 362, 44-52.	1.7	98
21	Overexpression of MiR-335-5p Promotes Bone Formation and Regeneration in Mice. <i>Journal of Bone and Mineral Research</i> , 2017, 32, 2466-2475.	2.8	92
22	Roles of SATB2 in Osteogenic Differentiation and Bone Regeneration. <i>Tissue Engineering - Part A</i> , 2011, 17, 1767-1776.	3.1	85
23	BSP and RANKL Induce Osteoclastogenesis and Bone Resorption Synergistically. <i>Journal of Bone and Mineral Research</i> , 2005, 20, 1669-1679.	2.8	67
24	Adiponectin Regulates Bone Marrow Mesenchymal Stem Cell Niche Through a Unique Signal Transduction Pathway: An Approach for Treating Bone Disease in Diabetes. <i>Stem Cells</i> , 2015, 33, 240-252.	3.2	65
25	Expression of Osterix in mechanical stress-induced osteogenic differentiation of periodontal ligament cells <i>in vitro</i> . <i>European Journal of Oral Sciences</i> , 2008, 116, 199-206.	1.5	58
26	Predicting adverse drug reaction profiles by integrating protein interaction networks with drug structures. <i>Proteomics</i> , 2013, 13, 313-324.	2.2	56
27	Tumor Necrosis Factor- α and Interleukin-1-Induced Cellular Responses: A Coupling Proteomic and Genomic Information. <i>Journal of Proteome Research</i> , 2007, 6, 2176-2185.	3.7	54
28	MicroRNA expression signature for Satb2-induced osteogenic differentiation in bone marrow stromal cells. <i>Molecular and Cellular Biochemistry</i> , 2014, 387, 227-239.	3.1	53
29	Central adiponectin administration reveals new regulatory mechanisms of bone metabolism in mice. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2014, 306, E1418-E1430.	3.5	51
30	Unraveling human complexity and disease with systems biology and personalized medicine. <i>Personalized Medicine</i> , 2010, 7, 275-289.	1.5	50
31	Semantic Web meets Integrative Biology: a survey. <i>Briefings in Bioinformatics</i> , 2013, 14, 109-125.	6.5	50
32	Overexpression of Bone Sialoprotein Leads to an Uncoupling of Bone Formation and Bone Resorption in Mice. <i>Journal of Bone and Mineral Research</i> , 2008, 23, 1775-1788.	2.8	46
33	A novel Lipidoid-MicroRNA formulation promotes calvarial bone regeneration. <i>Biomaterials</i> , 2018, 177, 88-97.	11.4	46
34	Runx2/DICER/miRNA Pathway in Regulating Osteogenesis. <i>Journal of Cellular Physiology</i> , 2017, 232, 182-191.	4.1	45
35	Effects of Platelet Concentrate on Palatal Wound Healing After Connective Tissue Graft Harvesting. <i>Journal of Periodontology</i> , 2007, 78, 601-610.	3.4	44
36	Sustained release of adiponectin improves osteogenesis around hydroxyapatite implants by suppressing osteoclast activity in ovariectomized rabbits. <i>Acta Biomaterialia</i> , 2012, 8, 734-743.	8.3	44

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37	Semantic web for integrated network analysis in biomedicine. <i>Briefings in Bioinformatics</i> , 2009, 10, 177-192.	6.5	43
38	HPD: an online integrated human pathway database enabling systems biology studies. <i>BMC Bioinformatics</i> , 2009, 10, S5.	2.6	42
39	Epigenetic Modulation in Periodontitis: Interaction of Adiponectin and JMJD3-IRF4 Axis in Macrophages. <i>Journal of Cellular Physiology</i> , 2016, 231, 1090-1096.	4.1	38
40	Haploinsufficiency of <i>Runx2</i> results in bone formation decrease and different BSP expression pattern changes in two transgenic mouse models. <i>Journal of Cellular Physiology</i> , 2008, 217, 40-47.	4.1	36
41	<i>Cbfa1/Runx2</i> -deficiency delays bone wound healing and locally delivered <i>Cbfa1/Runx2</i> promotes bone repair in animal models. <i>Wound Repair and Regeneration</i> , 2007, 15, 404-412.	3.0	35
42	Targeted overexpression of BSP in osteoclasts promotes bone metastasis of breast cancer cells. <i>Journal of Cellular Physiology</i> , 2009, 218, 135-145.	4.1	35
43	DMAP: a connectivity map database to enable identification of novel drug repositioning candidates. <i>BMC Bioinformatics</i> , 2015, 16, S4.	2.6	35
44	HAPPI-2: a Comprehensive and High-quality Map of Human Annotated and Predicted Protein Interactions. <i>BMC Genomics</i> , 2017, 18, 182.	2.8	35
45	Genome-wide meta-analysis of genetic susceptible genes for Type 2 Diabetes. <i>BMC Systems Biology</i> , 2012, 6, S16.	3.0	34
46	Altered Expression of Bone Sialoproteins in Vitamin D-Deficient <i>rBSP2.7Luc</i> Transgenic Mice. <i>Journal of Bone and Mineral Research</i> , 1999, 14, 221-229.	2.8	33
47	C2Maps: a network pharmacology database with comprehensive disease-gene-drug connectivity relationships. <i>BMC Genomics</i> , 2012, 13, S17.	2.8	33
48	Oracle Database 10g: a platform for BLAST search and Regular Expression pattern matching in life sciences. <i>Nucleic Acids Research</i> , 2004, 33, D675-D679.	14.5	32
49	Proteomic Characterization Reveals That MMP-3 Correlates With Bronchiolitis Obliterans Syndrome Following Allogeneic Hematopoietic Cell and Lung Transplantation. <i>American Journal of Transplantation</i> , 2016, 16, 2342-2351.	4.7	32
50	A systematic simulation-based meta-analytical framework for prediction of physiological biomarkers in alopecia. <i>Journal of Biological Research</i> , 2019, 26, 2.	2.1	31
51	Adiponectin Ameliorates Experimental Periodontitis in Diet-Induced Obesity Mice. <i>PLoS ONE</i> , 2014, 9, e97824.	2.5	31
52	ProteoLens: a visual analytic tool for multi-scale database-driven biological network data mining. <i>BMC Bioinformatics</i> , 2008, 9, S5.	2.6	30
53	Bone Tissue Regeneration - Application of Mesenchymal Stem Cells and Cellular and Molecular Mechanisms. <i>Current Stem Cell Research and Therapy</i> , 2017, 12, 357-364.	1.3	30
54	Discovery of pathway biomarkers from coupled proteomics and systems biology methods. <i>BMC Genomics</i> , 2010, 11, S12.	2.8	28

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55	Prioritizing drug targets in <i>Clostridium botulinum</i> with a computational systems biology approach. <i>Genomics</i> , 2014, 104, 24-35.	2.9	27
56	Computational Analysis of Drought Stress-Associated miRNAs and miRNA Co-Regulation Network in <i>Physcomitrella patens</i> . <i>Genomics, Proteomics and Bioinformatics</i> , 2011, 9, 37-44.	6.9	26
57	New threats to health data privacy. <i>BMC Bioinformatics</i> , 2011, 12, S7.	2.6	25
58	Repositioning drugs by targeting network modules: a Parkinson's disease case study. <i>BMC Bioinformatics</i> , 2017, 18, 532.	2.6	25
59	MicroRNA Expression Profiling of Human Respiratory Epithelium Affected by Invasive <i>Candida</i> Infection. <i>PLoS ONE</i> , 2015, 10, e0136454.	2.5	23
60	An integrated proteomics analysis of bone tissues in response to mechanical stimulation. <i>BMC Systems Biology</i> , 2011, 5, S7.	3.0	22
61	Epigenetically Modified Bone Marrow Stromal Cells in Silk Scaffolds Promote Craniofacial Bone Repair and Wound Healing. <i>Tissue Engineering - Part A</i> , 2015, 21, 2156-2165.	3.1	22
62	Potential roles of miR-335-5p on pathogenesis of experimental periodontitis. <i>Journal of Periodontal Research</i> , 2020, 55, 191-198.	2.7	22
63	Identification and characterization of a novel adiponectin receptor agonist adipo anti-inflammation agonist and its anti-inflammatory effects in vitro and in vivo. <i>British Journal of Pharmacology</i> , 2021, 178, 280-297.	5.4	22
64	Genomic data modeling. <i>Information Systems</i> , 2003, 28, 287-310.	3.6	21
65	PEPPI: a peptidomic database of human protein isoforms for proteomics experiments. <i>BMC Bioinformatics</i> , 2010, 11, S7.	2.6	21
66	PAGER: constructing PAGs and new PAG-PAG relationships for network biology. <i>Bioinformatics</i> , 2015, 31, i250-i257.	4.1	21
67	Dissecting the human plasma proteome and inflammatory response biomarkers. <i>Proteomics</i> , 2009, 9, 470-484.	2.2	20
68	Breast cancer subtyping from plasma proteins. <i>BMC Medical Genomics</i> , 2013, 6, S6.	1.5	20
69	Cellular Signaling Pathways in Insulin Resistance-Systems Biology Analyses of Microarray Dataset Reveals New Drug Target Gene Signatures of Type 2 Diabetes Mellitus. <i>Frontiers in Physiology</i> , 2017, 8, 13.	2.8	20
70	Systems-Scale Analysis Reveals Pathways Involved in Cellular Response to Methamphetamine. <i>PLoS ONE</i> , 2011, 6, e18215.	2.5	20
71	A SYSTEMS BIOLOGY APPROACH TO THE STUDY OF CISPLATIN DRUG RESISTANCE IN OVARIAN CANCERS. <i>Journal of Bioinformatics and Computational Biology</i> , 2007, 05, 383-405.	0.8	19
72	HOMER: a human organ-specific molecular electronic repository. <i>BMC Bioinformatics</i> , 2011, 12, S4.	2.6	19

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73	Metabolic alterations mediated by STAT3 promotes drug persistence in CML. <i>Leukemia</i> , 2021, 35, 3371-3382.	7.2	19
74	Over-expression of bone sialoprotein enhances bone metastasis of human breast cancer cells in a mouse model. <i>International Journal of Oncology</i> , 2003, 23, 1043-8.	3.3	19
75	PAGED: a pathway and gene-set enrichment database to enable molecular phenotype discoveries. <i>BMC Bioinformatics</i> , 2012, 13, S2.	2.6	18
76	PAGER 2.0: an update to the pathway, annotated-list and gene-signature electronic repository for Human Network Biology. <i>Nucleic Acids Research</i> , 2018, 46, D668-D676.	14.5	18
77	A case study of integrating protein interaction data using semantic web technology. <i>International Journal of Bioinformatics Research and Applications</i> , 2007, 3, 286.	0.2	16
78	Autoregulation of bone sialoprotein gene in pre-osteoblastic and non-osteoblastic cells. <i>Biochemical and Biophysical Research Communications</i> , 2004, 316, 461-467.	2.1	15
79	Reordering based integrative expression profiling for microarray classification. <i>BMC Bioinformatics</i> , 2012, 13, S1.	2.6	15
80	A nonredundant role for T _H cell-derived interleukin 22 in antibacterial defense of colonic crypts. <i>Immunity</i> , 2022, 55, 494-511.e11.	14.3	15
81	An In Vivo Model to Study Osteogenic Gene Regulation: Targeting an Avian Retroviral Receptor (TVA) to Bone With the Bone Sialoprotein (BSP) Promoter. <i>Journal of Bone and Mineral Research</i> , 2005, 20, 1403-1413.	2.8	14
82	Bowmanâ€™s inhibitor affects pathways associated with energy metabolism in <i>Drosophila melanogaster</i> . <i>Insect Molecular Biology</i> , 2010, 19, 303-313.	2.0	14
83	Identifying the key regulators that promote cell-cycle activity in the hearts of early neonatal pigs after myocardial injury. <i>PLoS ONE</i> , 2020, 15, e0232963.	2.5	14
84	Roles and Mechanisms of Irisin in Attenuating Pathological Features of Osteoarthritis. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 703670.	3.7	14
85	The Periodontal Pathogen <i>Fusobacterium nucleatum</i> Exacerbates Alzheimerâ€™s Pathogenesis via Specific Pathways. <i>Frontiers in Aging Neuroscience</i> , 0, 14, .	3.4	14
86	Gsslasso Cox: a Bayesian hierarchical model for predicting survival and detecting associated genes by incorporating pathway information. <i>BMC Bioinformatics</i> , 2019, 20, 94.	2.6	13
87	A SYSTEMS BIOLOGY CASE STUDY OF OVARIAN CANCER DRUG RESISTANCE. , 2006, , .		13
88	Applications of transgenics in studies of bone sialoprotein. <i>Journal of Cellular Physiology</i> , 2009, 220, 30-34.	4.1	12
89	A neural network approach to multi-biomarker panel discovery by high-throughput plasma proteomics profiling of breast cancer. <i>BMC Proceedings</i> , 2013, 7, S10.	1.6	11
90	Association of CMV genomic mutations with symptomatic infection and hearing loss in congenital CMV infection. <i>BMC Infectious Diseases</i> , 2019, 19, 1046.	2.9	11

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91	IL-23 Promotes a Coordinated B Cell Germinal Center Program for Class-Switch Recombination to IgG2b in BXD2 Mice. <i>Journal of Immunology</i> , 2020, 205, 346-358.	0.8	11
92	Connecting Protein Interaction Data, Mutations, and Disease Using Bioinformatics. <i>Methods in Molecular Biology</i> , 2009, 541, 449-461.	0.9	11
93	Single Nucleus Transcriptomics: Apical Resection in Newborn Pigs Extends the Time Window of Cardiomyocyte Proliferation and Myocardial Regeneration. <i>Circulation</i> , 2022, 145, 1744-1747.	1.6	11
94	Data mining in protein interactomics. <i>IEEE Engineering in Medicine and Biology Magazine</i> , 2005, 24, 95-102.	0.8	10
95	Network Medicine: Finding the Links to Personalized Therapy. <i>Clinical Pharmacology and Therapeutics</i> , 2013, 94, 613-616.	4.7	10
96	A method for identifying discriminative isoform-specific peptides for clinical proteomics application. <i>BMC Genomics</i> , 2016, 17, 522.	2.8	10
97	A GMM-IG framework for selecting genes as expression panel biomarkers. <i>Artificial Intelligence in Medicine</i> , 2010, 48, 75-82.	6.5	9
98	Integrative Approaches to Understanding the Pathogenic Role of Genetic Variation in Rheumatic Diseases. <i>Rheumatic Disease Clinics of North America</i> , 2017, 43, 449-466.	1.9	9
99	AdipoRon promotes diabetic fracture repair through endochondral ossification-based bone repair by enhancing survival and differentiation of chondrocytes. <i>Experimental Cell Research</i> , 2020, 387, 111757.	2.6	9
100	Systems biology visualization tools for drug target discovery. <i>Expert Opinion on Drug Discovery</i> , 2010, 5, 425-439.	5.0	8
101	PAGER-CoV: a comprehensive collection of pathways, annotated gene-lists and gene signatures for coronavirus disease studies. <i>Nucleic Acids Research</i> , 2021, 49, D589-D599.	14.5	8
102	A novel adiponectin receptor agonist (AdipoAI) ameliorates type 2 diabetes-associated periodontitis by enhancing autophagy in osteoclasts. <i>Journal of Periodontal Research</i> , 2022, 57, 381-391.	2.7	8
103	A systems biology case study of ovarian cancer drug resistance. <i>Computational Systems Bioinformatics / Life Sciences Society Computational Systems Bioinformatics Conference</i> , 2006, , 389-98.	0.4	8
104	Molecular Interaction Networks: Topological and Functional Characterizations. , 0, , 145-174.		7
105	Finding fractal patterns in molecular interaction networks: a case study in Alzheimer's disease. <i>International Journal of Computational Biology and Drug Design</i> , 2009, 2, 340.	0.3	7
106	Gene Terrain: Visual Exploration of Differential Gene Expression Profiles Organized in Native Biomolecular Interaction Networks. <i>Information Visualization</i> , 2010, 9, 1-12.	1.9	7
107	Disease gene-fishing in molecular interaction networks: A case study in colorectal cancer. , 2009, 2009, 6416-9.		6
108	Data Mining Methods in Omics-Based Biomarker Discovery. <i>Methods in Molecular Biology</i> , 2011, 719, 511-526.	0.9	6

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109	Simulation Study of cDNA Dataset to Investigate Possible Association of Differentially Expressed Genes of Human THP1-Monocytic Cells in Cancer Progression Affected by Bacterial Shiga Toxins. <i>Frontiers in Microbiology</i> , 2018, 9, 380.	3.5	6
110	A new approach to construct pathway connected networks and its application in dose responsive gene expression profiles of rat liver regulated by 2,4DNT. <i>BMC Genomics</i> , 2010, 11, S4.	2.8	5
111	Discovering breast cancer drug candidates from biomedical literature. <i>International Journal of Data Mining and Bioinformatics</i> , 2010, 4, 241.	0.1	5
112	Experimental investigation on pressure fluctuation of cryogenic liquid transport in pitching motion. <i>Cryogenics</i> , 2012, 52, 530-537.	1.7	5
113	Seed-weighted random walk ranking for cancer biomarker prioritisation: a case study in leukaemia. <i>International Journal of Data Mining and Bioinformatics</i> , 2014, 9, 135.	0.1	5
114	BEERE: a web server for biomedical entity expansion, ranking and explorations. <i>Nucleic Acids Research</i> , 2019, 47, W578-W586.	14.5	5
115	Network topological reordering revealing systemic patterns in yeast protein interaction networks. , 2009, 2009, 6954-7.		4
116	Data Mining in Bioinformatics: Selected Papers from BIODDD. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2010, 7, 195-196.	3.0	4
117	Predicting drug efficacy based on the integrated breast cancer pathway model. , 2011, , .		4
118	WIPER: Weighted in-Path Edge Ranking for biomolecular association networks. <i>Quantitative Biology</i> , 2019, 7, 313-326.	0.5	4
119	Central adiponectin induces trabecular bone mass partly through epigenetic downregulation of cannabinoid receptor CB1. <i>Journal of Cellular Physiology</i> , 2019, 234, 7062-7069.	4.1	4
120	Initial large-scale exploration of protein-protein interactions in human brain. <i>Proceedings</i> , 2003, 2, 229-34.	0.1	4
121	A statistical framework to discover true associations from multiprotein complex pull-down proteomics data sets. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 64, 436-443.	2.6	3
122	Biological Knowledge Discovery and Data Mining. <i>Scientific Programming</i> , 2012, 20, 1-2.	0.7	3
123	Predictive and preventive models for diabetes prevention using clinical information in electronic health record. , 2015, , .		3
124	Osteogenic effects of microRNA-335-5p/lipidoid nanoparticles coated on titanium surface. <i>Archives of Oral Biology</i> , 2021, 129, 105207.	1.8	3
125	Characterization and analysis of long non-coding rna (lncRNA) in In Vitro- and Ex Vivo-derived cardiac progenitor cells. <i>PLoS ONE</i> , 2017, 12, e0180096.	2.5	3
126	A Network Biology Approach to Predicting Drug Cardiotoxicity. , 2011, , .		2

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127	An evaluation for merging signaling pathways by using protein-protein interaction data. , 2012, , .		2
128	Multi-biomarker panel selection on a GPU. , 2012, , .		2
129	Multiscale and Multimodal Analysis for Computational Biology. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1951-1952.	3.0	2
130	“Super Gene Set” Causal Relationship Discovery from Functional Genomics Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1991-1998.	3.0	2
131	Graft-Versus-Host Disease “Free Antitumoral Signature After Allogeneic Donor Lymphocyte Injection Identified by Proteomics and Systems Biology. JCO Precision Oncology, 2019, 3, 1-11.	3.0	2
132	Scalable De Novo Genome Assembly Using a Pregel-Like Graph-Parallel System. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 731-744.	3.0	2
133	Linking clinotypes to phenotypes and genotypes from laboratory test results in comprehensive physical exams. BMC Medical Informatics and Decision Making, 2021, 21, 51.	3.0	2
134	Network expansion and pathway enrichment analysis towards biologically significant findings from microarrays. Journal of Integrative Bioinformatics, 2012, 9, 213.	1.5	2
135	Ethics and Privacy Considerations for Systems Biology Applications in Predictive and Personalized Medicine. , 2011, , 1-27.		2
136	PAGER Web APP: An Interactive, Online Gene Set and Network Interpretation Tool for Functional Genomics. Frontiers in Genetics, 2022, 13, 820361.	2.3	2
137	Identification and Characterization of a Novel Long Noncoding RNA that Regulates Osteogenesis in Diet-Induced Obesity Mice. Frontiers in Cell and Developmental Biology, 2022, 10, 832460.	3.7	2
138	Gene Selection using the GMM-IG Framework based Integrative Analysis. , 2008, , .		1
139	A neural network approach to multi-biomarker panel development based on LC/MS/MS proteomics profiles: A case study in breast cancer. , 2009, , .		1
140	Personal genome privacy protection with feature-based hierarchical dual-stage encryption. , 2011, , .		1
141	Network Expansion and Pathway Enrichment Analysis towards Biologically Significant Findings from Microarrays. Journal of Integrative Bioinformatics, 2012, 9, 113-125.	1.5	1
142	SLDR: a computational technique to identify novel genetic regulatory relationships. BMC Bioinformatics, 2014, 15, S1.	2.6	1
143	A method for developing regulatory gene set networks to characterize complex biological systems. BMC Genomics, 2015, 16, S4.	2.8	1
144	Knowledge Discovery Using Big Data in Biomedical Systems [Guest Editorial]. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 726-728.	3.0	1

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145	Towards constructing "Super Gene Sets" regulatory networks. , 2016, , .		1
146	DTMBIO 2016. , 2016, , .		1
147	Polyvalent therapeutic vaccine for type 2 diabetes mellitus: Immunoinformatics approach to study co-stimulation of cytokines and GLUT1 receptors. BMC Molecular and Cell Biology, 2020, 21, 56.	2.0	1
148	Guest Editorial for Selected Papers from BIOKDD 2018 and DMBIH 2018. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 1832-1834.	3.0	1
149	Statistical Enrichment Analysis of Samples: A General-Purpose Tool to Annotate Metadata Neighborhoods of Biological Samples. Frontiers in Big Data, 2021, 4, 725276.	2.9	1
150	Abstract P108: Identify Hypertension Risk from Health Exam Results. Hypertension, 2019, 74, .	2.7	1
151	Ethics and Privacy Considerations for Systems Biology Applications in Predictive and Personalized Medicine. , 0, , 1378-1404.		1
152	Polar Gini Curve: A Technique to Discover Gene Expression Spatial Patterns from Single-cell RNA-seq Data. Genomics, Proteomics and Bioinformatics, 2021, 19, 493-503.	6.9	1
153	INTRODUCTION. Journal of Bioinformatics and Computational Biology, 2008, 06, v-vi.	0.8	0
154	RIC: Ranking with Interaction Chains and Its Application in Computational Clinical Proteomics Studies. , 2009, , .		0
155	Data mining for biomarker discovery: The time is ripe. , 2009, , .		0
156	Seed-weighted random walks ranking method and its application to leukemia cancer biomarker prioritizations. , 2009, , .		0
157	Visualizing a Correlative Multi-level Graph of Biology Entity Interactions. , 2009, , .		0
158	Toward Ontology-Driven Omics Data Integration in Current Database Management Systems. , 2009, , .		0
159	Random walk ranking guided by disease association networks for lung cancer biomarker discovery. , 2010, , .		0
160	Breast cancer plasma protein biomarker discovery by coupling LC-MS/MS proteomics and systems biology. , 2010, , .		0
161	Towards a Metadata Model for Mass-Spectrometry Based Clinical Proteomics. Current Bioinformatics, 2012, 7, 246-254.	1.5	0
162	Constructing regulatory gene set networks to reveal novel insights into biological systems. , 2014, , .		0

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163	Empowering Team Science Across the Translational Spectrum with the UAB Biomedical Research Infrastructure Technology Enhancement (U-BRITE). , 2020, , .		0
164	Biological Network Mining. Methods in Molecular Biology, 2021, 2328, 139-151.	0.9	0
165	Guest Editorial for Selected Papers From BIOKDD 2019. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 809-810.	3.0	0
166	Design of an Online Physician-Mediated Personal Health Record System. Studies in Computational Intelligence, 2009, , 265-279.	0.9	0
167	Transplanted Bone Marrow Stromal Cells and Bone Tissue Regeneration. , 2013, , 22-43.		0
168	Computational Identification of De-Centric Genetic Regulatory Relationships from Functional Genomic Data. Lecture Notes in Computer Science, 2014, , 224-235.	1.3	0
169	Abstract 279: Long non-coding RNAs in glioblastoma tumor recurrence and therapy resistance. , 2020, , .		0
170	CBIO-12. THE ROLES OF lncRNAs IN GBM RADIATION RESISTANCE AND TUMOR RECURRENCE. Neuro-Oncology, 2020, 22, ii18-ii18.	1.2	0