Asmundur Oddsson

List of Publications by Year
in descending order

56 papers	5,022 citations	172386 29 h-index	155592 55 g-index
61 all docs	61 docs citations	61 times ranked	11131 citing authors

#	Article	IF	Citations
1	Rare SLC13A1 variants associate with intervertebral disc disorder highlighting role of sulfate in disc pathology. Nature Communications, 2022, 13, 634.	5.8	21
2	Population-level deficit of homozygosity unveils CPSF3 as an intellectual disability syndrome gene. Nature Communications, 2022, 13, 705.	5.8	7
3	A genome-wide meta-analysis identifies 50 genetic loci associated with carpal tunnel syndrome. Nature Communications, 2022, 13, 1598.	5.8	8
4	Multiomics analysis of rheumatoid arthritis yields sequence variants that have large effects on risk of the seropositive subset. Annals of the Rheumatic Diseases, 2022, 81, 1085-1095.	0.5	26
5	Genetic architecture of band neutrophil fraction in Iceland. Communications Biology, 2022, 5, .	2.0	1
6	A meta-analysis uncovers the first sequence variant conferring risk of Bellâ€™s palsy. Scientific Reports, 2021, 11, 4188.	1.6	8
7	Loss-of-Function Variants in the Tumor-Suppressor Gene PTPN14 Confer Increased Cancer Risk. Cancer Research, 2021, 81, 1954-1964.	0.4	15
8	A genome-wide meta-analysis yields 46 new loci associating with biomarkers of iron homeostasis. Communications Biology, 2021, 4, 156.	2.0	72
9	Genetic insight into sick sinus syndrome. European Heart Journal, 2021, 42, 1959-1971.	1.0	27
10	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
11	The genetic architecture of age-related hearing impairment revealed by genome-wide association analysis. Communications Biology, 2021, 4, 706.	2.0	30
12	Sequence variants in malignant hyperthermia genes in Iceland: classification and actionable findings in a population database. European Journal of Human Genetics, 2021, 29, 1819-1824.	1.4	4
13	Large-scale integration of the plasma proteome with genetics and disease. Nature Genetics, 2021, 53, 1712-1721.	9.4	340
14	Cohort profile: Copenhagen Hospital Biobank - Cardiovascular Disease Cohort (CHB-CVDC): Construction of a large-scale genetic cohort to facilitate a better understanding of heart diseases. BMJ Open, 2021, 11, e049709.	0.8	7
15	Sequence Variants in TAAR5 and Other Loci Affect Human Odor Perception and Naming. Current Biology, 2020, 30, 4643-4653.e3.	1.8	19
16	Genome-wide association identifies seven loci for pelvic organ prolapse in Iceland and the UK Biobank. Communications Biology, 2020, 3, 129.	2.0	20
17	Predicted loss and gain of function mutations in ACO1 are associated with erythropoiesis. Communications Biology, 2020, 3, 189.	2.0	30
18	Characterizing mutagenic effects of recombination through a sequence-level genetic map. Science, 2019, 363, .	6.0	252

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19	Sequence variation at ANAPC1 accounts for 24% of the variability in corneal endothelial cell density. Nature Communications, 2019, 10, 1284.	5.8	24
20	A loss-of-function variant in ALOX15 protects against nasal polyps and chronic rhinosinusitis. Nature Genetics, 2019, 51, 267-276.	9.4	83
21	Genetics of common complex kidney stone disease: insights from genome-wide association studies. Urolithiasis, 2019, 47, 11-21.	1.2	26
22	Sequence variants associating with urinary biomarkers. Human Molecular Genetics, 2019, 28, 1199-1211.	1.4	28
23	A rare missense variant in NR1H4 associates with lower cholesterol levels. Communications Biology, 2018, 1, 14.	2.0	6
24	The nature of nurture: Effects of parental genotypes. Science, 2018, 359, 424-428.	6.0	720
25	Genome-wide association meta-analysis yields 20 loci associated with gallstone disease. Nature Communications, 2018, 9, 5101.	5.8	73
26	A homozygous loss-of-function mutation leading to CYBC1 deficiency causes chronic granulomatous disease. Nature Communications, 2018, 9, 4447.	5.8	95
27	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
28	Variants associating with uterine leiomyoma highlight genetic background shared by various cancers and hormone-related traits. Nature Communications, 2018, 9, 3636.	5.8	74
29	A truncating mutation in EPOR leads to hypo-responsiveness to erythropoietin with normal haemoglobin. Communications Biology, 2018, 1, 49.	2.0	9
30	Sequence variant at 8q24.21 associates with sciatica caused by lumbar disc herniation. Nature Communications, 2017, 8, 14265.	5.8	48
31	Identification of sequence variants influencing immunoglobulin levels. Nature Genetics, 2017, 49, 1182-1191.	9.4	90
32	A rare splice donor mutation in the haptoglobin gene associates with blood lipid levels and coronary artery disease. Human Molecular Genetics, 2017, 26, 2364-2376.	1.4	17
33	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
34	Sequence variant at 4q25 near PITX2 associates with appendicitis. Scientific Reports, 2017, 7, 3119.	1.6	14
35	A frameshift deletion in the sarcomere geneMYL4causes early-onset familial atrial fibrillation. European Heart Journal, 2017, 38, 27-34.	1.0	89
36	Compound heterozygous mutations in UBA5 causing early-onset epileptic encephalopathy in two sisters. BMC Medical Genetics, 2017, 18, 103.	2.1	28

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37	COPA syndrome in an Icelandic family caused by a recurrent missense mutation in COPA. BMC Medical Genetics, 2017, 18, 129.	2.1	47
38	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
39	Epigenetic and genetic components of height regulation. Nature Communications, 2016, 7, 13490.	5.8	52
40	Common and rare variants associating with serum levels of creatine kinase and lactate dehydrogenase. Nature Communications, 2016, 7, 10572.	5.8	60
41	Weighting sequence variants based on their annotation increases power of whole-genome association studies. Nature Genetics, 2016, 48, 314-317.	9.4	178
42	Knockdown of Tmem234 in zebrafish results in proteinuria. American Journal of Physiology - Renal Physiology, 2015, 309, F955-F966.	1.3	5
43	Survival in patients with familial and sporadic myeloproliferative neoplasms. Blood, 2015, 125, 3665-3666.	0.6	8
44	Sequence variants from whole genome sequencing a large group of Icelanders. Scientific Data, 2015, 2, 150011.	2.4	59
45	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
46	Loss-of-function variants in ATM confer risk of gastric cancer. Nature Genetics, 2015, 47, 906-910.	9.4	155
47	Identification of a large set of rare complete human knockouts. Nature Genetics, 2015, 47, 448-452.	9.4	214
48	Large-scale whole-genome sequencing of the Icelandic population. Nature Genetics, 2015, 47, 435-444.	9.4	663
49	Common and rare variants associated with kidney stones and biochemical traits. Nature Communications, 2015, 6, 7975.	5.8	117
50	Glomerular Filtration Barrier. , 2014, , .		1
51	The germline sequence variant rs2736100_C in TERT associates with myeloproliferative neoplasms. Leukemia, 2014, 28, 1371-1374.	3.3	85
52	Nonsense mutation in the LGR4 gene is associated with several human diseases and other traits. Nature, 2013, 497, 517-520.	13.7	236
53	Zebrafish: a model system for the study of vertebrate renal development, function, and pathophysiology. Current Opinion in Nephrology and Hypertension, 2011, 20, 416-424.	1.0	54
54	Glcci1 Deficiency Leads to Proteinuria. Journal of the American Society of Nephrology: JASN, 2011, 22, 2037-2046.	3.0	39

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55	Expression and Subcellular Distribution of Novel Glomerulus-Associated Proteins Dendrin, Ehd3, Sh2d4a, Plekhh2, and 2310066E14Rik. Journal of the American Society of Nephrology: JASN, 2007, 18, 689-697.	3.0	72
56	Glomerulus proteome analysis with two-dimensional gel electrophoresis and mass spectrometry. Cellular and Molecular Life Sciences, 2007, 64, 3317-3335.	2.4	7