# Erwin P Bottinger

List of Publications by Year
in descending order



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|---|---|---|---|
| 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 | Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206. | 27.8 | 3,823 |
| 2 | 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 |
| 3 | 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 |
| 4 | 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 |
| 5 | 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 |
| 6 | Genetic analyses of diverse populations improves discovery for complex traits. Nature, 2019, 570, 514-518. | 27.8 | 679 |
| 7 | An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902. | 0.6 | 615 |
| 8 | The Electronic Medical Records and Genomics (eMERGE) Network: past, present, and future. Genetics in Medicine, 2013, 15, 761-771. | 2.4 | 611 |
| 9 | Association analyses based on false discovery rate implicate new loci for coronary artery disease. Nature Genetics, 2017, 49, 1385-1391. | 21.4 | 571 |
| 10 | A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972. | 21.4 | 549 |
| 11 | Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190. | 27.8 | 544 |
| 12 | AKI in Hospitalized Patients with COVID-19. Journal of the American Society of Nephrology: JASN, 2021, 32, 151-160. | 6.1 | 500 |
| 13 | Identification of type 2 diabetes subgroups through topological analysis of patient similarity. Science Translational Medicine, 2015, 7, 311ra174. | 12.4 | 426 |
| 14 | Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023. | 12.8 | 412 |
| 15 | The Polygenic and Monogenic Basis of Blood Traits and Diseases. Cell, 2020, 182, 1214-1231.e11. | 28.9 | 388 |
| 16 | Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. Nature Genetics, 2015, 47, 1415-1425. | 21.4 | 365 |
| 17 | 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 |
| 18 | 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 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | 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 |
| 20 | The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860. | 21.4 | 341 |
| 21 | 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 |
| 22 | 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 |
| 23 | TGF-Î² in Renal Injury and Disease. Seminars in Nephrology, 2007, 27, 309-320. | 1.6 | 320 |
| 24 | 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 |
| 25 | The phenotypic legacy of admixture between modern humans and Neandertals. Science, 2016, 351, 737-741. | 12.6 | 269 |
| 26 | 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 |
| 27 | Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474. | 21.4 | 251 |
| 28 | 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 |
| 29 | Exome sequencing of 20,791Âcases of type 2 diabetes and 24,440Âcontrols. Nature, 2019, 570, 71-76. | 27.8 | 248 |
| 30 | 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 |
| 31 | 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 |
| 32 | 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 |
| 33 | 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 |
| 34 | 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 |
| 35 | The IGNITE network: a model for genomic medicine implementation and research. BMC Medical Genomics, 2015, 9, 1. | 1.5 | 189 |
| 36 | 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 |

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|---|---|---|---|
| 37 | 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 |
| 38 | Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462. | 27.8 | 173 |
| 39 | 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 |
| 40 | Glomerular Endothelial Mitochondrial Dysfunction Is Essential and Characteristic of Diabetic Kidney Disease Susceptibility. Diabetes, 2017, 66, 763-778. | 0.6 | 165 |
| 41 | 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 |
| 42 | 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 |
| 43 | 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 |
| 44 | 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 |
| 45 | 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 |
| 46 | 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 |
| 47 | 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 |
| 48 | 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 |
| 49 | Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469. | 21.4 | 89 |
| 50 | 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 |
| 51 | 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 |
| 52 | Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. American Journal of Human Genetics, 2016, 99, 40-55. | 6.2 | 82 |
| 53 | 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 |
| 54 | Toward a fine-scale population health monitoring system. Cell, 2021, 184, 2068-2083.e11. | 28.9 | 78 |

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|---|---|---|---|
| 55 | 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 |
| 56 | CNV-association meta-analysis in 191,161 European adults reveals new loci associated with anthropometric traits. Nature Communications, 2017, 8, 744. | 12.8 | 64 |
| 57 | Exome Genotyping Identifies Pleiotropic Variants Associated with Red Blood Cell Traits. American Journal of Human Genetics, 2016, 99, 8-21. | 6.2 | 60 |
| 58 | 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 |
| 59 | Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542. | 12.8 | 59 |
| 60 | 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 |
| 61 | 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 |
| 62 | 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 |
| 63 | Determinants of penetrance and variable expressivity in monogenic metabolic conditions across 77,184 exomes. Nature Communications, 2021, 12, 3505. | 12.8 | 49 |
| 64 | 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 |
| 65 | 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 |
| 66 | Apolipoprotein L1 VariantsÂand Blood Pressure Traits inÂAfrican Americans. Journal of the American College of Cardiology, 2017, 69, 1564-1574. | 2.8 | 46 |
| 67 | Physician Attitudes toward Adopting Genome-Guided Prescribing through Clinical Decision Support. Journal of Personalized Medicine, 2014, 4, 35-49. | 2.5 | 43 |
| 68 | 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 |
| 69 | Meta-analysis uncovers genome-wide significant variants for rapid kidney function decline. Kidney International, 2021, 99, 926-939. | 5.2 | 42 |
| 70 | Practical considerations in genomic decision support: The eMERGE experience. Journal of Pathology Informatics, 2015, 6, 50. | 1.7 | 42 |
| 71 | Genome-wide association study of primary open-angle glaucoma in continental and admixed African populations. Human Genetics, 2018, 137, 847-862. | 3.8 | 40 |
| 72 | Medical student preparedness for an era of personalized medicine: findings from one US medical school. Personalized Medicine, 2016, 13, 129-141. | 1.5 | 36 |

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|---|---|---|---|
| 73 | 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 |
| 74 | 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 |
| 75 | 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 |
| 76 | Development and validation of an electronic phenotyping algorithm for chronic kidney disease. AMIA ... Annual Symposium proceedings, 2014, 2014, 907-16. | 0.2 | 31 |
| 77 | Combinatorial actions of Tgfî² and Activin ligands promote oligodendrocyte development and CNS myelination. Development (Cambridge), 2014, 141, 2414-2428. | 2.5 | 30 |
| 78 | Kidney disease genetic risk variants alter lysosomal beta-mannosidase ( MANBA ) expression and disease severity. Science Translational Medicine, 2021, 13, . | 12.4 | 30 |
| 79 | 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 |
| 80 | No Association of Coronary Artery Disease with X-Chromosomal Variants in Comprehensive International Meta-Analysis. Scientific Reports, 2016, 6, 35278. | 3.3 | 25 |
| 81 | Plasma biomarkers are associated with renal outcomes in individuals with APOL1 risk variants. Kidney International, 2018, 93, 1409-1416. | 5.2 | 25 |
| 82 | 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 |
| 83 | Foundations, promises and uncertainties of personalized medicine. Mount Sinai Journal of Medicine, 2007, 74, 15-21. | 1.9 | 24 |
| 84 | 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 |
| 85 | 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 |
| 86 | 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 |
| 87 | 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 |
| 88 | Institutional profile: translational pharmacogenomics at the Icahn School of Medicine at Mount Sinai. Pharmacogenomics, 2017, 18, 1381-1386. | 1.3 | 20 |
| 89 | Phe2vec: Automated disease phenotyping based on unsupervised embeddings from electronic health records. Patterns, 2021, 2, 100337. | 5.9 | 19 |
| 90 | 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 |

| # | Article | IF | Citations |
|---|---|---|---|
| 91 | 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 |
| 92 | A conceptual model for translating omic data into clinical action. Journal of Pathology Informatics, 2015, 6, 46. | 1.7 | 17 |
| 93 | 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 |
| 94 | 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 |
| 95 | 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 |
| 96 | 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 |
| 97 | 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 |
| 98 | 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 |
| 99 | 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 |
| 100 | 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 |
| 101 | Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. PLoS ONE, 2020, 15, e0230815. | 2.5 | 10 |
| 102 | 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 |
| 103 | Lights on for aminopeptidases in cystic kidney disease. Journal of Clinical Investigation, 2010, 120, 660-663. | 8.2 | 9 |
| 104 | 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 |
| 105 | iGAS: A framework for using electronic intraoperative medical records for genomic discovery. Journal of Biomedical Informatics, 2017, 67, 80-89. | 4.3 | 8 |
| 106 | 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 |
| 107 | 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 |
| 108 | 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 |

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|---|---|---|---|
| 109 | 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 |
| 110 | StudyU: A Platform for Designing and Conducting Innovative Digital N-of-1 Trials. Journal of Medical Internet Research, 2022, 24, e35884. | 4.3 | 4 |
| 111 | Monitoring of Sitting Postures With Sensor Networks in Controlled and Free-living Environments: Systematic Review. JMIR Biomedical Engineering, 2021, 6, e21105. | 1.2 | 2 |
| 112 | Unsupervised Learning to Subphenotype Heart Failure Patients from Electronic Health Records. Lecture Notes in Computer Science, 2021, , 219-228. | 1.3 | 1 |
| 113 | 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 |
| 114 | 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 |
| 115 | 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 |
| 116 | Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815. | | 0 |
| 117 | Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815. | | 0 |
| 118 | Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815. | | 0 |
| 119 | Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815. | | 0 |
| 120 | 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 |