Erwin P Bottinger

List of Publications by Year
in descending order

120 papers	23,638 citations	31976 53 h-index	20358 116 g-index
143 all docs	143 docs citations	143 times ranked	33946 citing authors

#	Article	IF	Citations
1	Rare coding variants in 35 genes associate with circulating lipid levelsâ€"A multi-ancestry analysis of 170,000 exomes. American Journal of Human Genetics, 2022, 109, 81-96.	6.2	24
2	Digital Therapeutic Care Apps With Decision-Support Interventions for People With Low Back Pain in Germany: Cost-Effectiveness Analysis. JMIR MHealth and UHealth, 2022, 10, e35042.	3.7	19
3	Effects of Testing and Disclosing Ancestry-Specific Genetic Risk for Kidney Failure on Patients and Health Care Professionals. JAMA Network Open, 2022, 5, e221048.	5.9	9
4	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. Nature Genetics, 2022, 54, 560-572.	21.4	250
5	StudyU: A Platform for Designing and Conducting Innovative Digital N-of-1 Trials. Journal of Medical Internet Research, 2022, 24, e35884.	4.3	4
6	Inducing and Recording Acute Stress Responses on a Large Scale With the Digital Stress Test (DST): Development and Evaluation Study. Journal of Medical Internet Research, 2022, 24, e32280.	4.3	0
7	Insights From a Large-Scale Whole-Genome Sequencing Study of Systolic Blood Pressure, Diastolic Blood Pressure, and Hypertension. Hypertension, 2022, 79, 1656-1667.	2.7	12
8	Rapid response to the alpha-1 adrenergic agent phenylephrine in the perioperative period is impacted by genomics and ancestry. Pharmacogenomics Journal, 2021, 21, 174-189.	2.0	0
9	Using interpretability approaches to update â€œblack-boxâ€•clinical prediction models: an external validation study in nephrology. Artificial Intelligence in Medicine, 2021, 111, 101982.	6.5	14
10	Meta-analysis uncovers genome-wide significant variants for rapid kidney function decline. Kidney International, 2021, 99, 926-939.	5.2	42
11	AKI in Hospitalized Patients with COVID-19. Journal of the American Society of Nephrology: JASN, 2021, 32, 151-160.	6.1	500
12	Kidney disease genetic risk variants alter lysosomal beta-mannosidase (MANBA) expression and disease severity. Science Translational Medicine, 2021, 13, .	12.4	30
13	Unsupervised Learning to Subphenotype Heart Failure Patients from Electronic Health Records. Lecture Notes in Computer Science, 2021, , 219-228.	1.3	1
14	Federated Learning of Electronic Health Records to Improve Mortality Prediction in Hospitalized Patients With COVID-19: Machine Learning Approach. JMIR Medical Informatics, 2021, 9, e24207.	2.6	108
15	Association of SARS-CoV-2 viral load at admission with in-hospital acute kidney injury: A retrospective cohort study. PLoS ONE, 2021, 16, e0247366.	2.5	5
16	Use of Physiological Data From a Wearable Device to Identify SARS-CoV-2 Infection and Symptoms and Predict COVID-19 Diagnosis: Observational Study. Journal of Medical Internet Research, 2021, 23, e26107.	4.3	91
17	Monitoring of Sitting Postures With Sensor Networks in Controlled and Free-living Environments: Systematic Review. JMIR Biomedical Engineering, 2021, 6, e21105.	1.2	2
18	Discovery and fine-mapping of height loci via high-density imputation of GWASs in individuals of African ancestry. American Journal of Human Genetics, 2021, 108, 564-582.	6.2	18

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19	Toward a fine-scale population health monitoring system. Cell, 2021, 184, 2068-2083.e11.	28.9	78
20	A Resilience-Building App to Support the Mental Health of Health Care Workers in the COVID-19 Era: Design Process, Distribution, and Evaluation. JMIR Formative Research, 2021, 5, e26590.	1.4	26
21	Predictive Approaches for Acute Dialysis Requirement and Death in COVID-19. Clinical Journal of the American Society of Nephrology: CJASN, 2021, 16, 1158-1168.	4.5	15
22	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	21.4	341
23	Determinants of penetrance and variable expressivity in monogenic metabolic conditions across 77,184 exomes. Nature Communications, 2021, 12, 3505.	12.8	49
24	Acute Kidney Injury in Patients Hospitalized With COVID-19 in New York City: Temporal Trends From March 2020 to April 2021. Kidney Medicine, 2021, 3, 877-879.	2.0	12
25	Phe2vec: Automated disease phenotyping based on unsupervised embeddings from electronic health records. Patterns, 2021, 2, 100337.	5.9	19
26	Factors Associated With Longitudinal Psychological and Physiological Stress in Health Care Workers During the COVID-19 Pandemic: Observational Study Using Apple Watch Data. Journal of Medical Internet Research, 2021, 23, e31295.	4.3	15
27	Mobile app requirements for patients with rare liver diseases: A single center survey for the ERN RARE-LIVERâ€¬â€¬â€¬. Clinics and Research in Hepatology and Gastroenterology, 2021, 45, 101760.	1.5	1
28	Digital Therapeutic Care and Decision Support Interventions for People With Low Back Pain: Systematic Review. JMIR Rehabilitation and Assistive Technologies, 2021, 8, e26612.	2.2	23
29	The Polygenic and Monogenic Basis of Blood Traits and Diseases. Cell, 2020, 182, 1214-1231.e11.	28.9	388
30	Utilization of Deep Learning for Subphenotype Identification in Sepsis-Associated Acute Kidney Injury. Clinical Journal of the American Society of Nephrology: CJASN, 2020, 15, 1557-1565.	4.5	59
31	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. Nature Genetics, 2020, 52, 1314-1332.	21.4	91
32	Retrospective cohort study of clinical characteristics of 2199 hospitalised patients with COVID-19 in New York City. BMJ Open, 2020, 10, e040736.	1.9	50
33	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. Cell, 2020, 182, 1198-1213.e14.	28.9	353
34	Characterization of Patients Who Return to Hospital Following Discharge from Hospitalization for COVID-19. Journal of General Internal Medicine, 2020, 35, 2838-2844.	2.6	79
35	Association of APOL1 Risk Genotype and Air Pollution for Kidney Disease. Clinical Journal of the American Society of Nephrology: CJASN, 2020, 15, 401-403.	4.5	14
36	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. PLoS ONE, 2020, 15, e0230815.	2.5	10

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37	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542.	12.8	59
38	Coronavirus 2019 and People Living With Human Immunodeficiency Virus: Outcomes for Hospitalized Patients in New York City. Clinical Infectious Diseases, 2020, 71, 2933-2938.	5.8	189
39	Machine Learning to Predict Mortality and Critical Events in a Cohort of Patients With COVID-19 in New York City: Model Development and Validation. Journal of Medical Internet Research, 2020, 22, e24018.	4.3	174
40	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815.		0
41	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815.		0
42	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815.		0
43	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815.		0
44	A Genome-Wide Association Study Identifies Blood Disorderâ€“Related Variants Influencing Hemoglobin A1c With Implications for Glycemic Status in U.S. Hispanics/Latinos. Diabetes Care, 2019, 42, 1784-1791.	8.6	9
45	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	21.4	251
46	Genetic analyses of diverse populations improves discovery for complex traits. Nature, 2019, 570, 514-518.	27.8	679
47	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	21.4	549
48	The role of country of birth, and genetic and self-identified ancestry, in obesity susceptibility among African and Hispanic Americans. American Journal of Clinical Nutrition, 2019, 110, 16-23.	4.7	13
49	Exome sequencing of 20,791Âcases of type 2 diabetes and 24,440Âcontrols. Nature, 2019, 570, 71-76.	27.8	248
50	A multi-ancestry genome-wide study incorporating geneâ€“smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. Human Molecular Genetics, 2019, 28, 2615-2633.	2.9	31
51	Multi-ancestry genome-wide geneâ€“smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. Nature Genetics, 2019, 51, 636-648.	21.4	112
52	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	21.4	89
53	Trans-ethnic kidney function association study reveals putative causal genes and effects on kidney-specific disease aetiologies. Nature Communications, 2019, 10, 29.	12.8	113
54	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. Nature Genetics, 2018, 50, 559-571.	21.4	356

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55	Transethnic Evaluation Identifies Low-Frequency Loci Associated With 25-Hydroxyvitamin D Concentrations. Journal of Clinical Endocrinology and Metabolism, 2018, 103, 1380-1392.	3.6	33
56	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. American Journal of Human Genetics, 2018, 102, 375-400.	6.2	123
57	Genome-wide Study of Atrial Fibrillation Identifies Seven Risk Loci and Highlights Biological Pathways and Regulatory Elements Involved in Cardiac Development. American Journal of Human Genetics, 2018, 102, 103-115.	6.2	86
58	Plasma biomarkers are associated with renal outcomes in individuals with APOL1 risk variants. Kidney International, 2018, 93, 1409-1416.	5.2	25
59	Genome-Wide Association Study of Heavy Smoking and Daily/Nondaily Smoking in the Hispanic Community Health Study/Study of Latinos (HCHS/SOL). Nicotine and Tobacco Research, 2018, 20, 448-457.	2.6	21
60	Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps. Nature Genetics, 2018, 50, 1505-1513.	21.4	1,331
61	Genome-wide association study of primary open-angle glaucoma in continental and admixed African populations. Human Genetics, 2018, 137, 847-862.	3.8	40
62	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. American Journal of Human Genetics, 2018, 103, 691-706.	6.2	326
63	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 2018, 50, 1412-1425.	21.4	924
64	The genetic underpinnings of variation in ages at menarche and natural menopause among women from the multi-ethnic Population Architecture using Genomics and Epidemiology (PAGE) Study: A trans-ethnic meta-analysis. PLoS ONE, 2018, 13, e0200486.	2.5	25
65	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
66	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	27.8	544
67	iGAS: A framework for using electronic intraoperative medical records for genomic discovery. Journal of Biomedical Informatics, 2017, 67, 80-89.	4.3	8
68	Genome-wide association analyses for lung function and chronic obstructive pulmonary disease identify new loci and potential druggable targets. Nature Genetics, 2017, 49, 416-425.	21.4	257
69	Trans-ethnic fine-mapping of genetic loci for body mass index in the diverse ancestral populations of the Population Architecture using Genomics and Epidemiology (PAGE) Study reveals evidence for multiple signals at established loci. Human Genetics, 2017, 136, 771-800.	3.8	31
70	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. Nature Communications, 2017, 8, 14977.	12.8	169
71	Glomerular Endothelial Mitochondrial Dysfunction Is Essential and Characteristic of Diabetic Kidney Disease Susceptibility. Diabetes, 2017, 66, 763-778.	0.6	165
72	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902.	0.6	615

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73	Apolipoprotein L1 VariantsÂand Blood Pressure Traits inÂAfrican Americans. Journal of the American College of Cardiology, 2017, 69, 1564-1574.	2.8	46
74	CNV-association meta-analysis in 191,161 European adults reveals new loci associated with anthropometric traits. Nature Communications, 2017, 8, 744.	12.8	64
75	Institutional profile: translational pharmacogenomics at the Icahn School of Medicine at Mount Sinai. Pharmacogenomics, 2017, 18, 1381-1386.	1.3	20
76	Association analyses based on false discovery rate implicate new loci for coronary artery disease. Nature Genetics, 2017, 49, 1385-1391.	21.4	571
77	Impact of common genetic determinants of Hemoglobin A1c on type 2 diabetes risk and diagnosis in ancestrally diverse populations: A transethnic genome-wide meta-analysis. PLoS Medicine, 2017, 14, e1002383.	8.4	341
78	Genetic identification of a common collagen disease in Puerto Ricans via identity-by-descent mapping in a health system. ELife, 2017, 6, .	6.0	65
79	Identification of new susceptibility loci for type 2 diabetes and shared etiological pathways with coronary heart disease. Nature Genetics, 2017, 49, 1450-1457.	21.4	218
80	Single-trait and multi-trait genome-wide association analyses identify novel loci for blood pressure in African-ancestry populations. PLoS Genetics, 2017, 13, e1006728.	3.5	88
81	Variant Discovery and Fine Mapping of Genetic Loci Associated with Blood Pressure Traits in Hispanics and African Americans. PLoS ONE, 2016, 11, e0164132.	2.5	24
82	Exome Genotyping Identifies Pleiotropic Variants Associated with Red Blood Cell Traits. American Journal of Human Genetics, 2016, 99, 8-21.	6.2	60
83	Development and preliminary evaluation of an online educational video about whole-genome sequencing for research participants, patients, and the general public. Genetics in Medicine, 2016, 18, 501-512.	2.4	51
84	Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. Nature Genetics, 2016, 48, 1162-1170.	21.4	223
85	No Association of Coronary Artery Disease with X-Chromosomal Variants in Comprehensive International Meta-Analysis. Scientific Reports, 2016, 6, 35278.	3.3	25
86	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. American Journal of Human Genetics, 2016, 99, 40-55.	6.2	82
87	Large-Scale Exome-wide Association Analysis Identifies Loci for White Blood Cell Traits and Pleiotropy with Immune-Mediated Diseases. American Journal of Human Genetics, 2016, 99, 22-39.	6.2	50
88	Analytical Validation of a Personalized Medicine APOL1 Genotyping Assay for Nondiabetic Chronic Kidney Disease Risk Assessment. Journal of Molecular Diagnostics, 2016, 18, 260-266.	2.8	10
89	Mitochondrial Pathology and Glycolytic Shift during Proximal Tubule Atrophy after Ischemic AKI. Journal of the American Society of Nephrology: JASN, 2016, 27, 3356-3367.	6.1	223
90	The phenotypic legacy of admixture between modern humans and Neandertals. Science, 2016, 351, 737-741.	12.6	269

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91	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	12.8	412
92	Medical student preparedness for an era of personalized medicine: findings from one US medical school. Personalized Medicine, 2016, 13, 129-141.	1.5	36
93	Association of Arrhythmia-Related Genetic Variants With Phenotypes Documented in Electronic Medical Records. JAMA - Journal of the American Medical Association, 2016, 315, 47.	7.4	148
94	The IGNITE network: a model for genomic medicine implementation and research. BMC Medical Genomics, 2015, 9, 1.	1.5	189
95	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	3,823
96	Meta-analysis of Correlated Traits via Summary Statistics from GWASs with an Application in Hypertension. American Journal of Human Genetics, 2015, 96, 21-36.	6.2	321
97	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	27.8	173
98	Incorporating temporal EHR data in predictive models for risk stratification of renal function deterioration. Journal of Biomedical Informatics, 2015, 53, 220-228.	4.3	108
99	Penetrance of Hemochromatosis in HFE Genotypes Resulting in p.Cys282Tyr and p.[Cys282Tyr];[His63Asp] in the eMERGE Network. American Journal of Human Genetics, 2015, 97, 512-520.	6.2	47
100	Identification of type 2 diabetes subgroups through topological analysis of patient similarity. Science Translational Medicine, 2015, 7, 311ra174.	12.4	426
101	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. Nature Genetics, 2015, 47, 1415-1425.	21.4	365
102	Defective fatty acid oxidation in renal tubular epithelial cells has a key role in kidney fibrosis development. Nature Medicine, 2015, 21, 37-46.	30.7	1,007
103	Microvascular Endothelial Cells Poised to Take Center Stage in Experimental Renal Fibrosis. Journal of the American Society of Nephrology: JASN, 2015, 26, 767-769.	6.1	7
104	A conceptual model for translating omic data into clinical action. Journal of Pathology Informatics, 2015, 6, 46.	1.7	17
105	Practical considerations in genomic decision support: The eMERGE experience. Journal of Pathology Informatics, 2015, 6, 50.	1.7	42
106	ePhenotyping for Abdominal Aortic Aneurysm in the Electronic Medical Records and Genomics (eMERGE) Network: Algorithm Development and Konstanz Information Miner Workflow. International Journal of Biomedical Data Mining, 2015, 4, .	0.1	5
107	Physician Attitudes toward Adopting Genome-Guided Prescribing through Clinical Decision Support. Journal of Personalized Medicine, 2014, 4, 35-49.	2.5	43
108	Mpv17 in mitochondria protects podocytes against mitochondrial dysfunction and apoptosis in vivo and in vitro. American Journal of Physiology - Renal Physiology, 2014, 306, F1372-F1380.	2.7	42

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109	Meta-Analysis of Genome-Wide Association Studies in African Americans Provides Insights into the Genetic Architecture of Type 2 Diabetes. PLoS Genetics, 2014, 10, e1004517.	3.5	191
110	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. American Journal of Human Genetics, 2014, 94, 233-245.	6.2	193
111	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	21.4	1,818
112	Combinatorial actions of Tgfî² and Activin ligands promote oligodendrocyte development and CNS myelination. Development (Cambridge), 2014, 141, 2414-2428.	2.5	30
113	Development and validation of an electronic phenotyping algorithm for chronic kidney disease. AMIA ... Annual Symposium proceedings, 2014, 2014, 907-16.	0.2	31
114	Disease progression subtype discovery from longitudinal EMR data with a majority of missing values and unknown initial time points. AMIA ... Annual Symposium proceedings, 2014, 2014, 709-18.	0.2	4
115	The Electronic Medical Records and Genomics (eMERGE) Network: past, present, and future. Genetics in Medicine, 2013, 15, 761-771.	2.4	611
116	Smad2 and Myocardin-Related Transcription Factor B Cooperatively Regulate Vascular Smooth Muscle Differentiation From Neural Crest Cells. Circulation Research, 2013, 113, e76-86.	4.5	46
117	Genome-Wide Association Study (GWAS) Of Venous Thromboembolism (VTE) In African-Americans From The Electronic Medical Records & Genomics (eMERGE) Networkm. Blood, 2013, 122, 458-458.	1.4	0
118	Lights on for aminopeptidases in cystic kidney disease. Journal of Clinical Investigation, 2010, 120, 660-663.	8.2	9
119	TGF-Î² in Renal Injury and Disease. Seminars in Nephrology, 2007, 27, 309-320.	1.6	320
120	Foundations, promises and uncertainties of personalized medicine. Mount Sinai Journal of Medicine, 2007, 74, 15-21.	1.9	24