Joshua C Denny

List of Publications by Year
in descending order

426	34,591	4658	5829
papers	citations	85 h-index	161 g-index

467	467	467	40487
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	CYP2C19 Loss-of-Function Associated with First-Time Ischemic Stroke in Non-surgical Asymptomatic Carotid Artery Stenosis During Clopidogrel Therapy. Translational Stroke Research, 2022, 13, 46-55.	4.2	3
2	Antibodies to Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) in All of Us Research Program Participants, 2 January to 18 March 2020. Clinical Infectious Diseases, 2022, 74, 584-590.	5.8	26
3	Phenome-Wide Association Studies. JAMA - Journal of the American Medical Association, 2022, 327, 75.	7.4	41
4	Integrating gene expression and clinical data to identify drug repurposing candidates for hyperlipidemia and hypertension. Nature Communications, 2022, 13, 46.	12.8	19
5	OUP accepted manuscript. Bioinformatics, 2022, , .	4.1	1
6	Genetically predicted sex hormone levels and health outcomes: phenome-wide Mendelian randomization investigation. International Journal of Epidemiology, 2022, 51, 1931-1942.	1.9	19
7	Uterine fibroid polygenic risk score (PRS) associates and predicts risk for uterine fibroid. Human Genetics, 2022, 141, 1739-1748.	3.8	4
8	The reckoning: The return of genomic results to 1444 participants across the eMERGE3 Network. Genetics in Medicine, 2022, 24, 1130-1138.	2.4	12
9	Arrhythmia Variant Associations and Reclassifications in the eMERGE-III Sequencing Study. Circulation, 2022, 145, 877-891.	1.6	18
10	The U.S. National Library of Medicineâ€™s impact on precision and genomic medicine. Information Services and Use, 2022, , 1-10.	0.2	0
11	Association of Pathogenic Variants in Hereditary Cancer Genes With Multiple Diseases. JAMA Oncology, 2022, 8, 835.	7.1	25
12	Psychiatric manifestations of rare variation in medically actionable genes: a PheWAS approach. BMC Genomics, 2022, 23, 385.	2.8	1
13	Large-scale genomic analyses reveal insights into pleiotropy across circulatory system diseases and nervous system disorders. Nature Communications, 2022, 13, .	12.8	6
14	PheWAS-ME: a web-app for interactive exploration of multimorbidity patterns in PheWAS. Bioinformatics, 2021, 37, 1778-1780.	4.1	7
15	Real-time clinical note monitoring to detect conditions for rapid follow-up: A case study of clinical trial enrollment in drug-induced torsades de pointes and Stevens-Johnson syndrome. Journal of the American Medical Informatics Association: JAMIA, 2021, 28, 126-131.	4.4	6
16	CYP2C19 Loss-of-Function is Associated with Increased Risk of Ischemic Stroke after Transient Ischemic Attack in Intracranial Atherosclerotic Disease. Journal of Stroke and Cerebrovascular Diseases, 2021, 30, 105464.	1.6	9
17	Association of Genetic Variation With Cirrhosis: A Multi-Trait Genome-Wide Association and Geneâ€“Environment Interaction Study. Gastroenterology, 2021, 160, 1620-1633.e13.	1.3	68
18	Evaluation of the MC4R gene across eMERGE network identifies many unreported obesity-associated variants. International Journal of Obesity, 2021, 45, 155-169.	3.4	19

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19	Precision Medicine and Informatics. , 2021, , 941-966.		0
20	Lossless integration of multiple electronic health records for identifying pleiotropy using summary statistics. Nature Communications, 2021, 12, 168.	12.8	2
21	Association between triglycerides, known risk SNVs and conserved rare variation in SLC25A40 in a multi-ancestry cohort. BMC Medical Genomics, 2021, 14, 11.	1.5	4
22	Meeting the challenge: Health information technologyâ€™s essential role in achieving precision medicine. Journal of the American Medical Informatics Association: JAMIA, 2021, 28, 1345-1352.	4.4	8
23	Precision medicine in 2030â€”seven ways to transform healthcare. Cell, 2021, 184, 1415-1419.	28.9	161
24	DDIWAS: High-throughput electronic health record-based screening of drug-drug interactions. Journal of the American Medical Informatics Association: JAMIA, 2021, 28, 1421-1430.	4.4	10
25	Medical records-based chronic kidney disease phenotype for clinical care and â€œbig dataâ€•observational and genetic studies. Npj Digital Medicine, 2021, 4, 70.	10.9	39
26	Medical Records-Based Genetic Studies of the Complement System. Journal of the American Society of Nephrology: JASN, 2021, 32, 2031-2047.	6.1	10
27	A Mendelian Randomization Approach Using 3-HMG-Coenzyme-A Reductase Gene Variation to Evaluate the Association of Statin-Induced Low-Density Lipoprotein Cholesterol Lowering With Noncardiovascular Disease Phenotypes. JAMA Network Open, 2021, 4, e2112820.	5.9	16
28	High-throughput framework forÂgenetic analyses of adverse drug reactions using electronic health records. PLoS Genetics, 2021, 17, e1009593.	3.5	5
29	Neptune: an environment for the delivery of genomic medicine. Genetics in Medicine, 2021, 23, 1838-1846.	2.4	3
30	Systemic inhibition of PTPN22 augments anticancer immunity. Journal of Clinical Investigation, 2021, 131, .	8.2	24
31	I can drive in Iceland: Enabling international joint analyses. Cell Genomics, 2021, 1, 100034.	6.5	2
32	APOL1 renal risk variants are associated with obesity and body composition in African ancestry adults. Medicine (United States), 2021, 100, e27785.	1.0	6
33	Association of Genetic Risk of Obesity with Postoperative Complications Using Mendelian Randomization. World Journal of Surgery, 2020, 44, 84-94.	1.6	4
34	A Polygenic and Phenotypic Risk Prediction for Polycystic Ovary Syndrome Evaluated by Phenome-Wide Association Studies. Journal of Clinical Endocrinology and Metabolism, 2020, 105, 1918-1936.	3.6	40
35	PheMap: a multi-resource knowledge base for high-throughput phenotyping within electronic health records. Journal of the American Medical Informatics Association: JAMIA, 2020, 27, 1675-1687.	4.4	28
36	Genetic Architecture of Abdominal Aortic Aneurysm in the Million Veteran Program. Circulation, 2020, 142, 1633-1646.	1.6	78

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37	The polygenic architecture of left ventricular mass mirrors the clinical epidemiology. Scientific Reports, 2020, 10, 7561.	3.3	13
38	Frequency of genomic secondaryÂfindings among 21,915 eMERGE network participants. Genetics in Medicine, 2020, 22, 1470-1477.	2.4	61
39	Mendelian Randomization of Circulating Polyunsaturated Fatty Acids and Colorectal Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 860-870.	2.5	26
40	Diversity and inclusion for the All of Us research program: A scoping review. PLoS ONE, 2020, 15, e0234962.	2.5	128
41	Phenome-wide association analysis suggests the APOL1 linked disease spectrum primarily drives kidney-specific pathways. Kidney International, 2020, 97, 1032-1041.	5.2	20
42	Leveraging Human Genetics to Identify Safety Signals Prior to Drug Marketing Approval and Clinical Use. Drug Safety, 2020, 43, 567-582.	3.2	9
43	Development of a System for Postmarketing Population Pharmacokinetic and Pharmacodynamic Studies Using Realâ€World Data From Electronic Health Records. Clinical Pharmacology and Therapeutics, 2020, 107, 934-943.	4.7	26
44	medExtractR: A targeted, customizable approach to medication extraction from electronic health records. Journal of the American Medical Informatics Association: JAMIA, 2020, 27, 407-418.	4.4	15
45	A missense variant in Mitochondrial Amidoxime Reducing Component 1 gene and protection against liver disease. PLoS Genetics, 2020, 16, e1008629.	3.5	101
46	Evaluating the Utility of Polygenic Risk Scores in Identifying High-Risk Individuals for Eight Common Cancers. JNCI Cancer Spectrum, 2020, 4, pkaa021.	2.9	75
47	LabWAS: Novel findings and study design recommendations from a meta-analysis of clinical labs in two independent biobanks. PLoS Genetics, 2020, 16, e1009077.	3.5	14
48	Diversity and inclusion for the All of Us research program: A scoping review. , 2020, 15, e0234962.		0
49	Diversity and inclusion for the All of Us research program: A scoping review. , 2020, 15, e0234962.		0
50	Diversity and inclusion for the All of Us research program: A scoping review. , 2020, 15, e0234962.		0
51	Diversity and inclusion for the All of Us research program: A scoping review. , 2020, 15, e0234962.		0
52	The â€œAll of Usâ€•Research Program. New England Journal of Medicine, 2019, 381, 668-676.	27.0	955
53	Hypertension is a modifiable risk factor for osteonecrosis in acute lymphoblastic leukemia. Blood, 2019, 134, 983-986.	1.4	12
54	Cost-aware active learning for named entity recognition in clinical text. Journal of the American Medical Informatics Association: JAMIA, 2019, 26, 1314-1322.	4.4	18

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55	Facilitating phenotype transfer using a common data model. Journal of Biomedical Informatics, 2019, 96, 103253.	4.3	49
56	Genetically determined serum urate levels and cardiovascular and other diseases in UK Biobank cohort: A phenome-wide mendelian randomization study. PLoS Medicine, 2019, 16, e1002937.	8.4	81
57	A stepwise approach to implementing pharmacogenetic testing in the primary care setting. Pharmacogenomics, 2019, 20, 1103-1112.	1.3	27
58	Making work visible for electronic phenotype implementation: Lessons learned from the eMERGE network. Journal of Biomedical Informatics, 2019, 99, 103293.	4.3	27
59	Improving the phenotype risk score as a scalable approach to identifying patients with Mendelian disease. Journal of the American Medical Informatics Association: JAMIA, 2019, 26, 1437-1447.	4.4	35
60	Phenome-wide association analysis of LDL-cholesterol lowering genetic variants in PCSK9. BMC Cardiovascular Disorders, 2019, 19, 240.	1.7	22
61	Automated grouping of medical codes via multiview banded spectral clustering. Journal of Biomedical Informatics, 2019, 100, 103322.	4.3	6
62	A Decision-Theoretic Approach to Panel-Based, Preemptive Genotyping. MDM Policy and Practice, 2019, 4, 238146831986433.	0.9	10
63	Harmonizing Clinical Sequencing and Interpretation for the eMERGE III Network. American Journal of Human Genetics, 2019, 105, 588-605.	6.2	99
64	Phenome-wide Mendelian-randomization study of genetically determined vitamin D on multiple health outcomes using the UK Biobank study. International Journal of Epidemiology, 2019, 48, 1425-1434.	1.9	61
65	Detecting time-evolving phenotypic topics via tensor factorization on electronic health records: Cardiovascular disease case study. Journal of Biomedical Informatics, 2019, 98, 103270.	4.3	32
66	Learning from Longitudinal Data in Electronic Health Record and Genetic Data to Improve Cardiovascular Event Prediction. Scientific Reports, 2019, 9, 717.	3.3	115
67	Association of Thyroid Function Genetic Predictors With Atrial Fibrillation. JAMA Cardiology, 2019, 4, 136.	6.1	23
68	Use of Genetic Variants Related to Antihypertensive Drugs to Inform on Efficacy and Side Effects. Circulation, 2019, 140, 270-279.	1.6	99
69	Discovery of Noncancer Drug Effects on Survival in Electronic Health Records of Patients With Cancer: A New Paradigm for Drug Repurposing. JCO Clinical Cancer Informatics, 2019, 3, 1-9.	2.1	25
70	A Trans-Ethnic Genome-Wide Association Study of Uterine Fibroids. Frontiers in Genetics, 2019, 10, 511.	2.3	32
71	CP Tensor Decomposition with Cannot-Link Intermode Constraints. , 2019, 2019, 711-719.		2
72	Heritability and genome-wide association study of benign prostatic hyperplasia (BPH) in the eMERGE network. Scientific Reports, 2019, 9, 6077.	3.3	21

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73	Increased monocyte count as a cellular biomarker for poor outcomes in fibrotic diseases: a retrospective, multicentre cohort study. Lancet Respiratory Medicine,the, 2019, 7, 497-508.	10.7	168
74	Case 40-2018: A Woman with Recurrent Sinusitis, Cough, and Bronchiectasis. New England Journal of Medicine, 2019, 380, 1382-1383.	27.0	4
75	Genomeâ€Wide Association and Functional Studies Reveal Novel Pharmacological Mechanisms for Allopurinol. Clinical Pharmacology and Therapeutics, 2019, 106, 623-631.	4.7	23
76	Using topic modeling via non-negative matrix factorization to identify relationships between genetic variants and disease phenotypes: A case study of Lipoprotein(a) (LPA). PLoS ONE, 2019, 14, e0212112.	2.5	20
77	GRIK5 Genetically Regulated Expression Associated with Eye and Vascular Phenomes: Discovery through Iteration among Biobanks, Electronic Health Records, and Zebrafish. American Journal of Human Genetics, 2019, 104, 503-519.	6.2	21
78	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	21.4	89
79	A phenome-wide association study to discover pleiotropic effects of PCSK9, APOB, and LDLR. Npj Genomic Medicine, 2019, 4, 3.	3.8	26
80	Translational Health Disparities Research in a Data-Rich World. Health Equity, 2019, 3, 588-600.	1.9	29
81	Cox regression increases power to detect genotype-phenotype associations in genomic studies using the electronic health record. BMC Genomics, 2019, 20, 805.	2.8	24
82	Development of the Initial Surveys for the All of Us Research Program. Epidemiology, 2019, 30, 597-608.	2.7	35
83	Trans-ethnic association study of blood pressure determinants in over 750,000 individuals. Nature Genetics, 2019, 51, 51-62.	21.4	328
84	Qualitative study of system-level factors related to genomic implementation. Genetics in Medicine, 2019, 21, 1534-1540.	2.4	26
85	Unfolding of hidden white blood cell count phenotypes for gene discovery using latent class mixed modeling. Genes and Immunity, 2019, 20, 555-565.	4.1	4
86	Artificial intelligence, bias and clinical safety. BMJ Quality and Safety, 2019, 28, 231-237.	3.7	469
87	Identifying lupus patients in electronic health records: Development and validation of machine learning algorithms and application of rule-based algorithms. Seminars in Arthritis and Rheumatism, 2019, 49, 84-90.	3.4	67
88	Phenome-wide association study identifies dsDNA as a driver of major organ involvement in systemic lupus erythematosus. Lupus, 2019, 28, 66-76.	1.6	7
89	Effect of <scp>CYP</scp>4F2,<scp>VKORC</scp>1, and <scp>CYP</scp>2C9 in Influencing Coumarin Dose: A Singleâ€Patient Data Metaâ€Analysis in More Than 15,000 Individuals. Clinical Pharmacology and Therapeutics, 2019, 105, 1477-1491.	4.7	23
90	The eMERGE genotype set of 83,717 subjects imputed to ~40â€‰million variants genome wide and association with the herpes zoster medical record phenotype. Genetic Epidemiology, 2019, 43, 63-81.	1.3	63

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91	Mapping ICD-10 and ICD-10-CM Codes to Phecodes: Workflow Development and Initial Evaluation. JMIR Medical Informatics, 2019, 7, e14325.	2.6	323
92	Detecting potential pleiotropy across cardiovascular and neurological diseases using univariate, bivariate, and multivariate methods on 43,870 individuals from the eMERGE network. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2019, 24, 272-283.	0.7	6
93	Comorbidity Characterization Among eMERGE Institutions: A Pilot Evaluation with the Johns Hopkins Adjusted Clinical GroupsÂ® System. AMIA Summits on Translational Science Proceedings, 2019, 2019, 145-152.	0.4	2
94	Research Directions in the Clinical Implementation of Pharmacogenomics: An Overview of US Programs and Projects. Clinical Pharmacology and Therapeutics, 2018, 103, 778-786.	4.7	110
95	Phenomeâ€Wide Association Studies Uncover a Novel Association of Increased Atrial Fibrillation in Male Patients With Systemic Lupus Erythematosus. Arthritis Care and Research, 2018, 70, 1630-1636.	3.4	22
96	Analysis of predicted loss-of-function variants in UK Biobank identifies variants protective for disease. Nature Communications, 2018, 9, 1613.	12.8	78
97	Evaluating statistical approaches to leverage large clinical datasets for uncovering therapeutic and adverse medication effects. Bioinformatics, 2018, 34, 2988-2996.	4.1	15
98	Clinical Features Associated With Nascent Left Ventricular Diastolic Dysfunction in a Population Aged 40 to 55 Years. American Journal of Cardiology, 2018, 121, 1552-1557.	1.6	8
99	Benefit of Preemptive Pharmacogenetic Information on Clinical Outcome. Clinical Pharmacology and Therapeutics, 2018, 103, 787-794.	4.7	77
100	Calcium channel blockers as drug repurposing candidates for gestational diabetes: Mining large scale genomic and electronic health records data to repurpose medications. Pharmacological Research, 2018, 130, 44-51.	7.1	18
101	MR-PheWAS: exploring the causal effect of SUA level on multiple disease outcomes by using genetic instruments in UK Biobank. Annals of the Rheumatic Diseases, 2018, 77, 1039-1047.	0.9	57
102	SJS/TEN 2017: Building Multidisciplinary Networks to Drive Science and Translation. Journal of Allergy and Clinical Immunology: in Practice, 2018, 6, 38-69.	3.8	134
103	Principles of Systems Biology, No. 28. Cell Systems, 2018, 6, 397-399.	6.2	0
104	Opportunities and Challenges in Cardiovascular Pharmacogenomics. Circulation Research, 2018, 122, 1176-1190.	4.5	23
105	LPA Variants Are Associated With Residual Cardiovascular Risk in Patients Receiving Statins. Circulation, 2018, 138, 1839-1849.	1.6	64
106	Phenotype risk scores identify patients with unrecognized Mendelian disease patterns. Science, 2018, 359, 1233-1239.	12.6	164
107	PRECISION MEDICINE: FROM DIPLOTYPES TO DISPARITIES TOWARDS IMPROVED HEALTH AND THERAPIES. , 2018, , .		3
108	Mining 100 million notes to find homelessness and adverse childhood experiences: 2 case studies of rare and severe social determinants of health in electronic health records. Journal of the American Medical Informatics Association: JAMIA, 2018, 25, 61-71.	4.4	81

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109	Multisite Investigation of Outcomes WithÂImplementation of CYP2C19 Genotype-Guided Antiplatelet Therapy After Percutaneous Coronary Intervention. JACC: Cardiovascular Interventions, 2018, 11, 181-191.	2.9	213
110	Uncovering exposures responsible for birth season â€“ disease effects: a global study. Journal of the American Medical Informatics Association: JAMIA, 2018, 25, 275-288.	4.4	33
111	The Influence of Big (Clinical) Data and Genomics on Precision Medicine and Drug Development. Clinical Pharmacology and Therapeutics, 2018, 103, 409-418.	4.7	42
112	Genomeâ€wide and Phenomeâ€wide Approaches to Understand Variable Drug Actions in Electronic Health Records. Clinical and Translational Science, 2018, 11, 112-122.	3.1	36
113	Using Human â€˜Experiments of Natureâ€™ to Predict Drug Safety Issues: An Example with PCSK9 Inhibitors. Drug Safety, 2018, 41, 303-311.	3.2	22
114	Research Directions in Genetic Predispositions to Stevensâ€“Johnson Syndrome / Toxic Epidermal Necrolysis. Clinical Pharmacology and Therapeutics, 2018, 103, 390-394.	4.7	15
115	MZ carrier state in alpha-1 antitrypsin deficiency: Summary of the 16th Gordon L. Snider critical issues workshop, Bethesda, Maryland, November 13, 2017. Translational Science of Rare Diseases, 2018, 3, 105-120.	1.5	0
116	Association of Obesity with Postoperative Complications Using Phenome-Wide Association Studies and Mendelian Randomization. Journal of the American College of Surgeons, 2018, 227, S95.	0.5	0
117	AA-01â€…Phenome-wide association studies uncover hierarchy of autoantibodies in systemic lupus erythematosus. , 2018, , .		0
118	Characterizing Design Patterns of EHR-Driven Phenotype Extraction Algorithms. , 2018, , .		2
119	Characteristics and treatment of African-American and European-American patients with resistant hypertension identified using the electronic health record in an academic health centre: a caseâ€control study. BMJ Open, 2018, 8, e021640.	1.9	15
120	Probing the Virtual Proteome to Identify Novel Disease Biomarkers. Circulation, 2018, 138, 2469-2481.	1.6	42
121	Pulling the covers in electronic health records for an association study with self-reported sleep behaviors. Chronobiology International, 2018, 35, 1702-1712.	2.0	2
122	A study paradigm integrating prospective epidemiologic cohorts and electronic health records to identify disease biomarkers. Nature Communications, 2018, 9, 3522.	12.8	13
123	A case study evaluating the portability of an executable computable phenotype algorithm across multiple institutions and electronic health record environments. Journal of the American Medical Informatics Association: JAMIA, 2018, 25, 1540-1546.	4.4	29
124	Relationship between very low low-density lipoprotein cholesterol concentrations not due to statin therapy and risk of type 2 diabetes: A US-based cross-sectional observational study using electronic health records. PLoS Medicine, 2018, 15, e1002642.	8.4	22
125	A Phenome-Wide Association Study Uncovers a Role for Autoimmunity in the Development of Chronic Obstructive Pulmonary Disease. American Journal of Respiratory Cell and Molecular Biology, 2018, 58, 777-779.	2.9	8
126	Association of ST2 polymorphisms with atopy, asthma, and leukemia. Journal of Allergy and Clinical Immunology, 2018, 142, 991-993.e3.	2.9	4

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127	PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and atrioventricular electrical activity. Nature Communications, 2018, 9, 2904.	12.8	71
128	Reply to Ward and Colleaguesâ€™ Comment on â€œUsing Human Experiments of Nature to Predict Drug Safety Issues: An Example with PCSK9 Inhibitorsâ€• Drug Safety, 2018, 41, 1101-1101.	3.2	1
129	Common variation near IRF6 is associated with IFN-Î²-induced liver injury in multiple sclerosis. Nature Genetics, 2018, 50, 1081-1085.	21.4	32
130	Preg<scp>OMICS</scp>â€”Leveraging systems biology and bioinformatics for drug repurposing in maternalâ€child health. American Journal of Reproductive Immunology, 2018, 80, e12971.	1.2	8
131	An integrative functional genomics framework for effective identification of novel regulatory variants in genomeâ€“phenome studies. Genome Medicine, 2018, 10, 7.	8.2	29
132	Defining Phenotypes from Clinical Data to Drive Genomic Research. Annual Review of Biomedical Data Science, 2018, 1, 69-92.	6.5	38
133	Phenome-wide association study identifies marked increased in burden of comorbidities in African Americans with systemic lupus erythematosus. Arthritis Research and Therapy, 2018, 20, 69.	3.5	23
134	Simmering Below the Surface: Sweet's Syndrome with Multiple Myeloma. American Journal of Medicine, 2018, 131, 1058-1060.	1.5	1
135	Evaluation of a Novel System to Enhance Clinicians' Recognition of Preadmission Adverse Drug Reactions. Applied Clinical Informatics, 2018, 09, 313-325.	1.7	7
136	Efficiently controlling for case-control imbalance and sample relatedness in large-scale genetic association studies. Nature Genetics, 2018, 50, 1335-1341.	21.4	896
137	An Atlas of Genetic Variation Linking Pathogen-Induced Cellular Traits to Human Disease. Cell Host and Microbe, 2018, 24, 308-323.e6.	11.0	48
138	Disease Heritability Studies Harness the Healthcare System to Achieve Massive Scale. Cell, 2018, 173, 1568-1570.	28.9	3
139	Rare Variants in the Gene ALPL That Cause Hypophosphatasia Are Strongly Associated With Ovarian and Uterine Disorders. Journal of Clinical Endocrinology and Metabolism, 2018, 103, 2234-2243.	3.6	7
140	Multi-ethnic genome-wide association study for atrial fibrillation. Nature Genetics, 2018, 50, 1225-1233.	21.4	552
141	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	21.4	286
142	Huge Cohorts, Genomics, and Clinical Data to Personalize Medicine. , 2018, , .		0
143	Detecting potential pleiotropy across cardiovascular and neurological diseases using univariate, bivariate, and multivariate methods on 43,870 individuals from the eMERGE network. , 2018, , .		6
144	A Crowdsourcing Framework for Medical Data Sets. AMIA Summits on Translational Science Proceedings, 2018, 2017, 273-280.	0.4	11

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145	PRECISION MEDICINE: FROM DIPLOTYPES TO DISPARITIES TOWARDS IMPROVED HEALTH AND THERAPIES. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2018, 23, 389-399.	0.7	1
146	Phenotyping through Semi-Supervised Tensor Factorization (PSST). AMIA ... Annual Symposium proceedings, 2018, 2018, 564-573.	0.2	3
147	The effect of genetic variation in PCSK9 on the LDL-cholesterol response to statin therapy. Pharmacogenomics Journal, 2017, 17, 204-208.	2.0	29
148	Effects of G6pc2 deletion on body weight and cholesterol in mice. Journal of Molecular Endocrinology, 2017, 58, 127-139.	2.5	5
149	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated WithÂCoronary ArteryÂDisease. Journal of the American College of Cardiology, 2017, 69, 823-836.	2.8	214
150	Accelerating Precision Drug Development and Drug Repurposing by Leveraging Human Genetics. Assay and Drug Development Technologies, 2017, 15, 113-119.	1.2	30
151	Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. Nature Genetics, 2017, 49, 946-952.	21.4	279
152	Investigating the Genetic Architecture of the PR Interval Using Clinical Phenotypes. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	8
153	Phenome-wide scanning identifies multiple diseases and disease severity phenotypes associated with HLA variants. Science Translational Medicine, 2017, 9, .	12.4	105
154	PCSK9 genetic variants and risk of type 2 diabetes: a mendelian randomisation study. Lancet Diabetes and Endocrinology,the, 2017, 5, 97-105.	11.4	298
155	Apolipoprotein L1 VariantsÂand Blood Pressure Traits inÂAfrican Americans. Journal of the American College of Cardiology, 2017, 69, 1564-1574.	2.8	46
156	SOS2 and ACP1 Loci Identified through Large-Scale Exome Chip Analysis Regulate Kidney Development and Function. Journal of the American Society of Nephrology: JASN, 2017, 28, 981-994.	6.1	39
157	Reply. Arthritis and Rheumatology, 2017, 69, 680-681.	5.6	0
158	STRATEGIES FOR EQUITABLE PHARMACOGENOMIC-GUIDED WARFARIN DOSING AMONG EUROPEAN AND AFRICAN AMERICAN INDIVIDUALS IN A CLINICAL POPULATION. , 2017, 22, 545-556.		6
159	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	21.4	470
160	The Gain-of-Function Integrin Î²3 Pro33 Variant Alters the Serotonin System in the Mouse Brain. Journal of Neuroscience, 2017, 37, 11271-11284.	3.6	22
161	A multi-stage genome-wide association study of uterine fibroids in African Americans. Human Genetics, 2017, 136, 1363-1373.	3.8	39
162	Granite: Diversified, Sparse Tensor Factorization for Electronic Health Record-Based Phenotyping. , 2017, , .		17

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163	Genetic Interactions with Age, Sex, Body Mass Index, and Hypertension in Relation to Atrial Fibrillation: The AFGen Consortium. Scientific Reports, 2017, 7, 11303.	3.3	15
164	Influence of Human Leukocyte Antigen (<scp>HLA</scp>) Alleles and Killer Cell Immunoglobulinâ€Like Receptors (<scp>KIR</scp>) Types on Heparinâ€Induced Thrombocytopenia (<scp>HIT</scp>). Pharmacotherapy, 2017, 37, 1164-1171.	2.6	14
165	A common deletion in the haptoglobin gene associated with blood cholesterol levels among Chinese women. Journal of Human Genetics, 2017, 62, 911-914.	2.3	14
166	A comparison of rule-based and machine learning approaches for classifying patient portal messages. International Journal of Medical Informatics, 2017, 105, 110-120.	3.3	60
167	Challenges and strategies for implementing genomic services in diverse settings: experiences from the Implementing GeNomics In pracTicE (IGNITE) network. BMC Medical Genomics, 2017, 10, 35.	1.5	99
168	A long journey to short abbreviations: developing an open-source framework for clinical abbreviation recognition and disambiguation (CARD). Journal of the American Medical Informatics Association: JAMIA, 2017, 24, e79-e86.	4.4	45
169	Developing Electronic Health Record Algorithms That Accurately Identify Patients With Systemic Lupus Erythematosus. Arthritis Care and Research, 2017, 69, 687-693.	3.4	61
170	Evaluating electronic health record data sources and algorithmic approaches to identify hypertensive individuals. Journal of the American Medical Informatics Association: JAMIA, 2017, 24, 162-171.	4.4	74
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