Bjarni V Halldorsson

List of Publications by Year
in descending order

109 papers	13,654 citations	41627 51 h-index	34195 103 g-index
129 all docs	129 docs citations	129 times ranked	23366 citing authors

#	Article	IF	Citations
1	Population-scale detection of non-reference sequence variants using colored de Bruijn graphs. Bioinformatics, 2022, 38, 604-611.	1.8	4
2	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals. Nature Genetics, 2022, 54, 437-449.	9.4	215
3	read_haps: using read haplotypes to detect same species contamination in DNA sequences. Bioinformatics, 2021, 37, 2215-2217.	1.8	1
4	Lifelong Reduction in LDL (Low-Density Lipoprotein) Cholesterol due to a Gain-of-Function Mutation in LDLR. Circulation Genomic and Precision Medicine, 2021, 14, e003029.	1.6	12
5	Local improvement algorithms for a path packing problem: A performance analysis based on linear programming. Operations Research Letters, 2021, 49, 62-68.	0.5	2
6	Ratatosk: hybrid error correction of long reads enables accurate variant calling and assembly. Genome Biology, 2021, 22, 28.	3.8	35
7	A meta-analysis uncovers the first sequence variant conferring risk of Bellâ€™s palsy. Scientific Reports, 2021, 11, 4188.	1.6	8
8	Loss-of-Function Variants in the Tumor-Suppressor Gene PTPN14 Confer Increased Cancer Risk. Cancer Research, 2021, 81, 1954-1964.	0.4	15
9	PopDel identifies medium-size deletions simultaneously in tens of thousands of genomes. Nature Communications, 2021, 12, 730.	5.8	9
10	Variable number tandem repeats mediate the expression of proximal genes. Nature Communications, 2021, 12, 2075.	5.8	47
11	Long-read sequencing of 3,622 Icelanders provides insight into the role of structural variants in human diseases and other traits. Nature Genetics, 2021, 53, 779-786.	9.4	156
12	The genetic architecture of age-related hearing impairment revealed by genome-wide association analysis. Communications Biology, 2021, 4, 706.	2.0	30
13	Large-Scale Screening for Monogenic and Clinically Defined Familial Hypercholesterolemia in Iceland. Arteriosclerosis, Thrombosis, and Vascular Biology, 2021, 41, 2616-2628.	1.1	16
14	Differences between germline genomes of monozygotic twins. Nature Genetics, 2021, 53, 27-34.	9.4	83
15	Large-scale integration of the plasma proteome with genetics and disease. Nature Genetics, 2021, 53, 1712-1721.	9.4	340
16	popSTR2 enables clinical and population-scale genotyping of microsatellites. Bioinformatics, 2020, 36, 2269-2271.	1.8	11
17	Sequence Variants in TAAR5 and Other Loci Affect Human Odor Perception and Naming. Current Biology, 2020, 30, 4643-4653.e3.	1.8	19
18	Genome-wide association identifies seven loci for pelvic organ prolapse in Iceland and the UK Biobank. Communications Biology, 2020, 3, 129.	2.0	20

#	Article	IF	Citations
19	Eighty-eight variants highlight the role of T cell regulation and airway remodeling in asthma pathogenesis. Nature Communications, 2020, 11, 393.	5.8	59
20	The nature of Neanderthal introgression revealed by 27,566 Icelandic genomes. Nature, 2020, 582, 78-83.	13.7	71
21	A Branch & Price algorithm for the minimum cost clique cover problem in max-point tolerance graphs. 4or, 2019, 17, 75-96.	1.0	0
22	Characterizing mutagenic effects of recombination through a sequence-level genetic map. Science, 2019, 363, .	6.0	252
23	GraphTyper2 enables population-scale genotyping of structural variation using pangenome graphs. Nature Communications, 2019, 10, 5402.	5.8	96
24	Lipoprotein(a) Concentration and Risks of Cardiovascular Disease and Diabetes. Journal of the American College of Cardiology, 2019, 74, 2982-2994.	1.2	127
25	A loss-of-function variant in ALOX15 protects against nasal polyps and chronic rhinosinusitis. Nature Genetics, 2019, 51, 267-276.	9.4	83
26	Sequence variants associating with urinary biomarkers. Human Molecular Genetics, 2019, 28, 1199-1211.	1.4	28
27	Clinical decision support system for the management of osteoporosis compared to NOGG guidelines and an osteology specialist: a validation pilot study. BMC Medical Informatics and Decision Making, 2019, 19, 27.	1.5	9
28	The nature of nurture: Effects of parental genotypes. Science, 2018, 359, 424-428.	6.0	720
29	Profile of common prostate cancer risk variants in an unscreened Romanian population. Journal of Cellular and Molecular Medicine, 2018, 22, 1574-1582.	1.6	4
30	Multiple transmissions of de novo mutations in families. Nature Genetics, 2018, 50, 1674-1680.	9.4	89
31	Identification of Lynch syndrome risk variants in the Romanian population. Journal of Cellular and Molecular Medicine, 2018, 22, 6068-6076.	1.6	5
32	Insights into imprinting from parent-of-origin phased methylomes and transcriptomes. Nature Genetics, 2018, 50, 1542-1552.	9.4	94
33	Variants associating with uterine leiomyoma highlight genetic background shared by various cancers and hormone-related traits. Nature Communications, 2018, 9, 3636.	5.8	74
34	Coding variants in RPL3L and MYZAP increase risk of atrial fibrillation. Communications Biology, 2018, 1, 68.	2.0	42
35	DNA methylation as a mediator of HLA-DRB1*15:01 and a protective variant in multiple sclerosis. Nature Communications, 2018, 9, 2397.	5.8	147
36	popSTR: population-scale detection of STR variants. Bioinformatics, 2017, 33, 4041-4048.	1.8	34

#	Article	IF	Citations
37	Max point-tolerance graphs. Discrete Applied Mathematics, 2017, 216, 84-97.	0.5	29
38	Diversity in non-repetitive human sequences not found in the reference genome. Nature Genetics, 2017, 49, 588-593.	9.4	70
39	Identification of sequence variants influencing immunoglobulin levels. Nature Genetics, 2017, 49, 1182-1191.	9.4	90
40	Whole genome characterization of sequence diversity of 15,220 Icelanders. Scientific Data, 2017, 4, 170115.	2.4	98
41	Graphtyper enables population-scale genotyping using pangenome graphs. Nature Genetics, 2017, 49, 1654-1660.	9.4	189
42	Parental influence on human germline de novo mutations in 1,548 trios from Iceland. Nature, 2017, 549, 519-522.	13.7	410
43	A sequence variant associating with educational attainment also affects childhood cognition. Scientific Reports, 2016, 6, 36189.	1.6	2
44	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	13.7	1,204
45	The rate of meiotic gene conversion varies by sex and age. Nature Genetics, 2016, 48, 1377-1384.	9.4	85
46	Genetic variants linked to education predict longevity. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13366-13371.	3.3	110
47	Streaming Algorithms for Independent Sets in Sparse Hypergraphs. Algorithmica, 2016, 76, 490-501.	1.0	10
48	Insertion of an SVA-E retrotransposon into theCASP8gene is associated with protection against prostate cancer. Human Molecular Genetics, 2016, 25, 1008-1018.	1.4	22
49	HLA class II sequence variants influence tuberculosis risk in populations of European ancestry. Nature Genetics, 2016, 48, 318-322.	9.4	123
50	The minimum vulnerability problem on specific graph classes. Journal of Combinatorial Optimization, 2016, 32, 1288-1304.	0.8	3
51	PopIns: population-scale detection of novel sequence insertions. Bioinformatics, 2016, 32, 961-967.	1.8	33
52	Methylation of Bone SOST, Its mRNA, and Serum Sclerostin Levels Correlate Strongly With Fracture Risk in Postmenopausal Women. Journal of Bone and Mineral Research, 2015, 30, 249-256.	3.1	85
53	Sequence variants from whole genome sequencing a large group of Icelanders. Scientific Data, 2015, 2, 150011.	2.4	59
54	A Clinical Decision Support System for the Diagnosis, Fracture Risks and Treatment of Osteoporosis. Computational and Mathematical Methods in Medicine, 2015, 2015, 1-7.	0.7	14

#	Article	IF	Citations
55	Large-scale whole-genome sequencing of the Icelandic population. Nature Genetics, 2015, 47, 435-444.	9.4	663
56	Causal mechanisms and balancing selection inferred from genetic associations with polycystic ovary syndrome. Nature Communications, 2015, 6, 8464.	5.8	304
57	New basal cell carcinoma susceptibility loci. Nature Communications, 2015, 6, 6825.	5.8	59
58	PopAlu: population-scale detection of Alu polymorphisms. PeerJ, 2015, 3, e1269.	0.9	6
59	A genome-wide copy number association study of osteoporotic fractures points to the 6p25.1 locus. Journal of Medical Genetics, 2014, 51, 122-131.	1.5	36
60	KmerStream: streaming algorithms for k -mer abundance estimation. Bioinformatics, 2014, 30, 3541-3547.	1.8	56
61	Estimating population size via line graph reconstruction. Algorithms for Molecular Biology, 2013, 8, 17.	0.3	1
62	Sleepâ€“wake dynamics under extended light and extended dark conditions in adult zebrafish. Behavioural Brain Research, 2013, 256, 377-390.	1.2	36
63	Network-Based Interpretation of Genomic Variation Data. Journal of Molecular Biology, 2013, 425, 3964-3969.	2.0	18
64	An Integer Programming Formulation of the Parsimonious Loss of Heterozygosity Problem. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 1391-1402.	1.9	3
65	DELISHUS: an efficient and exact algorithm for genome-wide detection of deletion polymorphism in autism. Bioinformatics, 2012, 28, i154-i162.	1.8	3
66	Invited: Algorithmic challenges in DNA sequencing and disease association. , 2012, , .		0
67	PAIR: polymorphic Alu insertion recognition. BMC Bioinformatics, 2012, 13, S7.	1.2	6
68	Estimating Population Size via Line Graph Reconstruction. Lecture Notes in Computer Science, 2012, , 69-80.	1.0	0
69	A Mixed Integer Programming Model for the Parsimonious Loss of Heterozygosity Problem. Lecture Notes in Computer Science, 2012, , 24-35.	1.0	0
70	Genetic variation near IRS1 associates with reduced adiposity and an impaired metabolic profile. Nature Genetics, 2011, 43, 753-760.	9.4	289
71	Meta-analysis of genome-wide association studies confirms a susceptibility locus for knee osteoarthritis on chromosome 7q22. Annals of the Rheumatic Diseases, 2011, 70, 349-355.	0.5	126
72	The Clark Phaseable Sample Size Problem: Long-Range Phasing and Loss of Heterozygosity in GWAS. Journal of Computational Biology, 2011, 18, 323-333.	0.8	16

#	Article	IF	Citations
73	An Algorithm for Detecting High Frequency Copy Number Polymorphisms Using SNP Arrays. Journal of Computational Biology, 2011, 18, 955-966.	0.8	2
74	Association of JAG1 with Bone Mineral Density and Osteoporotic Fractures: A Genome-wide Association Study and Follow-up Replication Studies. American Journal of Human Genetics, 2010, 86, 229-239.	2.6	188
75	A genomeâ€wide association study identifies an osteoarthritis susceptibility locus on chromosome 7q22. Arthritis and Rheumatism, 2010, 62, 499-510.	6.7	178
76	On shortest crucial words avoiding abelian powers. Discrete Applied Mathematics, 2010, 158, 605-607.	0.5	6
77	Streaming Algorithms for Independent Sets. Lecture Notes in Computer Science, 2010, , 641-652.	1.0	13
78	HAPLOTYPE PHASING BY MULTI-ASSEMBLY OF SHARED HAPLOTYPES: PHASE-DEPENDENT INTERACTIONS BETWEEN RARE VARIANTS. , 2010, , 88-99.		8
79	Ancestry-Shift Refinement Mapping of the C6orf97-ESR1 Breast Cancer Susceptibility Locus. PLoS Genetics, 2010, 6, e1001029.	1.5	82
80	European Bone Mineral Density Loci Are Also Associated with BMD in East-Asian Populations. PLoS ONE, 2010, 5, e13217.	1.1	81
81	The Clark Phase-able Sample Size Problem: Long-Range Phasing and Loss of Heterozygosity in GWAS. Lecture Notes in Computer Science, 2010, , 158-173.	1.0	1
82	Largeâ€scale analysis of association between GDF5 and FRZB variants and osteoarthritis of the hip, knee, and hand. Arthritis and Rheumatism, 2009, 60, 1710-1721.	6.7	181
83	New sequence variants associated with bone mineral density. Nature Genetics, 2009, 41, 15-17.	9.4	328
84	Sequence variants in the CLDN14 gene associate with kidney stones and bone mineral density. Nature Genetics, 2009, 41, 926-930.	9.4	248
85	Twenty bone-mineral-density loci identified by large-scale meta-analysis of genome-wide association studies. Nature Genetics, 2009, 41, 1199-1206.	9.4	660
86	Collaborative Meta-analysis: Associations of 150 Candidate Genes With Osteoporosis and Osteoporotic Fracture. Annals of Internal Medicine, 2009, 151, 528.	2.0	250
87	Crucial Words for Abelian Powers. Lecture Notes in Computer Science, 2009, , 264-275.	1.0	1
88	Impact of Genetics on Low Bone Mass in Adults. Journal of Bone and Mineral Research, 2008, 23, 1584-1590.	3.1	41
89	Large recurrent microdeletions associated with schizophrenia. Nature, 2008, 455, 232-236.	13.7	1,619
90	Many sequence variants affecting diversity of adult human height. Nature Genetics, 2008, 40, 609-615.	9.4	615

#	Article	IF	Citations
91	Lessons from the past: Familial aggregation analysis of fatal pandemic influenza (Spanish flu) in Iceland in 1918. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 1303-1308.	3.3	55
92	Multiple Genetic Loci for Bone Mineral Density and Fractures. New England Journal of Medicine, 2008, 358, 2355-2365.	13.9	582
93	Islands of Tractability for Parsimony Haplotyping. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2006, 3, 303-311.	1.9	24
94	A Hybrid Microâ€“Macroevolutionary Approach to Gene Tree Reconstruction. Journal of Computational Biology, 2006, 13, 320-335.	0.8	240
95	The linkage disequilibrium maps of three human chromosomes across four populations reflect their demographic history and a common underlying recombination pattern. Genome Research, 2005, 15, 454-462.	2.4	107
96	Islands of tractability for parsimony haplotyping. , 2005, , 65-72.		4
97	Optimal Haplotype Block-Free Selection of Tagging SNPs for Genome-Wide Association Studies. Genome Research, 2004, 14, 1633-1640.	2.4	113
98	Whole-genome shotgun assembly and comparison of human genome assemblies. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 1916-1921.	3.3	164
99	Comparative immunopeptidomics of humans and their pathogens. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 13268-13272.	3.3	38
100	Estrogen Receptor Genotypes and Haplotypes Associated with Breast Cancer Risk. Cancer Research, 2004, 64, 8891-8900.	0.4	97
101	Optimal Selection of SNP Markers for Disease Association Studies. Human Heredity, 2004, 58, 190-202.	0.4	63
102	A Survey of Computational Methods for Determining Haplotypes. Lecture Notes in Computer Science, 2004, , 26-47.	1.0	72
103	An Interior-Point Method for a Class of Saddle-Point Problems. Journal of Optimization Theory and Applications, 2003, 116, 559-590.	0.8	66
104	Approximation algorithms for the test cover problem. Mathematical Programming, 2003, 98, 477-491.	1.6	76
105	Robustness of Inference of Haplotype Block Structure. Journal of Computational Biology, 2003, 10, 13-19.	0.8	54
106	Combinatorial Problems Arising in SNP and Haplotype Analysis. Lecture Notes in Computer Science, 2003, , 26-47.	1.0	17
107	Haplotypes and informative SNP selection algorithms. , 2003, , .		52
108	Epitope prediction algorithms for peptide-based vaccine design. Proceedings, 2003, 2, 17-26.	0.1	16

#	Article	IF	Citations
109	Optimal Sequencing by Hybridization in Rounds. Journal of Computational Biology, 2002, 9, 355-369.	0.8	12