Ituro Inoue

List of Publications by Year
in descending order

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68 papers	2,145 citations	279798 23 h-index	254184 43 g-index
68 all docs	68 docs citations	68 times ranked	3838 citing authors

#	Article	IF	Citations
1	Allelic and haplotypic HLA diversity in indigenous Malaysian populations explored using Next Generation Sequencing. Human Immunology, 2022, 83, 17-26.	2.4	4
2	APOBEC mediated mutagenesis drives genomic heterogeneity in endometriosis. Journal of Human Genetics, 2022, 67, 323-329.	2.3	3
3	Genome-wide meta-analysis between renal overload type and renal underexcretion type of clinically defined gout in Japanese populations. Molecular Genetics and Metabolism, 2022, 136, 186-189.	1.1	6
4	Spatiotemporal dynamics of clonal selection and diversification in normal endometrial epithelium. Nature Communications, 2022, 13, 943.	12.8	24
5	Movements of Ancient Human Endogenous Retroviruses Detected in SOX2-Expressing Cells. Journal of Virology, 2022, 96, e0035622.	3.4	9
6	High incidence of PI3K pathway gene mutations in South Indian cervical cancers. Cancer Genetics, 2022, 264-265, 100-108.	0.4	0
7	Detection of Ancient Viruses and Long-Term Viral Evolution. Viruses, 2022, 14, 1336.	3.3	8
8	Extraction of CRISPR-targeted sequences from the metagenome. STAR Protocols, 2022, 3, 101525.	1.2	0
9	Population genetics: past, present, and future. Human Genetics, 2021, 140, 231-240.	3.8	5
10	HLA-B*39:01:01 is a novel risk factor for antithyroid drug-induced agranulocytosis in Japanese population. Pharmacogenomics Journal, 2021, 21, 94-101.	2.0	4
11	APOBEC: A molecular driver in cervical cancer pathogenesis. Cancer Letters, 2021, 496, 104-116.	7.2	79
12	Identification of ancient viruses from metagenomic data of the Jomon people. Journal of Human Genetics, 2021, 66, 287-296.	2.3	5
13	AMBRA1 controls antigen-driven activation and proliferation of naive T cells. International Immunology, 2021, 33, 107-118.	4.0	3
14	Analysis of HLA gene polymorphisms in East Africans reveals evidence of gene flow in two Semitic populations from Sudan. European Journal of Human Genetics, 2021, 29, 1259-1271.	2.8	1
15	Substantial anti-gout effect conferred by common and rare dysfunctional variants of URAT1/SLC22A12. Rheumatology, 2021, 60, 5224-5232.	1.9	10
16	Genetic variant rs10251977 (G>A) in EGFR-AS1 modulates the expression of EGFR isoforms A and D. Scientific Reports, 2021, 11, 8808.	3.3	9
17	Significance of Mitochondrial DNA Haplogroup on Epidermal Growth Factor Receptor Mutation in Japanese Patients With Lung Adenocarcinoma. Anticancer Research, 2021, 41, 3997-4004.	1.1	1
18	Proposing a molecular classification associated with hypercoagulation in ovarian clear cell carcinoma. Gynecologic Oncology, 2021, 163, 327-333.	1.4	5

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19	Comprehensive discovery of CRISPR-targeted terminally redundant sequences in the human gut metagenome: Viruses, plasmids, and more. PLoS Computational Biology, 2021, 17, e1009428.	3.2	7
20	Dysfunctional missense variant of OAT10/SLC22A13 decreases gout risk and serum uric acid levels. Annals of the Rheumatic Diseases, 2020, 79, 164-166.	0.9	26
21	Endogenous retroviruses drive KRAB zinc-finger protein family expression for tumor suppression. Science Advances, 2020, 6, .	10.3	36
22	ARID1A protein expression is retained in ovarian endometriosis with ARID1A loss-of-function mutations: implication for the two-hit hypothesis. Scientific Reports, 2020, 10, 14260.	3.3	18
23	Germline mutations of multiple breast cancer-related genes are differentially associated with triple-negative breast cancers and prognostic factors. Journal of Human Genetics, 2020, 65, 577-587.	2.3	14
24	XCL1 expression correlates with CD8-positive T cells infiltration and PD-L1 expression in squamous cell carcinoma arising from mature cystic teratoma of the ovary. Oncogene, 2020, 39, 3541-3554.	5.9	26
25	Subtype-specific gout susceptibility loci and enrichment of selection pressure on ABCG2 and ALDH2 identified by subtype genome-wide meta-analyses of clinically defined gout patients. Annals of the Rheumatic Diseases, 2020, 79, 657-665.	0.9	24
26	Next-generation sequencing identifies contribution of both class I and II HLA genes on susceptibility of multiple sclerosis in Japanese. Journal of Neuroinflammation, 2019, 16, 162.	7.2	22
27	Genome-wide association study revealed novel loci which aggravate asymptomatic hyperuricaemia into gout. Annals of the Rheumatic Diseases, 2019, 78, 1430-1437.	0.9	73
28	Exploration of intermediate-sized INDELs by next-generation multigene panel testing in Han Chinese patients with breast cancer. Human Genome Variation, 2019, 6, 51.	0.7	3
29	Different mutation profiles between epithelium and stroma in endometriosis and normal endometrium. Human Reproduction, 2019, 34, 1899-1905.	0.9	37
30	Genetic and phenotypic landscape of the major histocompatibilty complex region in the Japanese population. Nature Genetics, 2019, 51, 470-480.	21.4	75
31	Germline and somatic mutations of homologous recombination-associated genes in Japanese ovarian cancer patients. Scientific Reports, 2019, 9, 17808.	3.3	38
32	Sensitization of Gastric Cancer Cells to Irinotecan by p53 Activation. BPB Reports, 2019, 2, 130-133.	0.3	2
33	No novel, high penetrant gene might remain to be found in Japanese patients with unknown MODY. Journal of Human Genetics, 2018, 63, 821-829.	2.3	3
34	Novel therapeutic strategy for cervical cancer harboring FGFR3-TACC3 fusions. Oncogenesis, 2018, 7, 4.	4.9	41
35	Exome and copy number variation analyses of Mayerâ€“Rokitanskyâ€“KÃ¼sterâ€“ Hauser syndrome. Human Genome Variation, 2018, 5, 27.	0.7	9
36	Novel MXD4â€“NUTM1 fusion transcript identified in primary ovarian undifferentiated small round cell sarcoma. Genes Chromosomes and Cancer, 2018, 57, 557-563.	2.8	28

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37	The Relationship between TP53 Gene Status and Carboxylesterase 2 Expression in Human Colorectal Cancer. Disease Markers, 2018, 2018, 1-7.	1.3	13
38	Long non-coding RNA p10247, high expressed in breast cancer (lncRNA-BCHE), is correlated with metastasis. Clinical and Experimental Metastasis, 2018, 35, 109-121.	3.3	21
39	Clonal Expansion and Diversification of Cancer-Associated Mutations in Endometriosis and Normal Endometrium. Cell Reports, 2018, 24, 1777-1789.	6.4	296
40	Comprehensive microbiome analysis of tonsillar crypts in IgA nephropathy. Nephrology Dialysis Transplantation, 2017, 32, gfw343.	0.7	40
41	Comprehensive genetic testing approach for major inherited kidney diseases, using next-generation sequencing with a custom panel. Clinical and Experimental Nephrology, 2017, 21, 63-75.	1.6	47
42	Comprehensive genetic exploration of selective tooth agenesis of mandibular incisors by exome sequencing. Human Genome Variation, 2017, 4, 17005.	0.7	20
43	Rapid and cost-effective high-throughput sequencing for identification of germline mutations of BRCA1 and BRCA2. Journal of Human Genetics, 2017, 62, 561-567.	2.3	17
44	GWAS of clinically defined gout and subtypes identifies multiple susceptibility loci that include urate transporter genes. Annals of the Rheumatic Diseases, 2017, 76, 869-877.	0.9	114
45	Multiple common and rare variants of ABCG2 cause gout. RMD Open, 2017, 3, e000464.	3.8	46
46	AMBRA1 is involved in T cell receptor-mediated metabolic reprogramming through an ATG7-independent pathway. Biochemical and Biophysical Research Communications, 2017, 491, 1098-1104.	2.1	5
47	Identification of a novel variant of the RET proto-oncogene in a novel family with Hirschsprungâ€™s disease. Pediatric Surgery International, 2017, 33, 1041-1046.	1.4	3
48	Structure and evolution of the filaggrin gene repeated region in primates. BMC Evolutionary Biology, 2017, 17, 10.	3.2	23
49	Systematic identification and characterization of regulatory elements derived from human endogenous retroviruses. PLoS Genetics, 2017, 13, e1006883.	3.5	132
50	Allelic Imbalance in Regulation of ANRIL through Chromatin Interaction at 9p21 Endometriosis Risk Locus. PLoS Genetics, 2016, 12, e1005893.	3.5	40
51	Shared Genetic Risk Factors of Intracranial, Abdominal, and Thoracic Aneurysms. Journal of the American Heart Association, 2016, 5, .	3.7	45
52	Novel kinase fusion transcripts found in endometrial cancer. Scientific Reports, 2016, 5, 18657.	3.3	11
53	Genome-wide association study of clinically defined gout identifies multiple risk loci and its association with clinical subtypes. Annals of the Rheumatic Diseases, 2016, 75, 652-659.	0.9	144
54	Germline Variants of Prostate Cancer in Japanese Families. PLoS ONE, 2016, 11, e0164233.	2.5	21

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55	Identification of novel exonic mobile element insertions in epithelial ovarian cancers. Human Genome Variation, 2015, 2, 15030.	0.7	2
56	Silver Nanoscale Hexagonal Column Chips for Detecting Cell-free DNA and Circulating Nucleosomes in Cancer Patients. Scientific Reports, 2015, 5, 10455.	3.3	19
57	Distribution of HLA haplotypes across Japanese Archipelago: similarity, difference and admixture. Journal of Human Genetics, 2015, 60, 683-690.	2.3	14
58	Aggregation of rare/low-frequency variants of the mitochondria respiratory chain-related proteins in rheumatoid arthritis patients. Journal of Human Genetics, 2015, 60, 449-454.	2.3	21
59	The impact of next-generation sequencing technologies on HLA research. Journal of Human Genetics, 2015, 60, 665-673.	2.3	173
60	Possible Association between Dysfunction of Vitamin D Binding Protein (GC Globulin) and Migraine Attacks. PLoS ONE, 2014, 9, e105319.	2.5	9
61	Molecular Characterization of an Intact p53 Pathway Subtype in High-Grade Serous Ovarian Cancer. PLoS ONE, 2014, 9, e114491.	2.5	17
62	Genome-wide linkage and exome analyses identify variants of HMCN1for splenic epidermoid cyst. BMC Medical Genetics, 2014, 15, 115.	2.1	3
63	Gene Expression Profiling Reveals Distinct Molecular Signatures Associated With the Rupture of Intracranial Aneurysm. Stroke, 2014, 45, 2239-2245.	2.0	100
64	A Bead-based Normalization for Uniform Sequencing depth (BeNUS) protocol for multi-samples sequencing exemplified by HLA-B. BMC Genomics, 2014, 15, 645.	2.8	29
65	The Admixed Origin of Japanese Population from HLA Alleles. Major Histocompatibility Complex, 2014, 21, 37-44.	0.1	0
66	HLA-DPB1*04:01 allele is associated with non-obstructive azoospermia in Japanese patients. Human Genetics, 2013, 132, 1405-1411.	3.8	14
67	A genome-wide association study of third molar agenesis in Japanese and Korean populations. Journal of Human Genetics, 2013, 58, 799-803.	2.3	17
68	Detection of Ancestry Informative HLA Alleles Confirms the Admixed Origins of Japanese Population. PLoS ONE, 2013, 8, e60793.	2.5	31