Atul J Butte

List of Publications by Year in descending order

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202 papers	30,661 citations	11608 70 h-index	5519 163 g-index
211 all docs	211 docs citations	211 times ranked	48751 citing authors

#	Article	IF	Citations
1	xCell: digitally portraying the tissue cellular heterogeneity landscape. Genome Biology, 2017, 18, 220.	3.8	2,572
2	Reference-based analysis of lung single-cell sequencing reveals a transitional profibrotic macrophage. Nature Immunology, 2019, 20, 163-172.	7.0	2,330
3	Coordinated reduction of genes of oxidative metabolism in humans with insulin resistance and diabetes: Potential role ofPGC1andNRF1. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 8466-8471.	3.3	1,800
4	Scalable and accurate deep learning with electronic health records. Npj Digital Medicine, 2018, 1, 18.	5.7	1,440
5	Ten Years of Pathway Analysis: Current Approaches and Outstanding Challenges. PLoS Computational Biology, 2012, 8, e1002375.	1.5	1,267
6	Personal Omics Profiling Reveals Dynamic Molecular and Medical Phenotypes. Cell, 2012, 148, 1293-1307.	13.5	1,134
7	Systematic pan-cancer analysis of tumour purity. Nature Communications, 2015, 6, 8971.	5.8	937
8	Variation in the Human Immune System Is Largely Driven by Non-Heritable Influences. Cell, 2015, 160, 37-47.	13.5	828
9	ImmPort: disseminating data to the public for the future of immunology. Immunologic Research, 2014, 58, 234-239.	1.3	724
10	Discovery and Preclinical Validation of Drug Indications Using Compendia of Public Gene Expression Data. Science Translational Medicine, 2011, 3, 96ra77.	5.8	708
11	Clinical assessment incorporating a personal genome. Lancet, The, 2010, 375, 1525-1535.	6.3	637
12	Computational Repositioning of the Anticonvulsant Topiramate for Inflammatory Bowel Disease. Science Translational Medicine, 2011, 3, 96ra76.	5.8	534
13	ImmPort, toward repurposing of open access immunological assay data for translational and clinical research. Scientific Data, 2018, 5, 180015.	2.4	529
14	FoxO3 Regulates Neural Stem Cell Homeostasis. Cell Stem Cell, 2009, 5, 527-539.	5.2	526
15	An Environment-Wide Association Study (EWAS) on Type 2 Diabetes Mellitus. PLoS ONE, 2010, 5, e10746.	1.1	470
16	Performance comparison of exome DNA sequencing technologies. Nature Biotechnology, 2011, 29, 908-914.	9.4	464
17	Cell typeâ€“specific gene expression differences in complex tissues. Nature Methods, 2010, 7, 287-289.	9.0	460
18	A survey of current trends in computational drug repositioning. Briefings in Bioinformatics, 2016, 17, 2-12.	3.2	459

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19	Ethnic Differences in the Relationship Between Insulin Sensitivity and Insulin Response. Diabetes Care, 2013, 36, 1789-1796.	4.3	449
20	Exploiting drug-disease relationships for computational drug repositioning. Briefings in Bioinformatics, 2011, 12, 303-311.	3.2	448
21	Clinical Interpretation and Implications of Whole-Genome Sequencing. JAMA - Journal of the American Medical Association, 2014, 311, 1035.	3.8	398
22	A Drug Repositioning Approach Identifies Tricyclic Antidepressants as Inhibitors of Small Cell Lung Cancer and Other Neuroendocrine Tumors. Cancer Discovery, 2013, 3, 1364-1377.	7.7	366
23	SMYD3 links lysine methylation of MAP3K2 to Ras-driven cancer. Nature, 2014, 510, 283-287.	13.7	331
24	A longitudinal big data approach for precision health. Nature Medicine, 2019, 25, 792-804.	15.2	329
25	Network-Based Elucidation of Human Disease Similarities Reveals Common Functional Modules Enriched for Pluripotent Drug Targets. PLoS Computational Biology, 2010, 6, e1000662.	1.5	297
26	Performance comparison of whole-genome sequencing platforms. Nature Biotechnology, 2012, 30, 78-82.	9.4	281
27	Minimum information about clinical artificial intelligence modeling: the MI-CLAIM checklist. Nature Medicine, 2020, 26, 1320-1324.	15.2	262
28	Leveraging models of cell regulation and GWAS data in integrative network-based association studies. Nature Genetics, 2012, 44, 841-847.	9.4	252
29	MicroRNA Profiling of Human-Induced Pluripotent Stem Cells. Stem Cells and Development, 2009, 18, 749-757.	1.1	225
30	Challenges in the clinical application of whole-genome sequencing. Lancet, The, 2010, 375, 1749-1751.	6.3	207
31	Prediction of preadipocyte differentiation by gene expression reveals role of insulin receptor substrates and necdin. Nature Cell Biology, 2005, 7, 601-611.	4.6	202
32	A common rejection module (CRM) for acute rejection across multiple organs identifies novel therapeutics for organ transplantation. Journal of Experimental Medicine, 2013, 210, 2205-2221.	4.2	201
33	Mutations in NGLY1 cause an inherited disorder of the endoplasmic reticulumâ€“associated degradation pathway. Genetics in Medicine, 2014, 16, 751-758.	1.1	191
34	Creation and implications of a phenome-genome network. Nature Biotechnology, 2006, 24, 55-62.	9.4	190
35	Further defining housekeeping, or â€œmaintenance,â€•genes Focus on â€œA compendium of gene expression in normal human tissuesâ€• Physiological Genomics, 2001, 7, 95-96.	1.0	184
36	Sex Differences in Reported Pain Across 11,000 Patients Captured in Electronic Medical Records. Journal of Pain, 2012, 13, 228-234.	0.7	184

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37	Dynamic MicroRNA Expression Programs During Cardiac Differentiation of Human Embryonic Stem Cells. Circulation: Cardiovascular Genetics, 2010, 3, 426-435.	5.1	176
38	Genome-scale expression profiling of Hutchinson-Gilford progeria syndrome reveals widespread transcriptional misregulation leading to mesodermal/mesenchymal defects and accelerated atherosclerosis. Aging Cell, 2004, 3, 235-243.	3.0	171
39	A call for deep-learning healthcare. Nature Medicine, 2019, 25, 14-15.	15.2	161
40	Non-Synonymous and Synonymous Coding SNPs Show Similar Likelihood and Effect Size of Human Disease Association. PLoS ONE, 2010, 5, e13574.	1.1	157
41	Future cancer research priorities in the USA: a Lancet Oncology Commission. Lancet Oncology, The, 2017, 18, e653-e706.	5.1	153
42	Autoimmune Disease Classification by Inverse Association with SNP Alleles. PLoS Genetics, 2009, 5, e1000792.	1.5	151
43	Reversal of cancer gene expression correlates with drug efficacy and reveals therapeutic targets. Nature Communications, 2017, 8, 16022.	5.8	151
44	AILUN: reannotating gene expression data automatically. Nature Methods, 2007, 4, 879-879.	9.0	150
45	Evidence for benefit of statins to modify cognitive decline and risk in Alzheimerâ€™s disease. Alzheimer's Research and Therapy, 2017, 9, 10.	3.0	145
46	Expression-based genome-wide association study links the receptor CD44 in adipose tissue with type 2 diabetes. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 7049-7054.	3.3	144
47	Aging disrupts cell subpopulation dynamics and diminishes the function of mesenchymal stem cells. Scientific Reports, 2014, 4, 7144.	1.6	140
48	Hematopoietic Stem Cell Quiescence Is Maintained by Compound Contributions of the Retinoblastoma Gene Family. Cell Stem Cell, 2008, 3, 416-428.	5.2	139
49	Phased Whole-Genome Genetic Risk in a Family Quartet Using a Major Allele Reference Sequence. PLoS Genetics, 2011, 7, e1002280.	1.5	137
50	Assessment of a Deep Learning Model Based on Electronic Health Record Data to Forecast Clinical Outcomes in Patients With Rheumatoid Arthritis. JAMA Network Open, 2019, 2, e190606.	2.8	135
51	A Meta-analysis of Lung Cancer Gene Expression Identifies PTK7 as a Survival Gene in Lung Adenocarcinoma. Cancer Research, 2014, 74, 2892-2902.	0.4	131
52	Translational Bioinformatics: Coming of Age. Journal of the American Medical Informatics Association: JAMIA, 2008, 15, 709-714.	2.2	129
53	Robust meta-analysis of gene expression using the elastic net. Nucleic Acids Research, 2015, 43, e79-e79.	6.5	124
54	Systematic evaluation of environmental factors: persistent pollutants and nutrients correlated with serum lipid levels. International Journal of Epidemiology, 2012, 41, 828-843.	0.9	123

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55	A Nutrient-Wide Association Study on Blood Pressure. Circulation, 2012, 126, 2456-2464.	1.6	122
56	Expression of Complement Components Differs Between Kidney Allografts from Living and Deceased Donors. Journal of the American Society of Nephrology: JASN, 2009, 20, 1839-1851.	3.0	121
57	FoxO6 regulates memory consolidation and synaptic function. Genes and Development, 2012, 26, 2780-2801.	2.7	116
58	Type 2 Diabetes Risk Alleles Demonstrate Extreme Directional Differentiation among Human Populations, Compared to Other Diseases. PLoS Genetics, 2012, 8, e1002621.	1.5	106
59	Disease signatures are robust across tissues and experiments. Molecular Systems Biology, 2009, 5, 307.	3.2	101
60	Population Genetic Inference from Personal Genome Data: Impact of Ancestry and Admixture on Human Genomic Variation. American Journal of Human Genetics, 2012, 91, 660-671.	2.6	100
61	Identifying compartment-specific non-HLA targets after renal transplantation by integrating transcriptome and â€œantibodyomeâ€•measures. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 4148-4153.	3.3	98
62	Ontology-driven indexing of public datasets for translational bioinformatics. BMC Bioinformatics, 2009, 10, S1.	1.2	98
63	Systematic identification of interaction effects between genome- and environment-wide associations in type 2 diabetes mellitus. Human Genetics, 2013, 132, 495-508.	1.8	98
64	Progressive histological damage in renal allografts is associated with expression of innate and adaptive immunity genes. Kidney International, 2011, 80, 1364-1376.	2.6	96
65	Cross-Species Functional Analysis of Cancer-Associated Fibroblasts Identifies a Critical Role for CLCF1 and IL-6 in Nonâ€“Small Cell Lung Cancer In Vivo. Cancer Research, 2012, 72, 5744-5756.	0.4	96
66	PDX-MI: Minimal Information for Patient-Derived Tumor Xenograft Models. Cancer Research, 2017, 77, e62-e66.	0.4	92
67	Opportunities and challenges in using real-world data for health care. Journal of Clinical Investigation, 2020, 130, 565-574.	3.9	88
68	Widespread parainflammation in human cancer. Genome Biology, 2016, 17, 145.	3.8	87
69	Systematic functional regulatory assessment of disease-associated variants. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 9607-9612.	3.3	85
70	Computational Discovery of Niclosamide Ethanolamine, a Repurposed Drug Candidate That Reduces Growth of Hepatocellular Carcinoma Cells InÂVitro and in Mice by Inhibiting Cell Division Cycle 37 Signaling. Gastroenterology, 2017, 152, 2022-2036.	0.6	81
71	ZeitZeiger: supervised learning for high-dimensional data from an oscillatory system. Nucleic Acids Research, 2016, 44, e80-e80.	6.5	76
72	Translational bioinformatics in the cloud: an affordable alternative. Genome Medicine, 2010, 2, 51.	3.6	74

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73	Differentially Expressed RNA from Public Microarray Data Identifies Serum Protein Biomarkers for Cross-Organ Transplant Rejection and Other Conditions. PLoS Computational Biology, 2010, 6, e1000940.	1.5	72
74	FitSNPs: highly differentially expressed genes are more likely to have variants associated with disease. Genome Biology, 2008, 9, R170.	13.9	71
75	Whole-Exome Sequencing Reveals TopBP1 as a Novel Gene in Idiopathic Pulmonary Arterial Hypertension. American Journal of Respiratory and Critical Care Medicine, 2014, 189, 1260-1272.	2.5	70
76	The Case for Algorithmic Stewardship for Artificial Intelligence and Machine Learning Technologies. JAMA - Journal of the American Medical Association, 2020, 324, 1397.	3.8	69
77	Analysis of the Genetic Basis of Disease in the Context of Worldwide Human Relationships and Migration. PLoS Genetics, 2013, 9, e1003447.	1.5	67
78	Sex differences in disease risk from reported genome-wide association study findings. Human Genetics, 2012, 131, 353-364.	1.8	64
79	The receptor CD44 is associated with systemic insulin resistance and proinflammatory macrophages in human adipose tissue. Diabetologia, 2015, 58, 1579-1586.	2.9	64
80	Anti-CD44 Antibody Treatment Lowers Hyperglycemia and Improves Insulin Resistance, Adipose Inflammation, and Hepatic Steatosis in Diet-Induced Obese Mice. Diabetes, 2015, 64, 867-875.	0.3	62
81	Translational bioinformatics: linking knowledge across biological and clinical realms: Figure 1. Journal of the American Medical Informatics Association: JAMIA, 2011, 18, 354-357.	2.2	61
82	Drug Discovery in a Multidimensional World: Systems, Patterns, and Networks. Journal of Cardiovascular Translational Research, 2010, 3, 438-447.	1.1	59
83	Integrating multiple â€˜omicsâ€™ analyses identifies serological protein biomarkers for preeclampsia. BMC Medicine, 2013, 11, 236.	2.3	58
84	Disease Risk Factors Identified Through Shared Genetic Architecture and Electronic Medical Records. Science Translational Medicine, 2014, 6, 234ra57.	5.8	58
85	Diabetes Irreversibly Depletes Bone Marrowâ€“Derived Mesenchymal Progenitor Cell Subpopulations. Diabetes, 2014, 63, 3047-3056.	0.3	58
86	Collaborative Biomedicine in the Age of Big Data: The Case of Cancer. Journal of Medical Internet Research, 2014, 16, e101.	2.1	57
87	Relating hepatocellular carcinoma tumor samples and cell lines using gene expression data in translational research. BMC Medical Genomics, 2015, 8, S5.	0.7	56
88	Extreme Evolutionary Disparities Seen in Positive Selection across Seven Complex Diseases. PLoS ONE, 2010, 5, e12236.	1.1	55
89	Tissue- and age-specific changes in gene expression during disease induction and progression in NOD mice. Clinical Immunology, 2008, 129, 195-201.	1.4	53
90	Protein microarrays identify antibodies to protein kinase CÎ¶ that are associated with a greater risk of allograft loss in pediatric renal transplant recipients. Kidney International, 2009, 76, 1277-1283.	2.6	53

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91	Peptidomic Identification of Serum Peptides Diagnosing Preeclampsia. PLoS ONE, 2013, 8, e65571.	1.1	52
92	MetaCyto: A Tool for Automated Meta-analysis of Mass and Flow Cytometry Data. Cell Reports, 2018, 24, 1377-1388.	2.9	52
93	Evaluation and integration of 49 genome-wide experiments and the prediction of previously unknown obesity-related genes. Bioinformatics, 2007, 23, 2910-2917.	1.8	50
94	The Ultimate Model Organism. Science, 2008, 320, 325-327.	6.0	48
95	Are minor alleles more likely to be risk alleles?. BMC Medical Genomics, 2018, 11, 3.	0.7	48
96	ProfileChaser: searching microarray repositories based on genome-wide patterns of differential expression. Bioinformatics, 2011, 27, 3317-3318.	1.8	47
97	Personal Mutanomes Meet Modern Oncology Drug Discovery and Precision Health. Pharmacological Reviews, 2019, 71, 1-19.	7.1	47
98	Corticosteroid use is not associated with improved outcomes in acute exacerbation of IPF. Respirology, 2020, 25, 629-635.	1.3	47
99	Meta-Analysis of Vaginal Microbiome Data Provides New Insights Into Preterm Birth. Frontiers in Microbiology, 2020, 11, 476.	1.5	47
100	Whole genome sequencing in support of wellness and health maintenance. Genome Medicine, 2013, 5, 58.	3.6	46
101	Achieving high-sensitivity for clinical applications using augmented exome sequencing. Genome Medicine, 2015, 7, 71.	3.6	46
102	Microfluidic single-cell transcriptional analysis rationally identifies novel surface marker profiles to enhance cell-based therapies. Nature Communications, 2016, 7, 11945.	5.8	46
103	Solving Immunology?. Trends in Immunology, 2017, 38, 116-127.	2.9	45
104	A Quick Guide for Developing Effective Bioinformatics Programming Skills. PLoS Computational Biology, 2009, 5, e1000589.	1.5	44
105	Precision annotation of digital samples in NCBIâ€™s gene expression omnibus. Scientific Data, 2017, 4, 170125.	2.4	44
106	The "etiome": identification and clustering of human disease etiological factors. BMC Bioinformatics, 2009, 10, S14.	1.2	43
107	Repurpose terbutaline sulfate for amyotrophic lateral sclerosis using electronic medical records. Scientific Reports, 2015, 5, 8580.	1.6	43
108	Investigation of maternal environmental exposures in association with self-reported preterm birth. Reproductive Toxicology, 2014, 45, 1-7.	1.3	42

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109	Differential Phasing between Circadian Clocks in the Brain and Peripheral Organs in Humans. Journal of Biological Rhythms, 2016, 31, 588-597.	1.4	42
110	Time for NIH to lead on data sharing. Science, 2020, 367, 1308-1309.	6.0	42
111	Human genomic disease variants: A neutral evolutionary explanation. Genome Research, 2012, 22, 1383-1394.	2.4	41
112	The 10,000 Immunomes Project: Building a Resource for Human Immunology. Cell Reports, 2018, 25, 513-522.e3.	2.9	40
113	A robust and interpretable end-to-end deep learning model for cytometry data. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 21373-21380.	3.3	40
114	A Computational Model to Define the Molecular Causes of Type 2 Diabetes Mellitus. Diabetes Technology and Therapeutics, 2005, 7, 323-336.	2.4	39
115	Opening clinical trial data: are the voluntary data-sharing portals enough?. BMC Medicine, 2015, 13, 280.	2.3	38
116	Protected Health Information filter (Philter): accurately and securely de-identifying free-text clinical notes. Npj Digital Medicine, 2020, 3, 57.	5.7	38
117	Content-based microarray search using differential expression profiles. BMC Bioinformatics, 2010, 11, 603.	1.2	36
118	Heterogeneity in HIV and cellular transcription profiles in cell line models of latent and productive infection: implications for HIV latency. Retrovirology, 2019, 16, 32.	0.9	35
119	In silico and in vitro drug screening identifies new therapeutic approaches for Ewing sarcoma. Oncotarget, 2017, 8, 4079-4095.	0.8	34
120	Expression-Based Genome-Wide Association Study Links Vitamin Dâ€“Binding Protein With Autoantigenicity in Type 1 Diabetes. Diabetes, 2016, 65, 1341-1349.	0.3	33
121	Finding disease-related genomic experiments within an international repository: first steps in translational bioinformatics. AMIA ... Annual Symposium proceedings, 2006, , 106-10.	0.2	32
122	GeneChaser: Identifying all biological and clinical conditions in which genes of interest are differentially expressed. BMC Bioinformatics, 2008, 9, 548.	1.2	31
123	Organ Size Control Is Dominant over Rb Family Inactivation to Restrict Proliferation InÂVivo. Cell Reports, 2014, 8, 371-381.	2.9	30
124	Application of Machine Learning for Cytometry Data. Frontiers in Immunology, 2021, 12, 787574.	2.2	30
125	Sequencing and analysis of a South Asian-Indian personal genome. BMC Genomics, 2012, 13, 440.	1.2	29
126	Data-driven integration of epidemiological and toxicological data to select candidate interacting genes and environmental factors in association with disease. Bioinformatics, 2012, 28, i121-i126.	1.8	28

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127	PatientExploreR: an extensible application for dynamic visualization of patient clinical history from electronic health records in the OMOP common data model. Bioinformatics, 2019, 35, 4515-4518.	1.8	28
128	Likelihood ratios for genome medicine. Genome Medicine, 2010, 2, 30.	3.6	27
129	Constraints on Biological Mechanism from Disease Comorbidity Using Electronic Medical Records and Database of Genetic Variants. PLoS Computational Biology, 2016, 12, e1004885.	1.5	27
130	Protein Microarrays Discover Angiotensinogen and PRKRIP1 as Novel Targets for Autoantibodies in Chronic Renal Disease. Molecular and Cellular Proteomics, 2011, 10, M110.000497.	2.5	26
131	Identification of discriminating biomarkers for human disease using integrative network biology. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2009, , 27-38.	0.7	26
132	Robust prediction of clinical outcomes using cytometry data. Bioinformatics, 2019, 35, 1197-1203.	1.8	25
133	Characteristics of drug combination therapy in oncology by analyzing clinical trial data on ClinicalTrials.gov. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2015, , 68-79.	0.7	25
134	Comparing Ethnicity-Specific Reference Intervals for Clinical Laboratory Tests from EHR Data. journal of applied laboratory medicine, The, 2018, 3, 366-377.	0.6	24
135	Reanalysis of the Rituximab in ANCA-Associated Vasculitis trial identifies granulocyte subsets as a novel early marker of successful treatment. Arthritis Research and Therapy, 2015, 17, 262.	1.6	23
136	Use of machine learning in osteoarthritis research: a systematic literature review. RMD Open, 2022, 8, e001998.	1.8	23
137	Comparison of multiplex meta analysis techniques for understanding the acute rejection of solid organ transplants. BMC Bioinformatics, 2010, 11, S6.	1.2	20
138	Evolutionary Meta-Analysis of Association Studies Reveals Ancient Constraints Affecting Disease Marker Discovery. Molecular Biology and Evolution, 2012, 29, 2087-2094.	3.5	20
139	Digitally deconvolving the tumor microenvironment. Genome Biology, 2016, 17, 175.	3.8	20
140	Enabling integrative genomic analysis of high-impact human diseases through text mining. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2008, , 580-91.	0.7	20
141	Translational bioinformatics applications in genome medicine. Genome Medicine, 2009, 1, 64.	3.6	19
142	Predicting Inpatient Medication Orders From Electronic Health Record Data. Clinical Pharmacology and Therapeutics, 2020, 108, 145-154.	2.3	18
143	Human splice factors contribute to latent HIV infection in primary cell models and blood CD4+ T cells from ART-treated individuals. PLoS Pathogens, 2020, 16, e1009060.	2.1	18
144	A Classifier-based approach to identify genetic similarities between diseases. Bioinformatics, 2009, 25, i21-i29.	1.8	17

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145	Identification of Cell Surface Targets through Meta-analysis of Microarray Data. Neoplasia, 2012, 14, 666-669.	2.3	17
146	THE REFERENCE HUMAN GENOME DEMONSTRATES HIGH RISK OF TYPE 1 DIABETES AND OTHER DISORDERS. , 2010, , 231-242.		16
147	Computational prediction and experimental validation associating FABP-1 and pancreatic adenocarcinoma with diabetes. BMC Gastroenterology, 2011, 11, 5.	0.8	16
148	Big data opens a window onto wellness. Nature Biotechnology, 2017, 35, 720-721.	9.4	16
149	Open challenges in developing digital therapeutics in the United States. , 2022, 1, e0000008.		16
150	Novel integration of hospital electronic medical records and gene expression measurements to identify genetic markers of maturation. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2008, , 243-54.	0.7	15
151	Transmission Distortion in CrohnÊ¼s Disease Risk Gene ATG16L1 Leads to Sex Difference in Disease Association. Inflammatory Bowel Diseases, 2012, 18, 312-322.	0.9	14
152	Identification of Matrix Metalloproteinase-12 as a Candidate Molecule for Prevention and Treatment of Cardiometabolic Disease. Molecular Medicine, 2016, 22, 487-496.	1.9	14
153	Comparison of automated and human assignment of MeSH terms on publicly-available molecular datasets. Journal of Biomedical Informatics, 2011, 44, S39-S43.	2.5	13
154	Computationally translating molecular discoveries into tools for medicine: translational bioinformatics articles now featured inJAMIA. Journal of the American Medical Informatics Association: JAMIA, 2011, 18, 352-353.	2.2	13
155	Making it personal: translational bioinformatics. Journal of the American Medical Informatics Association: JAMIA, 2013, 20, 595-596.	2.2	13
156	Dynamism in gene expression across multiple studies. Physiological Genomics, 2010, 40, 128-140.	1.0	12
157	Systematic evaluation of personal genome services for Japanese individuals. Journal of Human Genetics, 2013, 58, 734-741.	1.1	12
158	Cancer Cellâ€“Autonomous Parainflammation Mimics Immune Cell Infiltration. Cancer Research, 2017, 77, 3740-3744.	0.4	12
159	Risky Business: Meeting the Structural Needs of Transdisciplinary Science. Journal of Pediatrics, 2017, 191, 255-258.	0.9	11
160	ROMOP: a light-weight R package for interfacing with OMOP-formatted electronic health record data. JAMIA Open, 2019, 2, 10-14.	1.0	11
161	Integrative Approach to Pain Genetics Identifies Pain Sensitivity Loci across Diseases. PLoS Computational Biology, 2012, 8, e1002538.	1.5	10
162	Tracing diagnosis trajectories over millions of patients reveal an unexpected risk in schizophrenia. Scientific Data, 2019, 6, 201.	2.4	10

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163	Assessment of Postdonation Outcomes in US Living Kidney Donors Using Publicly Available Data Sets. JAMA Network Open, 2019, 2, e191851.	2.8	10
164	Closing the Evidence Gap in Interstitial Lung Disease. The Promise of Real-World Data. American Journal of Respiratory and Critical Care Medicine, 2019, 199, 1061-1065.	2.5	10
165	Big Data in Nephrology. Nature Reviews Nephrology, 2021, 17, 676-687.	4.1	10
166	Towards a cytokine-cell interaction knowledgebase of the adaptive immune system. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2009, , 439-50.	0.7	10
167	Accuracy of medical billing data against the electronic health record in the measurement of colorectal cancer screening rates. BMJ Open Quality, 2020, 9, e000856.	0.4	9
168	Enabling precision medicine in neonatology, an integrated repository for preterm birth research. Scientific Data, 2018, 5, 180219.	2.4	9
169	Current methodologies for translational bioinformatics. Journal of Biomedical Informatics, 2010, 43, 355-357.	2.5	8
170	The role of bioinformatics in studying rheumatic and autoimmune disorders. Nature Reviews Rheumatology, 2011, 7, 489-494.	3.5	8
171	Gene expression deconvolution in linear space. Nature Methods, 2012, 9, 9-9.	9.0	8
172	RImmPort: an R/Bioconductor package that enables ready-for-analysis immunology research data. Bioinformatics, 2017, 33, 1101-1103.	1.8	8
173	Clinical arrays of laboratory measures, or "clinarrays", built from an electronic health record enable disease subtyping by severity. AMIA ... Annual Symposium proceedings, 2007, , 115-9.	0.2	8
174	Infection in the intensive care unit alters physiological networks. BMC Bioinformatics, 2009, 10, S4.	1.2	7
175	Biomarker and Drug Discovery for Gastroenterology Through Translational Bioinformatics. Gastroenterology, 2010, 139, 735-741.e1.	0.6	7
176	ImmPort: Shared research data for bioinformatics and immunology. , 2015, , .		7
177	Open data informatics and data repurposing for IBD. Nature Reviews Gastroenterology and Hepatology, 2018, 15, 715-716.	8.2	7
178	Clinical assessment incorporating a personal genome â€“ Authors' reply. Lancet, The, 2010, 376, 869-870.	6.3	6
179	Altering physiological networks using drugs: steps towards personalized physiology. BMC Medical Genomics, 2013, 6, S7.	0.7	6
180	Trials and Tribulationsâ€”11 Reasons Why We Need to Promote Clinical Trials Data Sharing. JAMA Network Open, 2021, 4, e2035043.	2.8	6

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181	Rethinking PICO in the Machine Learning Era: ML-PICO. Applied Clinical Informatics, 2021, 12, 407-416.	0.8	6
182	DO CANCER CLINICAL TRIAL POPULATIONS TRULY REPRESENT CANCER PATIENTS? A COMPARISON OF OPEN CLINICAL TRIALS TO THE CANCER GENOME ATLAS. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2016, 21, 309-20.	0.7	6
183	Systematic identification of risk factors for Alzheimer's disease through shared genetic architecture and electronic medical records. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2013, , 224-35.	0.7	6
184	Topics in Neonatal Informatics. NeoReviews, 2012, 13, e281-e284.	0.4	5
185	Database integration of 4923 publicly-available samples of breast cancer molecular and clinical data. AMIA Summits on Translational Science Proceedings, 2013, 2013, 138-42.	0.4	5
186	Translational Bioinformatics for Genomic Medicine. , 2013, , 272-286.		4
187	It takes a genome to understand a village: Population scale precision medicine. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 12344-12346.	3.3	4
188	PGAGENE: integrating quantitative gene-specific results from the NHLBI Programs for Genomic Applications. Bioinformatics, 2003, 19, 778-779.	1.8	3
189	Genetic analysis in a patient with nine primary malignant neoplasms: A rare case of Li-Fraumeni syndrome. Oncology Reports, 2016, 35, 1519-1528.	1.2	3
190	Immune modulators in disease: integrating knowledge from the biomedical literature and gene expression. Journal of the American Medical Informatics Association: JAMIA, 2016, 23, 617-626.	2.2	3
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