

# Lisa Bastarache

## List of Publications by Year in descending order

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Version: 2024-02-01

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	Laboratory Predictors of Hemolytic Anemia in Patients With Systemic Loxoscelism. American Journal of Clinical Pathology, 2022, 157, 566-572.	0.7	6
2	Phenome-Wide Association Studies. JAMA - Journal of the American Medical Association, 2022, 327, 75.	7.4	41
3	OUP accepted manuscript. Bioinformatics, 2022, , .	4.1	1
4	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
5	Penetrance of Deleterious Clinical Variants. JAMA - Journal of the American Medical Association, 2022, 327, 1926.	7.4	0
6	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
7	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
8	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
9	Host genetic effects in pneumonia. American Journal of Human Genetics, 2021, 108, 194-201.	6.2	17
10	Co-detection of SARS-CoV-2 with Secondary Respiratory Pathogen Infections. Journal of General Internal Medicine, 2021, 36, 1159-1160.	2.6	2
11	Commonalities across computational workflows for uncovering explanatory variants in undiagnosed cases. Genetics in Medicine, 2021, 23, 1075-1085.	2.4	16
12	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
13	Multi-omic analysis elucidates the genetic basis of hydrocephalus. Cell Reports, 2021, 35, 109085.	6.4	18
14	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
15	Phenotypic signatures in clinical data enable systematic identification of patients for genetic testing. Nature Medicine, 2021, 27, 1097-1104.	30.7	21
16	Association Between a Common, Benign Genotype and Unnecessary Bone Marrow Biopsies Among African American Patients. JAMA Internal Medicine, 2021, 181, 1100.	5.1	18
17	Aggregating Electronic Health Record Data for COVID-19 Research—Caveat Emptor. JAMA Network Open, 2021, 4, e2117175.	5.9	13
18	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

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19	One is the loneliest number: genotypic matchmaking using the electronic health record. <i>Genetics in Medicine</i> , 2021, 23, 1830-1832.	2.4	6
20	The Role of Electronic Health Records in Advancing Genomic Medicine. <i>Annual Review of Genomics and Human Genetics</i> , 2021, 22, 219-238.	6.2	11
21	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. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2021, 28, 393-401.	4.4	54
22	Mapping the Read2/CTV3 controlled clinical terminologies to Phecodes in UK Biobank primary care electronic health records: implementation and evaluation.. <i>AMIA ... Annual Symposium proceedings</i> , 2021, 2021, 362-371.	0.2	0
23	Association of Genetic Risk of Obesity with Postoperative Complications Using Mendelian Randomization. <i>World Journal of Surgery</i> , 2020, 44, 84-94.	1.6	4
24	EHRs could clarify drug safety in pregnant people. <i>Nature Medicine</i> , 2020, 26, 820-821.	30.7	5
25	Phenome-wide association analysis suggests the APOL1 linked disease spectrum primarily drives kidney-specific pathways. <i>Kidney International</i> , 2020, 97, 1032-1041.	5.2	20
26	Electronic health record phenotypes associated with genetically regulated expression of CFTR and application to cystic fibrosis. <i>Genetics in Medicine</i> , 2020, 22, 1191-1200.	2.4	6
27	NKCC1: Newly Found as a Human Disease-Causing Ion Transporter. <i>Function</i> , 2020, 2, zqaa028.	2.3	29
28	SAT-LB111 Improving Classification of Diabetes Etiology in Electronic Resources Using Phenotype Algorithms and Polygenic Risk Scores. <i>Journal of the Endocrine Society</i> , 2020, 4, .	0.2	0
29	Improving the phenotype risk score as a scalable approach to identifying patients with Mendelian disease. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2019, 26, 1437-1447.	4.4	35
30	The current state of omics technologies in the clinical management of asthma and allergic diseases. <i>Annals of Allergy, Asthma and Immunology</i> , 2019, 123, 550-557.	1.0	23
31	Association of Thyroid Function Genetic Predictors With Atrial Fibrillation. <i>JAMA Cardiology</i> , 2019, 4, 136.	6.1	23
32	IgG4-related disease: Association with a rare gene variant expressed in cytotoxic T cells. <i>Molecular Genetics &amp; Genomic Medicine</i> , 2019, 7, e686.	1.2	8
33	Case 40-2018: A Woman with Recurrent Sinusitis, Cough, and Bronchiectasis. <i>New England Journal of Medicine</i> , 2019, 380, 1382-1383.	27.0	4
34	GRIK5 Genetically Regulated Expression Associated with Eye and Vascular Phenomes: Discovery through Iteration among Biobanks, Electronic Health Records, and Zebrafish. <i>American Journal of Human Genetics</i> , 2019, 104, 503-519.	6.2	21
35	Cox regression increases power to detect genotype-phenotype associations in genomic studies using the electronic health record. <i>BMC Genomics</i> , 2019, 20, 805.	2.8	24
36	Mapping ICD-10 and ICD-10-CM Codes to Phecodes: Workflow Development and Initial Evaluation. <i>JMIR Medical Informatics</i> , 2019, 7, e14325.	2.6	323

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37	Glucagon-like peptide 1 receptor signaling attenuates respiratory syncytial virus-induced type 2 responses and immunopathology. <i>Journal of Allergy and Clinical Immunology</i> , 2018, 142, 683-687.e12.	2.9	41
38	Phenotype risk scores identify patients with unrecognized Mendelian disease patterns. <i>Science</i> , 2018, 359, 1233-1239.	12.6	164
39	Cardiovascular toxicities associated with immune checkpoint inhibitors: an observational, retrospective, pharmacovigilance study. <i>Lancet Oncology</i> , The, 2018, 19, 1579-1589.	10.7	742
40	Pulling the covers in electronic health records for an association study with self-reported sleep behaviors. <i>Chronobiology International</i> , 2018, 35, 1702-1712.	2.0	2
41	A study paradigm integrating prospective epidemiologic cohorts and electronic health records to identify disease biomarkers. <i>Nature Communications</i> , 2018, 9, 3522.	12.8	13
42	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. <i>PLoS Medicine</i> , 2018, 15, e1002642.	8.4	22
43	Exploring the role of low-frequency and rare exonic variants in alcohol and tobacco use. <i>Drug and Alcohol Dependence</i> , 2018, 188, 94-101.	3.2	10
44	Association of ST2 polymorphisms with atopy, asthma, and leukemia. <i>Journal of Allergy and Clinical Immunology</i> , 2018, 142, 991-993.e3.	2.9	4
45	Rare Variants in the Gene ALPL That Cause Hypophosphatasia Are Strongly Associated With Ovarian and Uterine Disorders. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2018, 103, 2234-2243.	3.6	7
46	Accelerating Precision Drug Development and Drug Repurposing by Leveraging Human Genetics. <i>Assay and Drug Development Technologies</i> , 2017, 15, 113-119.	1.2	30
47	Phenome-wide scanning identifies multiple diseases and disease severity phenotypes associated with HLA variants. <i>Science Translational Medicine</i> , 2017, 9, .	12.4	105
48	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>). <i>Pharmacotherapy</i> , 2017, 37, 1164-1171.	2.6	14
49	Comparison of HLA allelic imputation programs. <i>PLoS ONE</i> , 2017, 12, e0172444.	2.5	58
50	Defining the complex phenotype of severe systemic loxoscelism using a large electronic health record cohort. <i>PLoS ONE</i> , 2017, 12, e0174941.	2.5	12
51	Phenome-Wide Association Studies as a Tool to Advance Precision Medicine. <i>Annual Review of Genomics and Human Genetics</i> , 2016, 17, 353-373.	6.2	193
52	Joint mouseâ€human phenome-wide association to test gene function and disease risk. <i>Nature Communications</i> , 2016, 7, 10464.	12.8	190
53	The phenotypic legacy of admixture between modern humans and Neandertals. <i>Science</i> , 2016, 351, 737-741.	12.6	269
54	Using a gene-environment interaction study to evaluate risk for lung cancer.. <i>Journal of Clinical Oncology</i> , 2016, 34, 1524-1524.	1.6	0

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55	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
56	R PheWAS: data analysis and plotting tools for phenome-wide association studies in the R environment. Bioinformatics, 2014, 30, 2375-2376.	4.1	334
57	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
58	A General Purpose Phenotype Algorithm for Venous Thromboembolism Using Billing Codes and Natural Language Processing. , 2012, , .		0
59	Natural Language Processing Improves Identification of Colorectal Cancer Testing in the Electronic Medical Record. Medical Decision Making, 2012, 32, 188-197.	2.4	63
60	PheWAS: demonstrating the feasibility of a phenome-wide scan to discover gene-disease associations. Bioinformatics, 2010, 26, 1205-1210.	4.1	966