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	Open challenges in developing digital therapeutics in the United States. , 2022, 1, e0000008.		16
2	Use of machine learning in osteoarthritis research: a systematic literature review. RMD Open, 2022, 8, e001998.	1.8	23
3	Trials and Tribulationsâ€"11 Reasons Why We Need to Promote Clinical Trials Data Sharing. JAMA Network Open, 2021, 4, e2035043.	2.8	6
4	Algorithmic Stewardship in Health Careâ€"Reply. JAMA - Journal of the American Medical Association, 2021, 325, 588.	3.8	2
5	Rethinking PICO in the Machine Learning Era: ML-PICO. Applied Clinical Informatics, 2021, 12, 407-416.	0.8	6
6	Opportunities and Challenges in Democratizing Immunology Datasets. Frontiers in Immunology, 2021, 12, 647536.	2.2	2
7	Big Data in Nephrology. Nature Reviews Nephrology, 2021, 17, 676-687.	4.1	10
8	Five-year pediatric use of a digital wearable fitness device: lessons from a pilot case study. JAMIA Open, 2021, 4, ooab054.	1.0	2
9	Application of Machine Learning for Cytometry Data. Frontiers in Immunology, 2021, 12, 787574.	2.2	30
10	Corticosteroid use is not associated with improved outcomes in acute exacerbation of IPF. Respirology, 2020, 25, 629-635.	1.3	47
11	Protected Health Information filter (Philter): accurately and securely de-identifying free-text clinical notes. Npj Digital Medicine, 2020, 3, 57.	5.7	38
12	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
13	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
14	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
15	Minimum information about clinical artificial intelligence modeling: the MI-CLAIM checklist. Nature Medicine, 2020, 26, 1320-1324.	15.2	262
16	Predicting Inpatient Medication Orders From Electronic Health Record Data. Clinical Pharmacology and Therapeutics, 2020, 108, 145-154.	2.3	18
17	Time for NIH to lead on data sharing. Science, 2020, 367, 1308-1309.	6.0	42
18	Meta-Analysis of Vaginal Microbiome Data Provides New Insights Into Preterm Birth. Frontiers in Microbiology, 2020, 11, 476.	1.5	47

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19	Opportunities and challenges in using real-world data for health care. Journal of Clinical Investigation, 2020, 130, 565-574.	3.9	88
20	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
21	Tracing diagnosis trajectories over millions of patients reveal an unexpected risk in schizophrenia. Scientific Data, 2019, 6, 201.	2.4	10
22	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
23	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
24	A longitudinal big data approach for precision health. Nature Medicine, 2019, 25, 792-804.	15.2	329
25	ROMOP: a light-weight R package for interfacing with OMOP-formatted electronic health record data. JAMIA Open, 2019, 2, 10-14.	1.0	11
26	Assessment of Postdonation Outcomes in US Living Kidney Donors Using Publicly Available Data Sets. JAMA Network Open, 2019, 2, e191851.	2.8	10
27	A pilot study showing a stronger H1N1 influenza vaccination response during pregnancy in women who subsequently deliver preterm. Journal of Reproductive Immunology, 2019, 132, 16-20.	0.8	3
28	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
29	Robust prediction of clinical outcomes using cytometry data. Bioinformatics, 2019, 35, 1197-1203.	1.8	25
30	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
31	A call for deep-learning healthcare. Nature Medicine, 2019, 25, 14-15.	15.2	161
32	Reference-based analysis of lung single-cell sequencing reveals a transitional profibrotic macrophage. Nature Immunology, 2019, 20, 163-172.	7.0	2,330
33	Personal Mutanomes Meet Modern Oncology Drug Discovery and Precision Health. Pharmacological Reviews, 2019, 71, 1-19.	7.1	47
34	ImmPort, toward repurposing of open access immunological assay data for translational and clinical research. Scientific Data, 2018, 5, 180015.	2.4	529
35	The 10,000 Immunomes Project: Building a Resource for Human Immunology. Cell Reports, 2018, 25, 513-522.e3.	2.9	40
36	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

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37	Open data informatics and data repurposing for IBD. Nature Reviews Gastroenterology and Hepatology, 2018, 15, 715-716.	8.2	7
38	MetaCyto: A Tool for Automated Meta-analysis of Mass and Flow Cytometry Data. Cell Reports, 2018, 24, 1377-1388.	2.9	52
39	Scalable and accurate deep learning with electronic health records. Npj Digital Medicine, 2018, 1, 18.	5.7	1,440
40	Are minor alleles more likely to be risk alleles?. BMC Medical Genomics, 2018, 11, 3.	0.7	48
41	Enabling precision medicine in neonatology, an integrated repository for preterm birth research. Scientific Data, 2018, 5, 180219.	2.4	9
42	RImmPort: an R/Bioconductor package that enables ready-for-analysis immunology research data. Bioinformatics, 2017, 33, 1101-1103.	1.8	8
43	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
44	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
45	Solving Immunology?. Trends in Immunology, 2017, 38, 116-127.	2.9	45
46	Future cancer research priorities in the USA: a Lancet Oncology Commission. Lancet Oncology, The, 2017, 18, e653-e706.	5.1	153
47	PDX-MI: Minimal Information for Patient-Derived Tumor Xenograft Models. Cancer Research, 2017, 77, e62-e66.	0.4	92
48	Precision annotation of digital samples in NCBIâ€™s gene expression omnibus. Scientific Data, 2017, 4, 170125.	2.4	44
49	Big data opens a window onto wellness. Nature Biotechnology, 2017, 35, 720-721.	9.4	16
50	Reversal of cancer gene expression correlates with drug efficacy and reveals therapeutic targets. Nature Communications, 2017, 8, 16022.	5.8	151
51	Cancer Cellâ€“Autonomous Parainflammation Mimics Immune Cell Infiltration. Cancer Research, 2017, 77, 3740-3744.	0.4	12
52	Risky Business: Meeting the Structural Needs of Transdisciplinary Science. Journal of Pediatrics, 2017, 191, 255-258.	0.9	11
53	xCell: digitally portraying the tissue cellular heterogeneity landscape. Genome Biology, 2017, 18, 220.	3.8	2,572
54	In silico and in vitro drug screening identifies new therapeutic approaches for Ewing sarcoma. Oncotarget, 2017, 8, 4079-4095.	0.8	34

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55	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
56	Widespread parainflammation in human cancer. Genome Biology, 2016, 17, 145.	3.8	87
57	Digitally deconvolving the tumor microenvironment. Genome Biology, 2016, 17, 175.	3.8	20
58	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
59	ZeitZeiger: supervised learning for high-dimensional data from an oscillatory system. Nucleic Acids Research, 2016, 44, e80-e80.	6.5	76
60	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
61	Differential Phasing between Circadian Clocks in the Brain and Peripheral Organs in Humans. Journal of Biological Rhythms, 2016, 31, 588-597.	1.4	42
62	Microfluidic single-cell transcriptional analysis rationally identifies novel surface marker profiles to enhance cell-based therapies. Nature Communications, 2016, 7, 11945.	5.8	46
63	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
64	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
65	A survey of current trends in computational drug repositioning. Briefings in Bioinformatics, 2016, 17, 2-12.	3.2	459
66	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
67	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
68	Opening clinical trial data: are the voluntary data-sharing portals enough?. BMC Medicine, 2015, 13, 280.	2.3	38
69	Repurpose terbutaline sulfate for amyotrophic lateral sclerosis using electronic medical records. Scientific Reports, 2015, 5, 8580.	1.6	43
70	Relating hepatocellular carcinoma tumor samples and cell lines using gene expression data in translational research. BMC Medical Genomics, 2015, 8, S5.	0.7	56
71	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
72	Systematic pan-cancer analysis of tumour purity. Nature Communications, 2015, 6, 8971.	5.8	937

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73	ImmPort: Shared research data for bioinformatics and immunology. , 2015, , .		7
74	Variation in the Human Immune System Is Largely Driven by Non-Heritable Influences. Cell, 2015, 160, 37-47.	13.5	828
75	The receptor CD44 is associated with systemic insulin resistance and proinflammatory macrophages in human adipose tissue. Diabetologia, 2015, 58, 1579-1586.	2.9	64
76	Robust meta-analysis of gene expression using the elastic net. Nucleic Acids Research, 2015, 43, e79-e79.	6.5	124
77	Achieving high-sensitivity for clinical applications using augmented exome sequencing. Genome Medicine, 2015, 7, 71.	3.6	46
78	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
79	A systematic assessment of linking gene expression with genetic variants for prioritizing candidate targets. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2015, , 383-94.	0.7	2
80	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
81	Disease Risk Factors Identified Through Shared Genetic Architecture and Electronic Medical Records. Science Translational Medicine, 2014, 6, 234ra57.	5.8	58
82	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
83	RImmPort. , 2014, , .		1
84	Towards the characterization of normal peripheral immune cells with data from ImmPort. , 2014, , .		1
85	Clinical Interpretation and Implications of Whole-Genome Sequencing. JAMA - Journal of the American Medical Association, 2014, 311, 1035.	3.8	398
86	Mutations in NGLY1 cause an inherited disorder of the endoplasmic reticulumâ€“associated degradation pathway. Genetics in Medicine, 2014, 16, 751-758.	1.1	191
87	Organ Size Control Is Dominant over Rb Family Inactivation to Restrict Proliferation InÂVivo. Cell Reports, 2014, 8, 371-381.	2.9	30
88	Diabetes Irreversibly Depletes Bone Marrowâ€“Derived Mesenchymal Progenitor Cell Subpopulations. Diabetes, 2014, 63, 3047-3056.	0.3	58
89	ImmPort: disseminating data to the public for the future of immunology. Immunologic Research, 2014, 58, 234-239.	1.3	724
90	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

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91	Investigation of maternal environmental exposures in association with self-reported preterm birth. Reproductive Toxicology, 2014, 45, 1-7.	1.3	42
92	SMYD3 links lysine methylation of MAP3K2 to Ras-driven cancer. Nature, 2014, 510, 283-287.	13.7	331
93	Aging disrupts cell subpopulation dynamics and diminishes the function of mesenchymal stem cells. Scientific Reports, 2014, 4, 7144.	1.6	140
94	Collaborative Biomedicine in the Age of Big Data: The Case of Cancer. Journal of Medical Internet Research, 2014, 16, e101.	2.1	57
95	Systematic identification of DNA variants associated with ultraviolet radiation using a novel Geographic-Wide Association Study (GeoWAS). BMC Medical Genetics, 2013, 14, 62.	2.1	2
96	Altering physiological networks using drugs: steps towards personalized physiology. BMC Medical Genomics, 2013, 6, S7.	0.7	6
97	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
98	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
99	Translational Bioinformatics for Genomic Medicine. , 2013, , 272-286.		4
100	Integrating multiple â€˜omicsâ€™ analyses identifies serological protein biomarkers for preeclampsia. BMC Medicine, 2013, 11, 236.	2.3	58
101	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
102	Making it personal: translational bioinformatics. Journal of the American Medical Informatics Association: JAMIA, 2013, 20, 595-596.	2.2	13
103	Analysis of the Genetic Basis of Disease in the Context of Worldwide Human Relationships and Migration. PLoS Genetics, 2013, 9, e1003447.	1.5	67
104	Systematic evaluation of personal genome services for Japanese individuals. Journal of Human Genetics, 2013, 58, 734-741.	1.1	12
105	Ethnic Differences in the Relationship Between Insulin Sensitivity and Insulin Response. Diabetes Care, 2013, 36, 1789-1796.	4.3	449
106	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
107	Whole genome sequencing in support of wellness and health maintenance. Genome Medicine, 2013, 5, 58.	3.6	46
108	Peptidomic Identification of Serum Peptides Diagnosing Preeclampsia. PLoS ONE, 2013, 8, e65571.	1.1	52

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109	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
110	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
111	Integrative Approach to Pain Genetics Identifies Pain Sensitivity Loci across Diseases. PLoS Computational Biology, 2012, 8, e1002538.	1.5	10
112	Topics in Neonatal Informatics. NeoReviews, 2012, 13, e281-e284.	0.4	5
113	Ten Years of Pathway Analysis: Current Approaches and Outstanding Challenges. PLoS Computational Biology, 2012, 8, e1002375.	1.5	1,267
114	Type 2 Diabetes Risk Alleles Demonstrate Extreme Directional Differentiation among Human Populations, Compared to Other Diseases. PLoS Genetics, 2012, 8, e1002621.	1.5	106
115	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
116	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
117	FoxO6 regulates memory consolidation and synaptic function. Genes and Development, 2012, 26, 2780-2801.	2.7	116
118	A Nutrient-Wide Association Study on Blood Pressure. Circulation, 2012, 126, 2456-2464.	1.6	122
119	Leveraging models of cell regulation and GWAS data in integrative network-based association studies. Nature Genetics, 2012, 44, 841-847.	9.4	252
120	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
121	Gene expression deconvolution in linear space. Nature Methods, 2012, 9, 9-9.	9.0	8
122	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
123	Sex Differences in Reported Pain Across 11,000 Patients Captured in Electronic Medical Records. Journal of Pain, 2012, 13, 228-234.	0.7	184
124	Personal Omics Profiling Reveals Dynamic Molecular and Medical Phenotypes. Cell, 2012, 148, 1293-1307.	13.5	1,134
125	Evolutionary Meta-Analysis of Association Studies Reveals Ancient Constraints Affecting Disease Marker Discovery. Molecular Biology and Evolution, 2012, 29, 2087-2094.	3.5	20
126	Sequencing and analysis of a South Asian-Indian personal genome. BMC Genomics, 2012, 13, 440.	1.2	29

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127	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
128	Identification of Cell Surface Targets through Meta-analysis of Microarray Data. Neoplasia, 2012, 14, 666-669.	2.3	17
129	Performance comparison of whole-genome sequencing platforms. Nature Biotechnology, 2012, 30, 78-82.	9.4	281
130	Human genomic disease variants: A neutral evolutionary explanation. Genome Research, 2012, 22, 1383-1394.	2.4	41
131	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
132	Sex differences in disease risk from reported genome-wide association study findings. Human Genetics, 2012, 131, 353-364.	1.8	64
133	Quantifying multi-ethnic representation in genetic studies of high mortality diseases. AMIA Summits on Translational Science Proceedings, 2012, 2012, 11-8.	0.4	1
134	The role of bioinformatics in studying rheumatic and autoimmune disorders. Nature Reviews Rheumatology, 2011, 7, 489-494.	3.5	8
135	Exploiting drug-disease relationships for computational drug repositioning. Briefings in Bioinformatics, 2011, 12, 303-311.	3.2	448
136	Discovery and Preclinical Validation of Drug Indications Using Compendia of Public Gene Expression Data. Science Translational Medicine, 2011, 3, 96ra77.	5.8	708
137	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
138	Performance comparison of exome DNA sequencing technologies. Nature Biotechnology, 2011, 29, 908-914.	9.4	464
139	Personalized Medicine and Cardiovascular Disease: From Genome to Bedside. Current Cardiovascular Risk Reports, 2011, 5, 542-551.	0.8	1
140	Computational prediction and experimental validation associating FABP-1 and pancreatic adenocarcinoma with diabetes. BMC Gastroenterology, 2011, 11, 5.	0.8	16
141	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
142	Phased Whole-Genome Genetic Risk in a Family Quartet Using a Major Allele Reference Sequence. PLoS Genetics, 2011, 7, e1002280.	1.5	137
143	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
144	ProfileChaser: searching microarray repositories based on genome-wide patterns of differential expression. Bioinformatics, 2011, 27, 3317-3318.	1.8	47

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145	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
146	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
147	Computational Repositioning of the Anticonvulsant Topiramate for Inflammatory Bowel Disease. Science Translational Medicine, 2011, 3, 96ra76.	5.8	534
148	THE REFERENCE HUMAN GENOME DEMONSTRATES HIGH RISK OF TYPE 1 DIABETES AND OTHER DISORDERS. , 2010, , 231-242.		16
149	Drug Discovery in a Multidimensional World: Systems, Patterns, and Networks. Journal of Cardiovascular Translational Research, 2010, 3, 438-447.	1.1	59
150	Content-based microarray search using differential expression profiles. BMC Bioinformatics, 2010, 11, 603.	1.2	36
151	Comparison of multiplex meta analysis techniques for understanding the acute rejection of solid organ transplants. BMC Bioinformatics, 2010, 11, S6.	1.2	20
152	Current methodologies for translational bioinformatics. Journal of Biomedical Informatics, 2010, 43, 355-357.	2.5	8
153	Cell typeâ€“specific gene expression differences in complex tissues. Nature Methods, 2010, 7, 287-289.	9.0	460
154	Extreme Evolutionary Disparities Seen in Positive Selection across Seven Complex Diseases. PLoS ONE, 2010, 5, e12236.	1.1	55
155	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
156	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
157	Biomarker and Drug Discovery for Gastroenterology Through Translational Bioinformatics. Gastroenterology, 2010, 139, 735-741.e1.	0.6	7
158	Clinical assessment incorporating a personal genome. Lancet, The, 2010, 375, 1525-1535.	6.3	637
159	Challenges in the clinical application of whole-genome sequencing. Lancet, The, 2010, 375, 1749-1751.	6.3	207
160	Clinical assessment incorporating a personal genome â€“ Authors' reply. Lancet, The, 2010, 376, 869-870.	6.3	6
161	Bioinformatic and Computational Analysis for Genomic Medicine. , 2010, , 111-130.		0
162	Dynamic MicroRNA Expression Programs During Cardiac Differentiation of Human Embryonic Stem Cells. Circulation: Cardiovascular Genetics, 2010, 3, 426-435.	5.1	176

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163	Translational bioinformatics in the cloud: an affordable alternative. Genome Medicine, 2010, 2, 51.	3.6	74
164	Likelihood ratios for genome medicine. Genome Medicine, 2010, 2, 30.	3.6	27
165	Dynamism in gene expression across multiple studies. Physiological Genomics, 2010, 40, 128-140.	1.0	12
166	An Environment-Wide Association Study (EWAS) on Type 2 Diabetes Mellitus. PLoS ONE, 2010, 5, e10746.	1.1	470
167	Non-Synonymous and Synonymous Coding SNPs Show Similar Likelihood and Effect Size of Human Disease Association. PLoS ONE, 2010, 5, e13574.	1.1	157
168	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
169	Disease signatures are robust across tissues and experiments. Molecular Systems Biology, 2009, 5, 307.	3.2	101
170	A Quick Guide for Developing Effective Bioinformatics Programming Skills. PLoS Computational Biology, 2009, 5, e1000589.	1.5	44
171	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
172	Autoimmune Disease Classification by Inverse Association with SNP Alleles. PLoS Genetics, 2009, 5, e1000792.	1.5	151
173	A Classifier-based approach to identify genetic similarities between diseases. Bioinformatics, 2009, 25, i21-i29.	1.8	17
174	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
175	Ontology-driven indexing of public datasets for translational bioinformatics. BMC Bioinformatics, 2009, 10, S1.	1.2	98
176	The "etiome": identification and clustering of human disease etiological factors. BMC Bioinformatics, 2009, 10, S14.	1.2	43
177	Infection in the intensive care unit alters physiological networks. BMC Bioinformatics, 2009, 10, S4.	1.2	7
178	FoxO3 Regulates Neural Stem Cell Homeostasis. Cell Stem Cell, 2009, 5, 527-539.	5.2	526
179	MicroRNA Profiling of Human-Induced Pluripotent Stem Cells. Stem Cells and Development, 2009, 18, 749-757.	1.1	225
180	Translational bioinformatics applications in genome medicine. Genome Medicine, 2009, 1, 64.	3.6	19

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181	Bioinformatic and Computational Analysis for Genomic Medicine. , 2009, , 206-225.		0
182	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
183	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
184	GeneChaser: Identifying all biological and clinical conditions in which genes of interest are differentially expressed. BMC Bioinformatics, 2008, 9, 548.	1.2	31
185	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
186	FitSNPs: highly differentially expressed genes are more likely to have variants associated with disease. Genome Biology, 2008, 9, R170.	13.9	71
187	Hematopoietic Stem Cell Quiescence Is Maintained by Compound Contributions of the Retinoblastoma Gene Family. Cell Stem Cell, 2008, 3, 416-428.	5.2	139
188	Translational Bioinformatics: Coming of Age. Journal of the American Medical Informatics Association: JAMIA, 2008, 15, 709-714.	2.2	129
189	The Ultimate Model Organism. Science, 2008, 320, 325-327.	6.0	48
190	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
191	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
192	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
193	AILUN: reannotating gene expression data automatically. Nature Methods, 2007, 4, 879-879.	9.0	150
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