Hirofumi Nakaoka

List of Publications by Year
in descending order

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74 papers	2,750 citations	218381 26 h-index	197535 49 g-index
75 all docs	75 docs citations	75 times ranked	4730 citing authors

#	Article	IF	Citations
1	Clonal Expansion and Diversification of Cancer-Associated Mutations in Endometriosis and Normal Endometrium. Cell Reports, 2018, 24, 1777-1789.	2.9	296
2	The auxin-inducible degron 2 technology provides sharp degradation control in yeast, mammalian cells, and mice. Nature Communications, 2020, 11, 5701.	5.8	208
3	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.	0.5	144
4	Systematic identification and characterization of regulatory elements derived from human endogenous retroviruses. PLoS Genetics, 2017, 13, e1006883.	1.5	132
5	ABCG2 dysfunction causes hyperuricemia due to both renal urate underexcretion and renal urate overload. Scientific Reports, 2014, 4, 3755.	1.6	125
6	Phase-defined complete sequencing of the HLA genes by next-generation sequencing. BMC Genomics, 2013, 14, 355.	1.2	121
7	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.	0.5	114
8	Gene Expression Profiling Reveals Distinct Molecular Signatures Associated With the Rupture of Intracranial Aneurysm. Stroke, 2014, 45, 2239-2245.	1.0	100
9	Meta-analysis of genetic association studies: methodologies, between-study heterogeneity and winner's curse. Journal of Human Genetics, 2009, 54, 615-623.	1.1	91
10	Next generation sequencing: implications in personalized medicine and pharmacogenomics. Molecular BioSystems, 2016, 12, 1818-1830.	2.9	82
11	APOBEC: A molecular driver in cervical cancer pathogenesis. Cancer Letters, 2021, 496, 104-116.	3.2	79
12	Genetic and phenotypic landscape of the major histocompatibilty complex region in the Japanese population. Nature Genetics, 2019, 51, 470-480.	9.4	75
13	Genome-wide association study revealed novel loci which aggravate asymptomatic hyperuricaemia into gout. Annals of the Rheumatic Diseases, 2019, 78, 1430-1437.	0.5	73
14	Common dysfunctional variants of ABCG2 have stronger impact on hyperuricemia progression than typical environmental risk factors. Scientific Reports, 2014, 4, 5227.	1.6	70
15	Three-dimensional understanding of the morphological complexity of the human uterine endometrium. IScience, 2021, 24, 102258.	1.9	59
16	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.	0.7	47
17	Multiple common and rare variants of ABCG2 cause gout. RMD Open, 2017, 3, e000464.	1.8	46
18	Shared Genetic Risk Factors of Intracranial, Abdominal, and Thoracic Aneurysms. Journal of the American Heart Association, 2016, 5, .	1.6	45

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19	Novel therapeutic strategy for cervical cancer harboring FGFR3-TACC3 fusions. Oncogenesis, 2018, 7, 4.	2.1	41
20	Allelic Imbalance in Regulation of ANRIL through Chromatin Interaction at 9p21 Endometriosis Risk Locus. PLoS Genetics, 2016, 12, e1005893.	1.5	40
21	Germline and somatic mutations of homologous recombination-associated genes in Japanese ovarian cancer patients. Scientific Reports, 2019, 9, 17808.	1.6	38
22	Different mutation profiles between epithelium and stroma in endometriosis and normal endometrium. Human Reproduction, 2019, 34, 1899-1905.	0.4	37
23	Identification of rs671, a common variant of ALDH2, as a gout susceptibility locus. Scientific Reports, 2016, 6, 25360.	1.6	36
24	Endogenous retroviruses drive KRAB zinc-finger protein family expression for tumor suppression. Science Advances, 2020, 6, .	4.7	36
25	Clonal lineage from normal endometrium to ovarian clear cell carcinoma through ovarian endometriosis. Cancer Science, 2020, 111, 3000-3009.	1.7	34
26	Detection of Ancestry Informative HLA Alleles Confirms the Admixed Origins of Japanese Population. PLoS ONE, 2013, 8, e60793.	1.1	31
27	Differential Effects of Chromosome 9p21 Variation on Subphenotypes of Intracranial Aneurysm. Stroke, 2010, 41, 1593-1598.	1.0	28
28	Novel MXD4â€“NUTM1 fusion transcript identified in primary ovarian undifferentiated small round cell sarcoma. Genes Chromosomes and Cancer, 2018, 57, 557-563.	1.5	28
29	Dysfunctional missense variant of OAT10/SLC22A13 decreases gout risk and serum uric acid levels. Annals of the Rheumatic Diseases, 2020, 79, 164-166.	0.5	26
30	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.	2.6	26
31	A nonsynonymous variant of IL1A is associated with endometriosis in Japanese population. Journal of Human Genetics, 2013, 58, 517-520.	1.1	25
32	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.	0.5	24
33	Spatiotemporal dynamics of clonal selection and diversification in normal endometrial epithelium. Nature Communications, 2022, 13, 943.	5.8	24
34	Structure and evolution of the filaggrin gene repeated region in primates. BMC Evolutionary Biology, 2017, 17, 10.	3.2	23
35	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.	1.1	21
36	Long non-coding RNA p10247, high expressed in breast cancer (lncRNA-BCHE), is correlated with metastasis. Clinical and Experimental Metastasis, 2018, 35, 109-121.	1.7	21

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37	Germline Variants of Prostate Cancer in Japanese Families. PLoS ONE, 2016, 11, e0164233.	1.1	21
38	Comprehensive genetic exploration of selective tooth agenesis of mandibular incisors by exome sequencing. Human Genome Variation, 2017, 4, 17005.	0.4	20
39	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.	1.6	18
40	Biological significance of KRAS mutant allele expression in ovarian endometriosis. Cancer Science, 2021, 112, 2020-2032.	1.7	18
41	A genome-wide association study of third molar agenesis in Japanese and Korean populations. Journal of Human Genetics, 2013, 58, 799-803.	1.1	17
42	Molecular Characterization of an Intact p53 Pathway Subtype in High-Grade Serous Ovarian Cancer. PLoS ONE, 2014, 9, e114491.	1.1	17
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.	1.1	17
44	Selective breeding and selection mapping using a novel wild-derived heterogeneous stock of mice revealed two closely-linked loci for tameness. Scientific Reports, 2017, 7, 4607.	1.6	16
45	A Systems Genetics Approach Provides a Bridge from Discovered Genetic Variants to Biological Pathways in Rheumatoid Arthritis. PLoS ONE, 2011, 6, e25389.	1.1	16
46	Distribution of HLA haplotypes across Japanese Archipelago: similarity, difference and admixture. Journal of Human Genetics, 2015, 60, 683-690.	1.1	14
47	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.	1.1	14
48	The Relationship between TP53 Gene Status and Carboxylesterase 2 Expression in Human Colorectal Cancer. Disease Markers, 2018, 2018, 1-7.	0.6	13
49	IGF1 gene is epigenetically activated in preterm infants with intrauterine growth restriction. Clinical Epigenetics, 2020, 12, 108.	1.8	10
50	Substantial anti-gout effect conferred by common and rare dysfunctional variants of URAT1/SLC22A12. Rheumatology, 2021, 60, 5224-5232.	0.9	10
51	Exome and copy number variation analyses of Mayerâ€“Rokitanskyâ€“KÃ¼sterâ€“ Hauser syndrome. Human Genome Variation, 2018, 5, 27.	0.4	9
52	Combined change of behavioral traits for domestication and <scp>geneâ€networks</scp> in mice selectively bred for active tameness. Genes, Brain and Behavior, 2021, 20, e12721.	1.1	8
53	High Order Formation and Evolution of Hornerin in Primates. Genome Biology and Evolution, 2018, 10, 3167-3175.	1.1	7
54	Comprehensive discovery of CRISPR-targeted terminally redundant sequences in the human gut metagenome: Viruses, plasmids, and more. PLoS Computational Biology, 2021, 17, e1009428.	1.5	7

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55	Assessment of Artificial MiRNA Architectures for Higher Knockdown Efficiencies without the Undesired Effects in Mice. PLoS ONE, 2015, 10, e0135919.	1.1	6
56	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.	0.5	6
57	Identification of ancient viruses from metagenomic data of the Jomon people. Journal of Human Genetics, 2021, 66, 287-296.	1.1	5
58	Common variant of BCAS3 is associated with gout risk in Japanese population: the first replication study after gout GWAS in Han Chinese. BMC Medical Genetics, 2018, 19, 96.	2.1	4
59	Concurrent isolated retroperitoneal HGSC and STIC defined by somatic mutation analysis: a case report. Diagnostic Pathology, 2019, 14, 17.	0.9	4
60	HLA-B*39:01:01 is a novel risk factor for antithyroid drug-induced agranulocytosis in Japanese population. Pharmacogenomics Journal, 2021, 21, 94-101.	0.9	4
61	Allelic and haplotypic HLA diversity in indigenous Malaysian populations explored using Next Generation Sequencing. Human Immunology, 2022, 83, 17-26.	1.2	4
62	Biased expression of mutant alleles in cancer-related genes in esophageal squamous cell carcinoma. Esophagus, 2022, 19, 294-302.	1.0	4
63	Exploration of intermediate-sized INDELs by next-generation multigene panel testing in Han Chinese patients with breast cancer. Human Genome Variation, 2019, 6, 51.	0.4	3
64	é»'æ¯›å'Œç¨®ã«ãŠã'ã‚‹å…¨å›½çš„ã ç¨®ç‰›è©•ä¾¡ã®å¯èƒ½æ€§ãŠã‚ˆã³æ•°å¦ãƒ¢ãƒ‡ãƒ«ã«é–¢ã™ã‚‹ç"ç©¶. Nihon Chikusan Gakkaiho,	0	3
65	APOBEC mediated mutagenesis drives genomic heterogeneity in endometriosis. Journal of Human Genetics, 2022, 67, 323-329.	1.1	3
66	Identification of novel exonic mobile element insertions in epithelial ovarian cancers. Human Genome Variation, 2015, 2, 15030.	0.4	2
67	Sensitization of Gastric Cancer Cells to Irinotecan by p53 Activation. BPB Reports, 2019, 2, 130-133.	0.1	2
68	Adjusting for heterogeneity of variance for carcass traits affects single and multiple trait selections in genetic evaluation of Japanese Black cattle. Animal Science Journal, 2008, 79, 645-654.	0.6	1
69	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.	1.4	1
70	OP0047â€…A GENOME-WIDE ASSOCIATION STUDY IDENTIFIED NOVEL LOCI ASSOCIATED WITH THE PROGRESSION FROM ASYMPTOMATIC HYPERURICEMIA TO GOUT. , 2019, , .		0
71	Useful properties of Bayesian multiple QTL mapping with MCMC. Journal of Animal Genetics, 2006, 34, 17-29.	0.1	0
72	The Admixed Origin of Japanese Population from HLA Alleles. Major Histocompatibility Complex, 2014, 21, 37-44.	0.2	0

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73	High incidence of PI3K pathway gene mutations in South Indian cervical cancers. Cancer Genetics, 2022, 264-265, 100-108.	0.2	0
74	The landscape of genetic alterations of <scp>UVB</scp> â€induced skin tumors in <scp>DNA</scp> repairâ€deficient mice. Experimental Dermatology, 0, , .	1.4	0