

# Asmundur Oddsson

## List of Publications by Year in descending order

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Version: 2024-02-01

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	The nature of nurture: Effects of parental genotypes. <i>Science</i> , 2018, 359, 424-428.	6.0	720
2	Large-scale whole-genome sequencing of the Icelandic population. <i>Nature Genetics</i> , 2015, 47, 435-444.	9.4	663
3	Large-scale integration of the plasma proteome with genetics and disease. <i>Nature Genetics</i> , 2021, 53, 1712-1721.	9.4	340
4	Characterizing mutagenic effects of recombination through a sequence-level genetic map. <i>Science</i> , 2019, 363, .	6.0	252
5	Nonsense mutation in the LGR4 gene is associated with several human diseases and other traits. <i>Nature</i> , 2013, 497, 517-520.	13.7	236
6	Identification of a large set of rare complete human knockouts. <i>Nature Genetics</i> , 2015, 47, 448-452.	9.4	214
7	Variants with large effects on blood lipids and the role of cholesterol and triglycerides in coronary disease. <i>Nature Genetics</i> , 2016, 48, 634-639.	9.4	214
8	Weighting sequence variants based on their annotation increases power of whole-genome association studies. <i>Nature Genetics</i> , 2016, 48, 314-317.	9.4	178
9	Long-read sequencing of 3,622 Icelanders provides insight into the role of structural variants in human diseases and other traits. <i>Nature Genetics</i> , 2021, 53, 779-786.	9.4	156
10	Loss-of-function variants in ATM confer risk of gastric cancer. <i>Nature Genetics</i> , 2015, 47, 906-910.	9.4	155
11	Meta-analysis of Icelandic and UK data sets identifies missense variants in SMO, IL11, COL11A1 and 13 more new loci associated with osteoarthritis. <i>Nature Genetics</i> , 2018, 50, 1681-1687.	9.4	131
12	Common and rare variants associated with kidney stones and biochemical traits. <i>Nature Communications</i> , 2015, 6, 7975.	5.8	117
13	A homozygous loss-of-function mutation leading to CYBC1 deficiency causes chronic granulomatous disease. <i>Nature Communications</i> , 2018, 9, 4447.	5.8	95
14	Identification of sequence variants influencing immunoglobulin levels. <i>Nature Genetics</i> , 2017, 49, 1182-1191.	9.4	90
15	A frameshift deletion in the sarcomere gene <i>MYL4</i> causes early-onset familial atrial fibrillation. <i>European Heart Journal</i> , 2017, 38, 27-34.	1.0	89
16	The germline sequence variant rs2736100_C in TERT associates with myeloproliferative neoplasms. <i>Leukemia</i> , 2014, 28, 1371-1374.	3.3	85
17	A loss-of-function variant in ALOX15 protects against nasal polyps and chronic rhinosinusitis. <i>Nature Genetics</i> , 2019, 51, 267-276.	9.4	83
18	Whole-genome sequencing identifies rare genotypes in COMP and CHADL associated with high risk of hip osteoarthritis. <i>Nature Genetics</i> , 2017, 49, 801-805.	9.4	75

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19	Variants associating with uterine leiomyoma highlight genetic background shared by various cancers and hormone-related traits. <i>Nature Communications</i> , 2018, 9, 3636.	5.8	74
20	Genome-wide association meta-analysis yields 20 loci associated with gallstone disease. <i>Nature Communications</i> , 2018, 9, 5101.	5.8	73
21	Expression and Subcellular Distribution of Novel Glomerulus-Associated Proteins Dendrin, Ehd3, Sh2d4a, Plekhh2, and 2310066E14Rik. <i>Journal of the American Society of Nephrology: JASN</i> , 2007, 18, 689-697.	3.0	72
22	A genome-wide meta-analysis yields 46 new loci associating with biomarkers of iron homeostasis. <i>Communications Biology</i> , 2021, 4, 156.	2.0	72
23	Common and rare variants associating with serum levels of creatine kinase and lactate dehydrogenase. <i>Nature Communications</i> , 2016, 7, 10572.	5.8	60
24	Sequence variants from whole genome sequencing a large group of Icelanders. <i>Scientific Data</i> , 2015, 2, 150011.	2.4	59
25	Zebrafish: a model system for the study of vertebrate renal development, function, and pathophysiology. <i>Current Opinion in Nephrology and Hypertension</i> , 2011, 20, 416-424.	1.0	54
26	Epigenetic and genetic components of height regulation. <i>Nature Communications</i> , 2016, 7, 13490.	5.8	52
27	Sequence variant at 8q24.21 associates with sciatica caused by lumbar disc herniation. <i>Nature Communications</i> , 2017, 8, 14265.	5.8	48
28	COPA syndrome in an Icelandic family caused by a recurrent missense mutation in COPA. <i>BMC Medical Genetics</i> , 2017, 18, 129.	2.1	47
29	Glcc1 Deficiency Leads to Proteinuria. <i>Journal of the American Society of Nephrology: JASN</i> , 2011, 22, 2037-2046.	3.0	39
30	Predicted loss and gain of function mutations in ACO1 are associated with erythropoiesis. <i>Communications Biology</i> , 2020, 3, 189.	2.0	30
31	The genetic architecture of age-related hearing impairment revealed by genome-wide association analysis. <i>Communications Biology</i> , 2021, 4, 706.	2.0	30
32	Compound heterozygous mutations in UBA5 causing early-onset epileptic encephalopathy in two sisters. <i>BMC Medical Genetics</i> , 2017, 18, 103.	2.1	28
33	Sequence variants associating with urinary biomarkers. <i>Human Molecular Genetics</i> , 2019, 28, 1199-1211.	1.4	28
34	Genetic insight into sick sinus syndrome. <i>European Heart Journal</i> , 2021, 42, 1959-1971.	1.0	27
35	Genetics of common complex kidney stone disease: insights from genome-wide association studies. <i>Urolithiasis</i> , 2019, 47, 11-21.	1.2	26
36	Multimomics analysis of rheumatoid arthritis yields sequence variants that have large effects on risk of the seropositive subset. <i>Annals of the Rheumatic Diseases</i> , 2022, 81, 1085-1095.	0.5	26

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37	A Splice Region Variant in LDLR Lowers Non-high Density Lipoprotein Cholesterol and Protects against Coronary Artery Disease. <i>PLoS Genetics</i> , 2015, 11, e1005379.	1.5	24
38	Sequence variation at ANAPC1 accounts for 24% of the variability in corneal endothelial cell density. <i>Nature Communications</i> , 2019, 10, 1284.	5.8	24
39	Rare SLC13A1 variants associate with intervertebral disc disorder highlighting role of sulfate in disc pathology. <i>Nature Communications</i> , 2022, 13, 634.	5.8	21
40	Genome-wide association identifies seven loci for pelvic organ prolapse in Iceland and the UK Biobank. <i>Communications Biology</i> , 2020, 3, 129.	2.0	20
41	Sequence Variants in TAAR5 and Other Loci Affect Human Odor Perception and Naming. <i>Current Biology</i> , 2020, 30, 4643-4653.e3.	1.8	19
42	A rare splice donor mutation in the haptoglobin gene associates with blood lipid levels and coronary artery disease. <i>Human Molecular Genetics</i> , 2017, 26, 2364-2376.	1.4	17
43	Loss-of-Function Variants in the Tumor-Suppressor Gene <i>PTPN14</i> Confer Increased Cancer Risk. <i>Cancer Research</i> , 2021, 81, 1954-1964.	0.4	15
44	Sequence variant at 4q25 near PITX2 associates with appendicitis. <i>Scientific Reports</i> , 2017, 7, 3119.	1.6	14
45	A truncating mutation in EPOR leads to hypo-responsiveness to erythropoietin with normal haemoglobin. <i>Communications Biology</i> , 2018, 1, 49.	2.0	9
46	Survival in patients with familial and sporadic myeloproliferative neoplasms. <i>Blood</i> , 2015, 125, 3665-3666.	0.6	8
47	A meta-analysis uncovers the first sequence variant conferring risk of Bell's palsy. <i>Scientific Reports</i> , 2021, 11, 4188.	1.6	8
48	A genome-wide meta-analysis identifies 50 genetic loci associated with carpal tunnel syndrome. <i>Nature Communications</i> , 2022, 13, 1598.	5.8	8
49	Glomerulus proteome analysis with two-dimensional gel electrophoresis and mass spectrometry. <i>Cellular and Molecular Life Sciences</i> , 2007, 64, 3317-3335.	2.4	7
50	Population-level deficit of homozygosity unveils CPSF3 as an intellectual disability syndrome gene. <i>Nature Communications</i> , 2022, 13, 705.	5.8	7
51	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. <i>BMJ Open</i> , 2021, 11, e049709.	0.8	7
52	A rare missense variant in NR1H4 associates with lower cholesterol levels. <i>Communications Biology</i> , 2018, 1, 14.	2.0	6
53	Knockdown of Tmem234 in zebrafish results in proteinuria. <i>American Journal of Physiology - Renal Physiology</i> , 2015, 309, F955-F966.	1.3	5
54	Sequence variants in malignant hyperthermia genes in Iceland: classification and actionable findings in a population database. <i>European Journal of Human Genetics</i> , 2021, 29, 1819-1824.	1.4	4

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55	Glomerular Filtration Barrier. , 2014, , .		1
56	Genetic architecture of band neutrophil fraction in Iceland. Communications Biology, 2022, 5, .	2.0	1