Kaoru Ito

List of Publications by Year in Descending Order

21 papers	1,060 citations	11 h-index	26 g-index
26 ext. papers	1,884 ext. citations	15.1 avg, IF	2.93 L-index

#	Paper	IF	Citations
21	Genetic Analysis for Coronary Artery Disease Toward Diverse Populations. *Frontiers in Genetics*, **2021**, 12, 766485	4.5	0
20	The Evolving Story in the Genetic Analysis for Heart Failure. *Frontiers in Cardiovascular Medicine*, **2021**, 8, 646816	5.4	0
19	Association of an IGHV3-66 gene variant with Kawasaki disease. *Journal of Human Genetics*, **2021**, 66, 475-489	4.3	9
18	Genome-wide analysis identifies novel susceptibility loci for myocardial infarction. *European Heart Journal*, **2021**, 42, 919-933	9.5	14
17	Contribution of Noncanonical Splice Variants to Truncating Variant Cardiomyopathy. *Circulation Genomic and Precision Medicine*, **2021**, 14, e003389	5.2	0
16	A cross-population atlas of genetic associations for 220 human phenotypes. *Nature Genetics*, **2021**, 53, 1415-1424	36.3	40
15	Transethnic Meta-Analysis of Genome-Wide Association Studies Identifies Three New Loci and Characterizes Population-Specific Differences for Coronary Artery Disease. *Circulation Genomic and Precision Medicine*, **2020**, 13, e002670	5.2	9
14	Large-scale genome-wide association study in a Japanese population identifies novel susceptibility loci across different diseases. *Nature Genetics*, **2020**, 52, 669-679	36.3	85
13	Diagnosing Heart Failure from Chest X-Ray Images Using Deep Learning. *International Heart Journal* , **2020**, 61, 781-786	1.8	8
12	Population-specific and trans-ancestry genome-wide analyses identify distinct and shared genetic risk loci for coronary artery disease. *Nature Genetics*, **2020**, 52, 1169-1177	36.3	51
11	Genetic Variants Associated With Cancer Therapy-Induced Cardiomyopathy. *Circulation*, **2019**, 140, 31-41	16.7	110
10	Multi-ethnic genome-wide association study for atrial fibrillation. *Nature Genetics*, **2018**, 50, 1225-1233	36.3	277
9	In vivo and In vitro methods to identify DNA sequence variants that alter RNA Splicing. *Current Protocols in Human Genetics*, **2018**, 97, e60	3.2	2
8	Identification of LEF1 as a Susceptibility Locus for Kawasaki Disease in Patients Younger than 6 Months of Age. *Genomics and Informatics*, **2018**, 16, 36-41	1.9	3
7	Blood lipid-related low-frequency variants in LDLR and PCSK9 are associated with onset age and risk of myocardial infarction in Japanese. *Scientific Reports*, **2018**, 8, 8107	4.9	7
6	Identification of six new genetic loci associated with atrial fibrillation in the Japanese population. *Nature Genetics*, **2017**, 49, 953-958	36.3	89
5	A genome-wide association analysis identifies NMNAT2 and HCP5 as susceptibility loci for Kawasaki disease. *Journal of Human Genetics*, **2017**, 62, 1023-1029	4.3	29

4	Identification of pathogenic gene mutations in and that alter RNA splicing. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, 7689-7694	11.5	42
3	Increased frequency of de novo copy number variants in congenital heart disease by integrative analysis of single nucleotide polymorphism array and exome sequence data. *Circulation Research*, **2014**, 115, 884-896	15.7	158
2	Increased burden of cardiovascular disease in carriers of APOL1 genetic variants. *Circulation Research*, **2014**, 114, 845-50	15.7	119
1	Discovery and systematic characterization of risk variants and genes for coronary artery disease in over a million participants		5