Lisa Bastarache

List of Publications by Year in descending order

60 papers	5,191 citations	304743 22 h-index	155660 55 g-index
68 all docs	68 docs citations	68 times ranked	9316 citing authors

#	Article	IF	Citations
1	PheWAS: demonstrating the feasibility of a phenome-wide scan to discover geneâ€“disease associations. Bioinformatics, 2010, 26, 1205-1210.	4.1	966
2	Systematic comparison of phenome-wide association study of electronic medical record data and genome-wide association study data. Nature Biotechnology, 2013, 31, 1102-1111.	17.5	846
3	Cardiovascular toxicities associated with immune checkpoint inhibitors: an observational, retrospective, pharmacovigilance study. Lancet Oncology, The, 2018, 19, 1579-1589.	10.7	742
4	R PheWAS: data analysis and plotting tools for phenome-wide association studies in the R environment. Bioinformatics, 2014, 30, 2375-2376.	4.1	334
5	Mapping ICD-10 and ICD-10-CM Codes to Phecodes: Workflow Development and Initial Evaluation. JMIR Medical Informatics, 2019, 7, e14325.	2.6	323
6	The phenotypic legacy of admixture between modern humans and Neandertals. Science, 2016, 351, 737-741.	12.6	269
7	Phenome-Wide Association Studies as a Tool to Advance Precision Medicine. Annual Review of Genomics and Human Genetics, 2016, 17, 353-373.	6.2	193
8	Joint mouseâ€“human phenome-wide association to test gene function and disease risk. Nature Communications, 2016, 7, 10464.	12.8	190
9	Phenotype risk scores identify patients with unrecognized Mendelian disease patterns. Science, 2018, 359, 1233-1239.	12.6	164
10	TYK2 Protein-Coding Variants Protect against Rheumatoid Arthritis and Autoimmunity, with No Evidence of Major Pleiotropic Effects on Non-Autoimmune Complex Traits. PLoS ONE, 2015, 10, e0122271.	2.5	120
11	Phenome-wide scanning identifies multiple diseases and disease severity phenotypes associated with HLA variants. Science Translational Medicine, 2017, 9, .	12.4	105
12	Using Phecodes for Research with the Electronic Health Record: From PheWAS to PheRS. Annual Review of Biomedical Data Science, 2021, 4, 1-19.	6.5	75
13	A multiancestry genome-wide association study of unexplained chronic ALT elevation as a proxy for nonalcoholic fatty liver disease with histological and radiological validation. Nature Genetics, 2022, 54, 761-771.	21.4	68
14	Natural Language Processing Improves Identification of Colorectal Cancer Testing in the Electronic Medical Record. Medical Decision Making, 2012, 32, 188-197.	2.4	63
15	Comparison of HLA allelic imputation programs. PLoS ONE, 2017, 12, e0172444.	2.5	58
16	Use of electronic health records to support a public health response to the COVID-19 pandemic in the United States: a perspective from 15 academic medical centers. Journal of the American Medical Informatics Association: JAMIA, 2021, 28, 393-401.	4.4	54
17	Glucagon-like peptide 1 receptor signaling attenuates respiratory syncytial virusâ€“induced type 2 responses and immunopathology. Journal of Allergy and Clinical Immunology, 2018, 142, 683-687.e12.	2.9	41
18	Phenome-Wide Association Studies. JAMA - Journal of the American Medical Association, 2022, 327, 75.	7.4	41

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19	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
20	Accelerating Precision Drug Development and Drug Repurposing by Leveraging Human Genetics. Assay and Drug Development Technologies, 2017, 15, 113-119.	1.2	30
21	NKCC1: Newly Found as a Human Disease-Causing Ion Transporter. Function, 2020, 2, zqaa028.	2.3	29
22	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
23	The current state of omics technologies in the clinical management of asthma and allergic diseases. Annals of Allergy, Asthma and Immunology, 2019, 123, 550-557.	1.0	23
24	Association of Thyroid Function Genetic Predictors With Atrial Fibrillation. JAMA Cardiology, 2019, 4, 136.	6.1	23
25	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
26	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
27	Phenotypic signatures in clinical data enable systematic identification of patients for genetic testing. Nature Medicine, 2021, 27, 1097-1104.	30.7	21
28	Phenome-wide association analysis suggests the APOL1 linked disease spectrum primarily drives kidney-specific pathways. Kidney International, 2020, 97, 1032-1041.	5.2	20
29	Predictive Accuracy of a Polygenic Risk Score for Postoperative Atrial Fibrillation After Cardiac Surgery. Circulation Genomic and Precision Medicine, 2021, 14, e003269.	3.6	18
30	Multi-omic analysis elucidates the genetic basis of hydrocephalus. Cell Reports, 2021, 35, 109085.	6.4	18
31	Association Between a Common, Benign Genotype and Unnecessary Bone Marrow Biopsies Among African American Patients. JAMA Internal Medicine, 2021, 181, 1100.	5.1	18
32	Host genetic effects in pneumonia. American Journal of Human Genetics, 2021, 108, 194-201.	6.2	17
33	Commonalities across computational workflows for uncovering explanatory variants in undiagnosed cases. Genetics in Medicine, 2021, 23, 1075-1085.	2.4	16
34	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
35	A study paradigm integrating prospective epidemiologic cohorts and electronic health records to identify disease biomarkers. Nature Communications, 2018, 9, 3522.	12.8	13
36	Aggregating Electronic Health Record Data for COVID-19 Researchâ€"Caveat Emptor. JAMA Network Open, 2021, 4, e2117175.	5.9	13

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37	Defining the complex phenotype of severe systemic loxoscelism using a large electronic health record cohort. PLoS ONE, 2017, 12, e0174941.	2.5	12
38	Phenotyping coronavirus disease 2019 during a global health pandemic: Lessons learned from the characterization of an early cohort. Journal of Biomedical Informatics, 2021, 117, 103777.	4.3	11
39	The Role of Electronic Health Records in Advancing Genomic Medicine. Annual Review of Genomics and Human Genetics, 2021, 22, 219-238.	6.2	11
40	Exploring the role of low-frequency and rare exonic variants in alcohol and tobacco use. Drug and Alcohol Dependence, 2018, 188, 94-101.	3.2	10
41	New Insights into Clinical and Mechanistic Heterogeneity of the Acute Respiratory Distress Syndrome: Summary of the Aspen Lung Conference 2021. American Journal of Respiratory Cell and Molecular Biology, 2022, 67, 284-308.	2.9	9
42	IgG4â€related disease: Association with a rare gene variant expressed in cytotoxic T cells. Molecular Genetics & Genomic Medicine, 2019, 7, e686.	1.2	8
43	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
44	Electronic health record phenotypes associated with genetically regulated expression of CFTR and application to cystic fibrosis. Genetics in Medicine, 2020, 22, 1191-1200.	2.4	6
45	One is the loneliest number: genotypic matchmaking using the electronic health record. Genetics in Medicine, 2021, 23, 1830-1832.	2.4	6
46	Laboratory Predictors of Hemolytic Anemia in Patients With Systemic Loxoscelism. American Journal of Clinical Pathology, 2022, 157, 566-572.	0.7	6
47	EHRs could clarify drug safety in pregnant people. Nature Medicine, 2020, 26, 820-821.	30.7	5
48	Frequency of benign neutropenia among Black versus White individuals undergoing a bone marrow assessment. Journal of Cellular and Molecular Medicine, 2022, 26, 3628-3635.	3.6	5
49	Association of ST2 polymorphisms with atopy, asthma, and leukemia. Journal of Allergy and Clinical Immunology, 2018, 142, 991-993.e3.	2.9	4
50	Case 40-2018: A Woman with Recurrent Sinusitis, Cough, and Bronchiectasis. New England Journal of Medicine, 2019, 380, 1382-1383.	27.0	4
51	Association of Genetic Risk of Obesity with Postoperative Complications Using Mendelian Randomization. World Journal of Surgery, 2020, 44, 84-94.	1.6	4
52	A research agenda to support the development and implementation of genomics-based clinical informatics tools and resources. Journal of the American Medical Informatics Association: JAMIA, 2022, 29, 1342-1349.	4.4	4
53	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
54	Co-detection of SARS-CoV-2 with Secondary Respiratory Pathogen Infections. Journal of General Internal Medicine, 2021, 36, 1159-1160.	2.6	2

#	Article	IF	Citations
55	OUP accepted manuscript. Bioinformatics, 2022, , .	4.1	1
56	A General Purpose Phenotype Algorithm for Venous Thromboembolism Using Billing Codes and Natural Language Processing. , 2012, , .		0
57	Using a gene-environment interaction study to evaluate risk for lung cancer.. Journal of Clinical Oncology, 2016, 34, 1524-1524.	1.6	0
58	SAT-LB111 Improving Classification of Diabetes Etiology in Electronic Resources Using Phenotype Algorithms and Polygenic Risk Scores. Journal of the Endocrine Society, 2020, 4, .	0.2	0
59	Mapping the Read2/CTV3 controlled clinical terminologies to Phecodes in UK Biobank primary care electronic health records: implementation and evaluation.. AMIA ... Annual Symposium proceedings, 2021, 2021, 362-371.	0.2	0
60	Penetrance of Deleterious Clinical Variants. JAMA - Journal of the American Medical Association, 2022, 327, 1926.	7.4	0