Ingo Ruczinski

List of Publications by Year
in descending order

103 papers	7,728 citations	109137 35 h-index	64668 79 g-index
106 all docs	106 docs citations	106 times ranked	12323 citing authors

#	Article	IF	Citations
1	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	13.7	1,069
2	A genome-wide association study of cleft lip with and without cleft palate identifies risk variants near MAFB and ABCA4. Nature Genetics, 2010, 42, 525-529.	9.4	518
3	Ab initio protein structure prediction of CASP III targets using ROSETTA. Proteins: Structure, Function and Bioinformatics, 1999, 37, 171-176.	1.5	435
4	Improved recognition of native-like protein structures using a combination of sequence-dependent and sequence-independent features of proteins. , 1999, 34, 82-95.		389
5	Experiment and theory highlight role of native state topology in SH3 folding. Nature Structural Biology, 1999, 6, 1016-1024.	9.7	349
6	Genome-wide meta-analyses of nonsyndromic cleft lip with or without cleft palate identify six new risk loci. Nature Genetics, 2012, 44, 968-971.	9.4	311
7	Logic Regression. Journal of Computational and Graphical Statistics, 2003, 12, 475-511.	0.9	274
8	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.	9.4	257
9	Rosetta in CASP4: Progress in ab initio protein structure prediction. Proteins: Structure, Function and Bioinformatics, 2001, 45, 119-126.	1.5	242
10	Detecting significant changes in protein abundance. EuPA Open Proteomics, 2015, 7, 11-19.	2.5	240
11	Protein folding: Defining a â€œstandardâ€•set of experimental conditions and a preliminary kinetic data set of two-state proteins. Protein Science, 2005, 14, 602-616.	3.1	207
12	Genome-wide analyses of non-syndromic cleft lip with palate identify 14 novel loci and genetic heterogeneity. Nature Communications, 2017, 8, 14364.	5.8	207
13	Genomeâ€wide association study of schizophrenia in Ashkenazi Jews. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2015, 168, 649-659.	1.1	203
14	Identifying interacting SNPs using Monte Carlo logic regression. Genetic Epidemiology, 2005, 28, 157-170.	0.6	195
15	Ab initio protein structure prediction of CASP III targets using ROSETTA. Proteins: Structure, Function and Bioinformatics, 1999, Suppl 3, 171-6.	1.5	191
16	Identification of Functional Variants for Cleft Lip with or without Cleft Palate in or near PAX7, FGFR2, and NOG by Targeted Sequencing of GWAS Loci. American Journal of Human Genetics, 2015, 96, 397-411.	2.6	150
17	Evidence for gene-environment interaction in a genome wide study of nonsyndromic cleft palate. Genetic Epidemiology, 2011, 35, n/a-n/a.	0.6	145
18	A continuum of admixture in the Western Hemisphere revealed by the African Diaspora genome. Nature Communications, 2016, 7, 12522.	5.8	136

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19	Statistical Inference from Multiple iTRAQ Experiments without Using Common Reference Standards. Journal of Proteome Research, 2013, 12, 594-604.	1.8	130
20	Sequence Analysis Using Logic Regression. Genetic Epidemiology, 2001, 21, S626-31.	0.6	114
21	Ab initio protein structure prediction of CASP III targets using ROSETTA. Proteins: Structure, Function and Bioinformatics, 1999, 37, 171-176.	1.5	99
22	Contact order and ab initio protein structure prediction. Protein Science, 2002, 11, 1937-1944.	3.1	95
23	Whole Exome Sequencing of Distant Relatives in Multiplex Families Implicates Rare Variants in Candidate Genes for Oral Clefts. Genetics, 2014, 197, 1039-1044.	1.2	79
24	Association study in African-admixed populations across the Americas recapitulates asthma risk loci in non-African populations. Nature Communications, 2019, 10, 880.	5.8	71
25	Distributions of beta sheets in proteins with application to structure prediction. Proteins: Structure, Function and Bioinformatics, 2002, 48, 85-97.	1.5	69
26	Challenges and disparities in the application of personalized genomic medicine to populations with African ancestry. Nature Communications, 2016, 7, 12521.	5.8	68
27	Exploring interactions in high-dimensional genomic data: an overview of Logic Regression, with applications. Journal of Multivariate Analysis, 2004, 90, 178-195.	0.5	67
28	Large-Scale Genome-Wide Association Studies and Meta-Analyses of Longitudinal Change in Adult Lung Function. PLoS ONE, 2014, 9, e100776.	1.1	52
29	Genome-wide Enrichment of De Novo Coding Mutations in Orofacial Cleft Trios. American Journal of Human Genetics, 2020, 107, 124-136.	2.6	48
30	Surfactant protein D is a causal risk factor for COPD: results of Mendelian randomisation. European Respiratory Journal, 2017, 50, 1700657.	3.1	45
31	Imputation methods to improve inference in SNP association studies. Genetic Epidemiology, 2006, 30, 690-702.	0.6	44
32	Targeted deep sequencing identifies rare loss-of-function variants in IFNGR1 for risk of atopic dermatitis complicated by eczema herpeticum. Journal of Allergy and Clinical Immunology, 2015, 136, 1591-1600.	1.5	42
33	Impact of methods used to express levels of circulating fatty acids on the degree and direction of associations with blood lipids in humans. British Journal of Nutrition, 2016, 115, 251-261.	1.2	42
34	On the precision of experimentally determined protein folding rates and Â-values. Protein Science, 2006, 15, 553-563.	3.1	41
35	The FGF and FGFR Gene Family and Risk of Cleft Lip with or Without Cleft Palate. Cleft Palate-Craniofacial Journal, 2013, 50, 96-103.	0.5	39
36	Evolution of Hominin Polyunsaturated Fatty Acid Metabolism: From Africa to the New World. Genome Biology and Evolution, 2019, 11, 1417-1430.	1.1	38

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37	Testing SNPs and sets of SNPs for importance in association studies. Biostatistics, 2011, 12, 18-32.	0.9	36
38	The MALT1 locus and peanut avoidance in the risk for peanut allergy. Journal of Allergy and Clinical Immunology, 2019, 143, 2326-2329.	1.5	36
39	Rapid Testing of SNPs and Geneâ€"Environment Interactions in Caseâ€"Parent Trio Data Based on Exact Analytic Parameter Estimation. Biometrics, 2012, 68, 766-773.	0.8	34
40	Evidence of Geneâ^'Environment Interaction for Two Genes on Chromosome 4 and Environmental Tobacco Smoke in Controlling the Risk of Nonsyndromic Cleft Palate. PLoS ONE, 2014, 9, e88088.	1.1	33
41	Logic Regression and Its Extensions. Advances in Genetics, 2010, 72, 25-45.	0.8	32
42	Whole exome sequencing analysis in severe chronic obstructive pulmonary disease. Human Molecular Genetics, 2018, 27, 3801-3812.	1.4	32
43	Whole genome sequence analysis of pulmonary function and COPD in 19,996 multi-ethnic participants. Nature Communications, 2020, 11, 5182.	5.8	32
44	A combined genome-wide linkage and association approach to find susceptibility loci for platelet function phenotypes in European American and African American families with coronary artery disease. BMC Medical Genomics, 2010, 3, 22.	0.7	31
45	Inferring rare disease risk variants based on exact probabilities of sharing by multiple affected relatives. Bioinformatics, 2014, 30, 2189-2196.	1.8	30
46	Tissue-specific impact of FADS cluster variants on FADS1 and FADS2 gene expression. PLoS ONE, 2018, 13, e0194610.	1.1	29
47	Genome sequencing unveils a regulatory landscape of platelet reactivity. Nature Communications, 2021, 12, 3626.	5.8	29
48	An IL-13 Promoter Polymorphism Associated with Liver Fibrosis in Patients with Schistosoma japonicum. PLoS ONE, 2015, 10, e0135360.	1.1	29
49	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. Cell Genomics, 2022, 2, 100084.	3.0	29
50	Examining Markers in 8q24 to Explain Differences in Evidence for Association With Cleft Lip With/Without Cleft Palate Between <scp>A</scp>sians and <scp>E</scp>uropeans. Genetic Epidemiology, 2012, 36, 392-399.	0.6	28
51	Genome-Wide Association Study Identification of Novel Loci Associated with Airway Responsiveness in Chronic Obstructive Pulmonary Disease. American Journal of Respiratory Cell and Molecular Biology, 2015, 53, 226-234.	1.4	27
52	Comprehensive Profiling of HIV Antibody Evolution. Cell Reports, 2019, 27, 1422-1433.e4.	2.9	27
53	Evidence for SNP-SNP interaction identified through targeted sequencing of cleft case-parent trios. Genetic Epidemiology, 2017, 41, 244-250.	0.6	24
54	Uncovering the DNA methylation landscape in key regulatory regions within the FADS cluster. PLoS ONE, 2017, 12, e0180903.	1.1	23

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55	Replicated methylation changes associated with eczema herpeticum and allergic response. Clinical Epigenetics, 2019, 11, 122.	1.8	22
56	Plasma Proteome Biomarkers of Inflammation in School Aged Children in Nepal. PLoS ONE, 2015, 10, e0144279.	1.1	22
57	A genome-wide study of de novo deletions identifies a candidate locus for non-syndromic isolated cleft lip/palate risk. BMC Genetics, 2014, 15, 24.	2.7	21
58	Transcriptional profile of platelets and iPSC-derived megakaryocytes from whole-genome and RNA sequencing. Blood, 2021, 137, 959-968.	0.6	21
59	Detection of SNPâ€SNP interactions in trios of parents with schizophrenic children. Genetic Epidemiology, 2010, 34, 396-406.	0.6	20
60	Whole genome sequencing identifies novel genetic mutations in patients with eczema herpeticum. Allergy: European Journal of Allergy and Clinical Immunology, 2021, 76, 2510-2523.	2.7	20
61	Detecting Disease Variants in Case-Parent Trio Studies Using the Bioconductor Software Package<tt>trio</tt>. Genetic Epidemiology, 2014, 38, 516-522.	0.6	19
62	Targeted deep sequencing of the PEAR1 locus for platelet aggregation in European and African American families. Platelets, 2019, 30, 380-386.	1.1	19
63	Pleiotropy method reveals genetic overlap between orofacial clefts at multiple novel loci from GWAS of multi-ethnic trios. PLoS Genetics, 2021, 17, e1009584.	1.5	18
64	Protective effect of club cell secretory protein (CC-16) on COPD risk and progression: a Mendelian randomisation study. Thorax, 2020, 75, 934-943.	2.7	17
65	The role of ST2 and ST2 genetic variants in schistosomiasis. Journal of Allergy and Clinical Immunology, 2017, 140, 1416-1422.e6.	1.5	15
66	Multiethnic genome-wide and HLA association study of total serum IgE level. Journal of Allergy and Clinical Immunology, 2021, 148, 1589-1595.	1.5	15
67	HLA alleles and sustained peanut consumption promote IgG4 responses in subjects protected from peanut allergy. Journal of Clinical Investigation, 2022, 132, .	3.9	15
68	Geneâ€based segregation method for identifying rare variants in familyâ€based sequencing studies. Genetic Epidemiology, 2017, 41, 309-319.	0.6	14
69	The pharmacogenomics of inhaled corticosteroids and lung function decline in COPD. European Respiratory Journal, 2019, 54, 1900521.	3.1	14
70	Association of HLA-DRB1âˆ—09:01 with tIgE levels among African-ancestry individuals with asthma. Journal of Allergy and Clinical Immunology, 2020, 146, 147-155.	1.5	14
71	Importance Measures for Epistatic Interactions in Case-Parent Trios. Annals of Human Genetics, 2011, 75, 122-132.	0.3	13
72	Fast detection of de novo copy number variants from SNP arrays for case-parent trios. BMC Bioinformatics, 2012, 13, 330.	1.2	13

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73	Incorporating Genotype Uncertainties Into the Genotypic TDT for Main Effects and Geneâ€Environment Interactions. Genetic Epidemiology, 2012, 36, 225-234.	0.6	13
74	Methods for the accurate estimation of confidence intervals on protein folding Ït-values. Protein Science, 2006, 15, 2257-2264.	3.1	12
75	A genomeâ€wide study of inherited deletions identified two regions associated with nonsyndromic isolated oral clefts. Birth Defects Research Part A: Clinical and Molecular Teratology, 2015, 103, 276-283.	1.6	11
76	The genetics of smoking in individuals with chronic obstructive pulmonary disease. Respiratory Research, 2018, 19, 59.	1.4	11
77	Whole exome association of rare deletions in multiplex oral cleft families. Genetic Epidemiology, 2017, 41, 61-69.	0.6	10
78	Genomic integrity of human induced pluripotent stem cells across nine studies in the NHLBI NextGen program. Stem Cell Research, 2020, 46, 101803.	0.3	10
79	Oesophageal squamous cell carcinoma in high-risk Chinese populations: Possible role for vascular epithelial growth factor A. European Journal of Cancer, 2014, 50, 2855-2865.	1.3	9
80	Improved recognition of native-like protein structures using a combination of sequence-dependent and sequence-independent features of proteins. , 1999, 34, 82.		9
81	Integrity of Induced Pluripotent Stem Cell (iPSC) Derived Megakaryocytes as Assessed by Genetic and Transcriptomic Analysis. PLoS ONE, 2017, 12, e0167794.	1.1	9
82	A Risk Prediction Model for Mortality Among Smokers in the COPDGeneÂ® Study. Chronic Obstructive Pulmonary Diseases (Miami, Fla), 2020, 7, 346-361.	0.5	9
83	Candidate Pathway Based Analysis for Cleft Lip with or without Cleft Palate. Statistical Applications in Genetics and Molecular Biology, 2012, 11, .	0.2	7
84	Polygenic transcriptome risk scores for COPD and lung function improve cross-ethnic portability of prediction in the NHLBI TOPMed program. American Journal of Human Genetics, 2022, 109, 857-870.	2.6	7
85	Detection of rare disease variants in extended pedigrees using RVS. Bioinformatics, 2019, 35, 2509-2511.	1.8	6
86	Inferring disease risk genes from sequencing data in multiplex pedigrees through sharing of rare variants. Genetic Epidemiology, 2019, 43, 37-49.	0.6	6
87	HIV Antibody Profiles in HIV Controllers and Persons With Treatment-Induced Viral Suppression. Frontiers in Immunology, 2021, 12, 740395.	2.2	6
88	Identifying a Deletion Affecting Total Lung Capacity Among Subjects in the COPDGene Study Cohort. Genetic Epidemiology, 2016, 40, 81-88.	0.6	5
89	Polymorphisms Influencing Prostate-Specific Antigen Concentration May Bias Genome-Wide Association Studies on Prostate Cancer. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 88-93.	1.1	4
90	Optimized distributed systems achieve significant performance improvement on sorted merging of massive VCF files. GigaScience, 2018, 7, .	3.3	4

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91	A flexible and nearly optimal sequential testing approach to randomized testing: QUICKâ€STOP. Genetic Epidemiology, 2020, 44, 139-147.	0.6	4
92	Hemizygous Deletion on Chromosome 3p26.1 Is Associated with Heavy Smoking among African American Subjects in the COPDGene Study. PLoS ONE, 2016, 11, e0164134.	1.1	4
93	Efficient Simulation of Epistatic Interactions in Case-Parent Trios. Human Heredity, 2013, 75, 12-22.	0.4	3
94	A top scoring pairs classifier for recent HIV infections. Statistics in Medicine, 2021, 40, 2604-2612.	0.8	3
95	Ab initio protein structure prediction of CASP III targets using ROSETTA. , 1999, 37, 171.		3
96	Some recommendations for the practitioner to improve the precision of experimentally determined protein folding rates and Ï• values. Proteins: Structure, Function and Bioinformatics, 2009, 74, 461-474.	1.5	2
97	Detection of de novo copy number deletions from targeted sequencing of trios. Bioinformatics, 2019, 35, 571-578.	1.8	2
98	Detecting Gene-Environment Interaction for Maternal Exposures Using Case-Parent Trios Ascertained Through a Case With Non-Syndromic Orofacial Cleft. Frontiers in Cell and Developmental Biology, 2021, 9, 621018.	1.8	2
99	Secondary analyses for genomeâ€wide association studies using expression quantitative trait loci. Genetic Epidemiology, 2022, , .	0.6	2
100	Identification of interactions of binary variables associated with survival time using survivalFS. Archives of Toxicology, 2019, 93, 585-602.	1.9	0
101	Bayesian copy number detection and association in large-scale studies. BMC Cancer, 2020, 20, 856.	1.1	0
102	A preâ€processing pipeline to quantify, visualize, and reduce technical variation in protein microarray studies. Proteomics, 2022, 22, e2100033.	1.3	0
103	Effects of Antenatal Micronutrient Supplementation on Plasma Protein Profiles in Nepalese Children. FASEB Journal, 2013, 27, 1080.7.	0.2	0