Thorunn Rafnar

List of Publications by Year
in descending order

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84 papers	15,832 citations	34493 54 h-index	60403 85 g-index
89 all docs	89 docs citations	89 times ranked	24052 citing authors

#	Article	IF	Citations
1	Functional dissection of inherited non-coding variation influencing multiple myeloma risk. Nature Communications, 2022, 13, 151.	5.8	10
2	Genetic architecture of band neutrophil fraction in Iceland. Communications Biology, 2022, 5, .	2.0	1
3	Loss-of-Function Variants in the Tumor-Suppressor Gene PTPN14 Confer Increased Cancer Risk. Cancer Research, 2021, 81, 1954-1964.	0.4	15
4	Germline variants at SOHLH2 influence multiple myeloma risk. Blood Cancer Journal, 2021, 11, 76.	2.8	6
5	Predicting the probability of death using proteomics. Communications Biology, 2021, 4, 758.	2.0	10
6	Identification of 22 susceptibility loci associated with testicular germ cell tumors. Nature Communications, 2021, 12, 4487.	5.8	27
7	Genetic variants associated with platelet count are predictive of human disease and physiological markers. Communications Biology, 2021, 4, 1132.	2.0	7
8	The CRTAC1 Protein in Plasma Is Associated With Osteoarthritis and Predicts Progression to Joint Replacement: A Largeâ€Scale Proteomics Scan in Iceland. Arthritis and Rheumatology, 2021, 73, 2025-2034.	2.9	27
9	Large-scale integration of the plasma proteome with genetics and disease. Nature Genetics, 2021, 53, 1712-1721.	9.4	340
10	FLT3 stop mutation increases FLT3 ligand level and risk of autoimmune thyroid disease. Nature, 2020, 584, 619-623.	13.7	81
11	Genome-wide association identifies seven loci for pelvic organ prolapse in Iceland and the UK Biobank. Communications Biology, 2020, 3, 129.	2.0	20
12	Predicted loss and gain of function mutations in ACO1 are associated with erythropoiesis. Communications Biology, 2020, 3, 189.	2.0	30
13	A PRPH splice-donor variant associates with reduced sural nerve amplitude and risk of peripheral neuropathy. Nature Communications, 2019, 10, 1777.	5.8	7
14	Clinical characteristics of patients with colorectal cancer with double somatic mismatch repair mutations compared with Lynch syndrome. Journal of Medical Genetics, 2019, 56, 462-470.	1.5	61
15	A Missense Variant in PTPN22 is a Risk Factor for Drug-induced Liver Injury. Gastroenterology, 2019, 156, 1707-1716.e2.	0.6	97
16	Common and rare sequence variants influencing tumor biomarkers in blood. Cancer Epidemiology Biomarkers and Prevention, 2019, 29, cebp.1060.2018.	1.1	9
17	A loss-of-function variant in ALOX15 protects against nasal polyps and chronic rhinosinusitis. Nature Genetics, 2019, 51, 267-276.	9.4	83
18	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

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19	Genome-wide associations for benign prostatic hyperplasia reveal a genetic correlation with serum levels of PSA. Nature Communications, 2018, 9, 4568.	5.8	44
20	Genome-wide association meta-analysis yields 20 loci associated with gallstone disease. Nature Communications, 2018, 9, 5101.	5.8	73
21	Meta-analysis of Icelandic and UK data sets identifies missense variants in SMO, IL11, COL11A1 and 13 more new loci associated with osteoarthritis. Nature Genetics, 2018, 50, 1681-1687.	9.4	131
22	Insights into imprinting from parent-of-origin phased methylomes and transcriptomes. Nature Genetics, 2018, 50, 1542-1552.	9.4	94
23	Identification of multiple risk loci and regulatory mechanisms influencing susceptibility to multiple myeloma. Nature Communications, 2018, 9, 3707.	5.8	86
24	Variants associating with uterine leiomyoma highlight genetic background shared by various cancers and hormone-related traits. Nature Communications, 2018, 9, 3636.	5.8	74
25	Association of BRCA2 K3326* With Small Cell Lung Cancer and Squamous Cell Cancer of the Skin. Journal of the National Cancer Institute, 2018, 110, 967-974.	3.0	29
26	A genome-wide association study yields five novel thyroid cancer risk loci. Nature Communications, 2017, 8, 14517.	5.8	117
27	Sequence variants in ARHGAP15, COLQ and FAM155A associate with diverticular disease and diverticulitis. Nature Communications, 2017, 8, 15789.	5.8	67
28	Large-scale association analysis identifies new lung cancer susceptibility loci and heterogeneity in genetic susceptibility across histological subtypes. Nature Genetics, 2017, 49, 1126-1132.	9.4	472
29	Whole-genome sequencing identifies rare genotypes in COMP and CHADL associated with high risk of hip osteoarthritis. Nature Genetics, 2017, 49, 801-805.	9.4	75
30	Whole genome characterization of sequence diversity of 15,220 Icelanders. Scientific Data, 2017, 4, 170115.	2.4	98
31	Fourteen sequence variants that associate with multiple sclerosis discovered by meta-analysis informed by genetic correlations. Npj Genomic Medicine, 2017, 2, 24.	1.7	16
32	Sequence variant at 4q25 near PITX2 associates with appendicitis. Scientific Reports, 2017, 7, 3119.	1.6	14
33	VariantASGR1Associated with a Reduced Risk of Coronary Artery Disease. New England Journal of Medicine, 2016, 374, 2131-2141.	13.9	137
34	Variants with large effects on blood lipids and the role of cholesterol and triglycerides in coronary disease. Nature Genetics, 2016, 48, 634-639.	9.4	214
35	Cross-Cancer Genome-Wide Analysis of Lung, Ovary, Breast, Prostate, and Colorectal Cancer Reveals Novel Pleiotropic Associations. Cancer Research, 2016, 76, 5103-5114.	0.4	100
36	Epigenetic and genetic components of height regulation. Nature Communications, 2016, 7, 13490.	5.8	52

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37	Genome-wide association study identifies multiple susceptibility loci for multiple myeloma. Nature Communications, 2016, 7, 12050.	5.8	146
38	Identification of a novel susceptibility locus at 13q34 and refinement of the 20p12.2 region as a multi-signal locus associated with bladder cancer risk in individuals of European ancestry. Human Molecular Genetics, 2016, 25, 1203-1214.	1.4	38
39	Sequence variants in the PTCH1 gene associate with spine bone mineral density and osteoporotic fractures. Nature Communications, 2016, 7, 10129.	5.8	58
40	Comprehensive population-wide detection of Lynch syndrome in Iceland.. Journal of Clinical Oncology, 2016, 34, 1542-1542.	0.8	3
41	A Splice Region Variant in LDLR Lowers Non-high Density Lipoprotein Cholesterol and Protects against Coronary Artery Disease. PLoS Genetics, 2015, 11, e1005379.	1.5	24
42	Loss-of-function variants in ATM confer risk of gastric cancer. Nature Genetics, 2015, 47, 906-910.	9.4	155
43	Large-scale whole-genome sequencing of the Icelandic population. Nature Genetics, 2015, 47, 435-444.	9.4	663
44	Variants in ELL2 influencing immunoglobulin levels associate with multiple myeloma. Nature Communications, 2015, 6, 7213.	5.8	101
45	New basal cell carcinoma susceptibility loci. Nature Communications, 2015, 6, 6825.	5.8	59
46	A Method for Detecting Long Non-Coding RNAs with Tiled RNA Expression Microarrays. PLoS ONE, 2014, 9, e99899.	1.1	12
47	Germline sequence variants in TGM3 and RGS22 confer risk of basal cell carcinoma. Human Molecular Genetics, 2014, 23, 3045-3053.	1.4	48
48	Rare variants of large effect in BRCA2 and CHEK2 affect risk of lung cancer. Nature Genetics, 2014, 46, 736-741.	9.4	360
49	Nonsense mutation in the LGR4 gene is associated with several human diseases and other traits. Nature, 2013, 497, 517-520.	13.7	236
50	A common variant at 8q24.21 is associated with renal cell cancer. Nature Communications, 2013, 4, 2776.	5.8	56
51	A study based on whole-genome sequencing yields a rare variant at 8q24 associated with prostate cancer. Nature Genetics, 2012, 44, 1326-1329.	9.4	178
52	Discovery of common variants associated with low TSH levels and thyroid cancer risk. Nature Genetics, 2012, 44, 319-322.	9.4	208
53	Mutations in BRIP1 confer high risk of ovarian cancer. Nature Genetics, 2011, 43, 1104-1107.	9.4	338
54	A germline variant in the TP53 polyadenylation signal confers cancer susceptibility. Nature Genetics, 2011, 43, 1098-1103.	9.4	251

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55	Identification of low-frequency variants associated with gout and serum uric acid levels. Nature Genetics, 2011, 43, 1127-1130.	9.4	134
56	A rare variant in MYH6 is associated with high risk of sick sinus syndrome. Nature Genetics, 2011, 43, 316-320.	9.4	275
57	Genome-Wide Significant Association Between a Sequence Variant at 15q15.2 and Lung Cancer Risk. Cancer Research, 2011, 71, 1356-1361.	0.4	26
58	European genome-wide association study identifies SLC14A1 as a new urinary bladder cancer susceptibility gene. Human Molecular Genetics, 2011, 20, 4268-4281.	1.4	134
59	A sequence variant at 4p16.3 confers susceptibility to urinary bladder cancer. Nature Genetics, 2010, 42, 415-419.	9.4	169
60	Genome-wide association study identifies a sequence variant within the DAB2IP gene conferring susceptibility to abdominal aortic aneurysm. Nature Genetics, 2010, 42, 692-697.	9.4	181
61	Common variants at 19p13 are associated with susceptibility to ovarian cancer. Nature Genetics, 2010, 42, 880-884.	9.4	235
62	A genome-wide association study identifies susceptibility loci for ovarian cancer at 2q31 and 8q24. Nature Genetics, 2010, 42, 874-879.	9.4	321
63	A multi-stage genome-wide association study of bladder cancer identifies multiple susceptibility loci. Nature Genetics, 2010, 42, 978-984.	9.4	493
64	Replication of Lung Cancer Susceptibility Loci at Chromosomes 15q25, 5p15, and 6p21: A Pooled Analysis From the International Lung Cancer Consortium. Journal of the National Cancer Institute, 2010, 102, 959-971.	3.0	174
65	Genetic Correction of PSA Values Using Sequence Variants Associated with PSA Levels. Science Translational Medicine, 2010, 2, 62ra92.	5.8	140
66	Ancestry-Shift Refinement Mapping of the C6orf97-ESR1 Breast Cancer Susceptibility Locus. PLoS Genetics, 2010, 6, e1001029.	1.5	82
67	Evaluation of Association of HNF1B Variants with Diverse Cancers: Collaborative Analysis of Data from 19 Genome-Wide Association Studies. PLoS ONE, 2010, 5, e10858.	1.1	28
68	Sequence variants at the TERT-CLPTM1L locus associate with many cancer types. Nature Genetics, 2009, 41, 221-227.	9.4	572
69	Common variants on 9q22.33 and 14q13.3 predispose to thyroid cancer in European populations. Nature Genetics, 2009, 41, 460-464.	9.4	353
70	Genome-wide association study identifies sequence variants on 6q21 associated with age at menarche. Nature Genetics, 2009, 41, 734-738.	9.4	199
71	New common variants affecting susceptibility to basal cell carcinoma. Nature Genetics, 2009, 41, 909-914.	9.4	303
72	Genome-wide association and replication studies identify four variants associated with prostate cancer susceptibility. Nature Genetics, 2009, 41, 1122-1126.	9.4	313

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73	A Genome-wide Association Study of Lung Cancer Identifies a Region of Chromosome 5p15 Associated with Risk for Adenocarcinoma. American Journal of Human Genetics, 2009, 85, 679-691.	2.6	489
74	A variant associated with nicotine dependence, lung cancer and peripheral arterial disease. Nature, 2008, 452, 638-642.	13.7	1,399
75	Many sequence variants affecting diversity of adult human height. Nature Genetics, 2008, 40, 609-615.	9.4	615
76	ASIP and TYR pigmentation variants associate with cutaneous melanoma and basal cell carcinoma. Nature Genetics, 2008, 40, 886-891.	9.4	306
77	Detection of sharing by descent, long-range phasing and haplotype imputation. Nature Genetics, 2008, 40, 1068-1075.	9.4	409
78	Sequence variant on 8q24 confers susceptibility to urinary bladder cancer. Nature Genetics, 2008, 40, 1307-1312.	9.4	377
79	Common variants on 1p36 and 1q42 are associated with cutaneous basal cell carcinoma but not with melanoma or pigmentation traits. Nature Genetics, 2008, 40, 1313-1318.	9.4	111
80	Genome-wide association study identifies a second prostate cancer susceptibility variant at 8q24. Nature Genetics, 2007, 39, 631-637.	9.4	818
81	Two variants on chromosome 17 confer prostate cancer risk, and the one in TCF2 protects against type 2 diabetes. Nature Genetics, 2007, 39, 977-983.	9.4	670
82	Common variants on chromosomes 2q35 and 16q12 confer susceptibility to estrogen receptorâ€“positive breast cancer. Nature Genetics, 2007, 39, 865-869.	9.4	774
83	The Icelandic Cancer Project â€“ a population-wide approach to studying cancer. Nature Reviews Cancer, 2004, 4, 488-492.	12.8	15
84	BRCA2, but not BRCA1, mutations account for familial ovarian cancer in Iceland: a population-based study. European Journal of Cancer, 2004, 40, 2788-2793.	1.3	50