GÃ-sli MÃ¡sson

List of Publications by Year
in descending order

38 papers	12,670 citations	109321 35 h-index	315739 38 g-index
41 all docs	41 docs citations	41 times ranked	25250 citing authors

#	Article	IF	Citations
1	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.	3.6	12
2	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.	21.4	156
3	Differences between germline genomes of monozygotic twins. Nature Genetics, 2021, 53, 27-34.	21.4	83
4	Humoral Immune Response to SARS-CoV-2 in Iceland. New England Journal of Medicine, 2020, 383, 1724-1734.	27.0	845
5	Eighty-eight variants highlight the role of T cell regulation and airway remodeling in asthma pathogenesis. Nature Communications, 2020, 11, 393.	12.8	59
6	Spread of SARS-CoV-2 in the Icelandic Population. New England Journal of Medicine, 2020, 382, 2302-2315.	27.0	1,093
7	Characterizing mutagenic effects of recombination through a sequence-level genetic map. Science, 2019, 363, .	12.6	252
8	A loss-of-function variant in ALOX15 protects against nasal polyps and chronic rhinosinusitis. Nature Genetics, 2019, 51, 267-276.	21.4	83
9	The nature of nurture: Effects of parental genotypes. Science, 2018, 359, 424-428.	12.6	720
10	Relatedness disequilibrium regression estimates heritability without environmental bias. Nature Genetics, 2018, 50, 1304-1310.	21.4	147
11	Selection against variants in the genome associated with educational attainment. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E727-E732.	7.1	149
12	Whole genome characterization of sequence diversity of 15,220 Icelanders. Scientific Data, 2017, 4, 170115.	5.3	98
13	Graphtyper enables population-scale genotyping using pangenome graphs. Nature Genetics, 2017, 49, 1654-1660.	21.4	189
14	Parental influence on human germline de novo mutations in 1,548 trios from Iceland. Nature, 2017, 549, 519-522.	27.8	410
15	A frameshift deletion in the sarcomere geneMYL4causes early-onset familial atrial fibrillation. European Heart Journal, 2017, 38, 27-34.	2.2	89
16	A rare IL33 loss-of-function mutation reduces blood eosinophil counts and protects from asthma. PLoS Genetics, 2017, 13, e1006659.	3.5	126
17	VariantASGR1Associated with a Reduced Risk of Coronary Artery Disease. New England Journal of Medicine, 2016, 374, 2131-2141.	27.0	137
18	Variants with large effects on blood lipids and the role of cholesterol and triglycerides in coronary disease. Nature Genetics, 2016, 48, 634-639.	21.4	214

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19	The rate of meiotic gene conversion varies by sex and age. Nature Genetics, 2016, 48, 1377-1384.	21.4	85
20	Epigenetic and genetic components of height regulation. Nature Communications, 2016, 7, 13490.	12.8	52
21	GORpipe: a query tool for working with sequence data based on a Genomic Ordered Relational (GOR) architecture. Bioinformatics, 2016, 32, 3081-3088.	4.1	17
22	Weighting sequence variants based on their annotation increases power of whole-genome association studies. Nature Genetics, 2016, 48, 314-317.	21.4	178
23	Comprehensive population-wide detection of Lynch syndrome in Iceland.. Journal of Clinical Oncology, 2016, 34, 1542-1542.	1.6	3
24	Multi-nucleotide de novo Mutations in Humans. PLoS Genetics, 2016, 12, e1006315.	3.5	111
25	Sequence variants from whole genome sequencing a large group of Icelanders. Scientific Data, 2015, 2, 150011.	5.3	59
26	Identification of a large set of rare complete human knockouts. Nature Genetics, 2015, 47, 448-452.	21.4	214
27	Large-scale whole-genome sequencing of the Icelandic population. Nature Genetics, 2015, 47, 435-444.	21.4	663
28	Variants in ELL2 influencing immunoglobulin levels associate with multiple myeloma. Nature Communications, 2015, 6, 7213.	12.8	101
29	Rare mutations associating with serum creatinine and chronic kidney disease. Human Molecular Genetics, 2014, 23, 6935-6943.	2.9	52
30	Common and low-frequency variants associated with genome-wide recombination rate. Nature Genetics, 2014, 46, 11-16.	21.4	116
31	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97.	27.8	548
32	Loss-of-function mutations in SLC30A8 protect against type 2 diabetes. Nature Genetics, 2014, 46, 357-363.	21.4	428
33	Nonsense mutation in the LGR4 gene is associated with several human diseases and other traits. Nature, 2013, 497, 517-520.	27.8	236
34	Rate of de novo mutations and the importance of fatherâ€™s age to disease risk. Nature, 2012, 488, 471-475.	27.8	1,880
35	Fine-scale recombination rate differences between sexes, populations and individuals. Nature, 2010, 467, 1099-1103.	27.8	559
36	Parental origin of sequence variants associated with complex diseases. Nature, 2009, 462, 868-874.	27.8	521

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37	Detection of sharing by descent, long-range phasing and haplotype imputation. Nature Genetics, 2008, 40, 1068-1075.	21.4	409
38	A high-resolution recombination map of the human genome. Nature Genetics, 2002, 31, 241-247.	21.4	1,571