Yoshinori Murakami

List of Publications by Year in Descending Order

127 papers	4,666 citations	40 h-index	64 g-index
141 ext. papers	6,672 ext. citations	10.7 avg, IF	5.03 L-index

#	Paper	IF	Citations
127	Usefulness of circulating tumor DNA by targeting human papilloma virus-derived sequences as a biomarker in p16-positive oropharyngeal cancer.. *Scientific Reports*, **2022**, 12, 572	4.9	0
126	Leveraging fine-mapping and multipopulation training data to improve cross-population polygenic risk scores.. *Nature Genetics*, **2022**, 54, 450-458	36.3	3
125	Expansion of Cancer Risk Profile for BRCA1 and BRCA2 Pathogenic Variants.. *JAMA Oncology*, **2022**,	13.4	1
124	The power of genetic diversity in genome-wide association studies of lipids. *Nature*, **2021**,	50.4	24
123	Pharmacological inhibition of Mint3 attenuates tumour growth, metastasis, and endotoxic shock. *Communications Biology*, **2021**, 4, 1165	6.7	1
122	Hematopoietic mosaic chromosomal alterations increase the risk for diverse types of infection. *Nature Medicine*, **2021**, 27, 1012-1024	50.5	16
121	Combined landscape of single-nucleotide variants and copy number alterations in clonal hematopoiesis. *Nature Medicine*, **2021**, 27, 1239-1249	50.5	10
120	CADM1 promotes malignant features of small-cell lung cancer by recruiting 4.1R to the plasma membrane. *Biochemical and Biophysical Research Communications*, **2021**, 534, 172-178	3.4	4
119	Short somatic alterations at the site of copy number variation in breast cancer. *Cancer Science*, **2021**, 112, 444-453	6.9	0
118	Susceptibility loci and polygenic architecture highlight population specific and common genetic features in inguinal hernias: genetics in inguinal hernias. *EBioMedicine*, **2021**, 70, 103532	8.8	1
117	A cross-population atlas of genetic associations for 220 human phenotypes. *Nature Genetics*, **2021**, 53, 1415-1424	36.3	40
116	Circulating tumor DNA harboring the V600E mutation may predict poor outcomes of primary papillary thyroid cancer patients. *Thyroid*, **2021**,	6.2	2
115	Mathematical Modeling of the Dimerization of EGFR and ErbB3 in Lung Adenocarcinoma. *Springer Proceedings in Mathematics and Statistics*, **2021**, 195-202	0.2	
114	Population-based Screening for Hereditary Colorectal Cancer Variants in Japan. *Clinical Gastroenterology and Hepatology*, **2020**,	6.9	3
113	Fine Mapping of the Major Histocompatibility Complex Region and Association of the HLA-B*52:01 Allele With Cervical Cancer in Japanese Women. *JAMA Network Open*, **2020**, 3, e2023248	10.4	3
112	Reciprocal expression of trefoil factor-1 and thyroid transcription factor-1 in lung adenocarcinomas. *Cancer Science*, **2020**, 111, 2183-2195	6.9	7
111	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

110	Chromosomal alterations among age-related haematopoietic clones in Japan. *Nature*, **2020**, 584, 130-135	50.4	38
109	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
108	EXOSC9 depletion attenuates P-body formation, stress resistance, and tumorigenicity of cancer cells. *Scientific Reports*, **2020**, 10, 9275	4.9	10
107	Trans-biobank analysis with 676,000 individuals elucidates the association of polygenic risk scores of complex traits with human lifespan. *Nature Medicine*, **2020**, 26, 542-548	50.5	36
106	Genetic and phenotypic landscape of the mitochondrial genome in the Japanese population. *Communications Biology*, **2020**, 3, 104	6.7	9
105	CADM1 suppresses c-Src activation by binding with Cbp on membrane lipid rafts and intervenes colon carcinogenesis. *Biochemical and Biophysical Research Communications*, **2020**, 529, 854-860	3.4	4
104	Genome-wide association meta-analysis identifies GP2 gene risk variants for pancreatic cancer. *Nature Communications*, **2020**, 11, 3175	17.4	14
103	GWAS of 165,084 Japanese individuals identified nine loci associated with dietary habits. *Nature Human Behaviour*, **2020**, 4, 308-316	12.8	28
102	Dimensionality reduction reveals fine-scale structure in the Japanese population with consequences for polygenic risk prediction. *Nature Communications*, **2020**, 11, 1569	17.4	22
101	Mint3 is dispensable for pancreatic and kidney functions in mice. *Biochemistry and Biophysics Reports*, **2020**, 24, 100872	2.2	2
100	Genome-Wide Natural Selection Signatures Are Linked to Genetic Risk of Modern Phenotypes in the Japanese Population. *Molecular Biology and Evolution*, **2020**, 37, 1306-1316	8.3	6
99	GWAS of five gynecologic diseases and cross-trait analysis in Japanese. *European Journal of Human Genetics*, **2020**, 28, 95-107	5.3	15
98	HLA-B*51:01 and CYP2C9*3 Are Risk Factors for Phenytoin-Induced Eruption in the Japanese Population: Analysis of Data From the Biobank Japan Project. *Clinical Pharmacology and Therapeutics*, **2020**, 107, 1170-1178	6.1	8
97	Genetic characterization of pancreatic cancer patients and prediction of carrier status of germline pathogenic variants in cancer-predisposing genes. *EBioMedicine*, **2020**, 60, 103033	8.8	10
96	The Polygenic and Monogenic Basis of Blood Traits and Diseases. *Cell*, **2020**, 182, 1214-1231.e11	56.2	96
95	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
94	Improving the trans-ancestry portability of polygenic risk scores by prioritizing variants in predicted cell-type-specific regulatory elements. *Nature Genetics*, **2020**, 52, 1346-1354	36.3	37
93	Endogenization and excision of human herpesvirus 6 in human genomes. *PLoS Genetics*, **2020**, 16, e1008915	8	8

92	A Mendelian randomization study identified obesity as a causal risk factor of uterine endometrial cancer in Japanese. *Cancer Science*, **2020**, 111, 4646-4651	6.9	13
91	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. *Cell*, **2020**, 182, 1198-1213.e14	56.2	88
90	Mint3 depletion restricts tumor malignancy of pancreatic cancer cells by decreasing SKP2 expression via HIF-1. *Oncogene*, **2020**, 39, 6218-6230	9.2	9
89	Functional variants in ADH1B and ALDH2 are non-additively associated with all-cause mortality in Japanese population. *European Journal of Human Genetics*, **2020**, 28, 378-382	5.3	7
88	Characterizing rare and low-frequency height-associated variants in the Japanese population. *Nature Communications*, **2019**, 10, 4393	17.4	51
87	Comparison of effects of UGT1A1*6 and UGT1A1*28 on irinotecan-induced adverse reactions in the Japanese population: analysis of the Biobank Japan Project. *Journal of Human Genetics*, **2019**, 64, 1195-1202	4.2	10
86	CADM1 associates with Hippo pathway core kinases; membranous co-expression of CADM1 and LATS2 in lung tumors predicts good prognosis. *Cancer Science*, **2019**, 110, 2284-2295	6.9	10
85	A case of an elderly patient with high-grade colorectal cancer in poor general condition who showed near complete response to chemotherapy and achieved long-term survival. *International Journal of Surgery Case Reports*, **2019**, 58, 186-189	0.8	1
84	Genome-wide meta-analysis identifies multiple novel loci associated with serum uric acid levels in Japanese individuals. *Communications Biology*, **2019**, 2, 115	6.7	42
83	GWAS of mosaic loss of chromosome Y highlights genetic effects on blood cell differentiation. *Nature Communications*, **2019**, 10, 4719	17.4	18
82	Associations of autozygosity with a broad range of human phenotypes. *Nature Communications*, **2019**, 10, 4957	17.4	40
81	Identification of 28 new susceptibility loci for type 2 diabetes in the Japanese population. *Nature Genetics*, **2019**, 51, 379-386	36.3	83
80	Mathematical analysis of gefitinib resistance of lung adenocarcinoma caused by MET amplification. *Biochemical and Biophysical Research Communications*, **2019**, 511, 544-550	3.4	9
79	Genetic predisposition to mosaic Y chromosome loss in blood. *Nature*, **2019**, 575, 652-657	50.4	83
78	Identification of two novel breast cancer loci through large-scale genome-wide association study in the Japanese population. *Scientific Reports*, **2019**, 9, 17332	4.9	5
77	Expression profile of CADM1 and CADM4 in triple negative breast cancer with primary systemic therapy. *Oncology Letters*, **2019**, 17, 921-926	2.6	2
76	Decreased expression of CADM1 and CADM4 are associated with advanced stage breast cancer. *Oncology Letters*, **2018**, 15, 2401-2406	2.6	12
75	GWAS identifies two novel colorectal cancer loci at 16q24.1 and 20q13.12. *Carcinogenesis*, **2018**, 39, 652-660	4.6	32

74	Development of a Highly Sensitive Device for Counting the Number of Disease-Specific Exosomes in Human Sera. *Clinical Chemistry*, **2018**, 64, 1463-1473	5.5	35
73	Progression of Pulmonary Emphysema and Continued Increase in Ectodomain Shedding of Cell Adhesion Molecule 1 After Cessation of Cigarette Smoke Exposure in Mice. *Frontiers in Cell and Developmental Biology*, **2018**, 6, 52	5.7	5
72	Quantitative Analysis of Interaction Between CADM1 and Its Binding Cell-Surface Proteins Using Surface Plasmon Resonance Imaging. *Frontiers in Cell and Developmental Biology*, **2018**, 6, 86	5.7	4
71	Characterization of KIF11 as a novel prognostic biomarker and therapeutic target for oral cancer. *International Journal of Oncology*, **2018**, 52, 155-165	4.4	24
70	Genome-wide association study (GWAS) of ovarian cancer in Japanese predicted regulatory variants in 22q13.1. *PLoS ONE*, **2018**, 13, e0209096	3.7	5
69	Genome-wide association study identifies gastric cancer susceptibility loci at 12q24.11-12 and 20q11.21. *Cancer Science*, **2018**, 109, 4015-4024	6.9	22
68	Mathematical modeling and analysis of ErbB3 and EGFR dimerization process for the gefitinib resistance. *JSIAM Letters*, **2018**, 10, 33-36	0.2	2
67	Cross-sectional analysis of BioBank Japan clinical data: A large cohort of 200,000 patients with 47 common diseases. *Journal of Epidemiology*, **2017**, 27, S9-S21	3.4	85
66	Mechanistic insights into ectodomain shedding: susceptibility of CADM1 adhesion molecule is determined by alternative splicing and O-glycosylation. *Scientific Reports*, **2017**, 7, 46174	4.9	14
65	Control of metastatic niche formation by targeting APBA3/Mint3 in inflammatory monocytes. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, E4416-E4424	11.5	18
64	Overview of the BioBank Japan Project: Study design and profile. *Journal of Epidemiology*, **2017**, 27, S2-S8	3.4	239
63	Overview of BioBank Japan follow-up data in 32 diseases. *Journal of Epidemiology*, **2017**, 27, S22-S28	3.4	41
62	Establishment of highly metastatic KRAS mutant lung cancer cell sublines in long-term three-dimensional low attachment cultures. *PLoS ONE*, **2017**, 12, e0181342	3.7	12
61	Mint3 in bone marrow-derived cells promotes lung metastasis in breast cancer model mice. *Biochemical and Biophysical Research Communications*, **2017**, 490, 688-692	3.4	8
60	A One-Pot Three-Component Double-Click Method for Synthesis of [Cu]-Labeled Biomolecular Radiotherapeutics. *Scientific Reports*, **2017**, 7, 1912	4.9	20
59	Mint3/Apba3 depletion ameliorates severe murine influenza pneumonia and macrophage cytokine production in response to the influenza virus. *Scientific Reports*, **2016**, 6, 37815	4.9	14
58	Loss of YAP1 defines neuroendocrine differentiation of lung tumors. *Cancer Science*, **2016**, 107, 1527-1538	3.9	44
57	Cell division cycle associated 1 as a novel prognostic biomarker and therapeutic target for oral cancer. *International Journal of Oncology*, **2016**, 49, 1385-93	4.4	13

56	NECAB3 Promotes Activation of Hypoxia-inducible factor-1 during Normoxia and Enhances Tumourigenicity of Cancer Cells. *Scientific Reports*, **2016**, 6, 22784	4.9	21
55	CRTAM determines the CD4+ cytotoxic T lymphocyte lineage. *Journal of Experimental Medicine*, **2016**, 213, 123-38	16.6	86
54	Measles virus selectively blind to signaling lymphocyte activity molecule has oncolytic efficacy against nectin-4-expressing pancreatic cancer cells. *Cancer Science*, **2016**, 107, 1647-1652	6.9	19
53	The ERK signaling target RNF126 regulates anoikis resistance in cancer cells by changing the mitochondrial metabolic flux. *Cell Discovery*, **2016**, 2, 16019	22.3	32
52	Xanthohumol inhibits STAT3 activation pathway leading to growth suppression and apoptosis induction in human cholangiocarcinoma cells. *Oncology Reports*, **2016**, 35, 2065-72	3.5	25
51	Dynamic regulation of a cell adhesion protein complex including CADM1 by combinatorial analysis of FRAP with exponential curve-fitting. *PLoS ONE*, **2015**, 10, e0116637	3.7	11
50	A measles virus selectively blind to signaling lymphocytic activation molecule shows anti-tumor activity against lung cancer cells. *Oncotarget*, **2015**, 6, 24895-903	3.3	17
49	Genomic and transcriptional alterations of cholangiocarcinoma. *Journal of Hepato-Biliary-Pancreatic Sciences*, **2014**, 21, 380-7	2.8	17
48	Expression of PRMT5 in lung adenocarcinoma and its significance in epithelial-mesenchymal transition. *Human Pathology*, **2014**, 45, 1397-405	3.7	52
47	Increased ectodomain shedding of lung epithelial cell adhesion molecule 1 as a cause of increased alveolar cell apoptosis in emphysema. *Thorax*, **2014**, 69, 223-31	7.3	26
46	Trans-homophilic interaction of CADM1 activates PI3K by forming a complex with MAGuK-family proteins MPP3 and Dlg. *PLoS ONE*, **2014**, 9, e82894	3.7	22
45	Detection of lung tumors in mice using a 1-tesla compact magnetic resonance imaging system. *PLoS ONE*, **2014**, 9, e94945	3.7	7
44	Lung cancer with loss of BRG1/BRM, shows epithelial mesenchymal transition phenotype and distinct histologic and genetic features. *Cancer Science*, **2013**, 104, 266-73	6.9	80
43	Cell adhesion molecule 1 is a new osteoblastic cell adhesion molecule and a diagnostic marker for osteosarcoma. *Life Sciences*, **2013**, 92, 91-9	6.8	22
42	Expression of a splicing variant of the CADM1 specific to small cell lung cancer. *Cancer Science*, **2012**, 103, 1051-7	6.9	19
41	Aberrations of a cell adhesion molecule CADM4 in renal clear cell carcinoma. *International Journal of Cancer*, **2012**, 130, 1329-37	7.5	44
40	Identification of CCDC6-RET fusion in the human lung adenocarcinoma cell line, LC-2/ad. *Journal of Thoracic Oncology*, **2012**, 7, 1872-1876	8.9	71
39	Tumor suppressor cell adhesion molecule 1 (CADM1) is cleaved by a disintegrin and metalloprotease 10 (ADAM10) and subsequently cleaved by γ-secretase complex. *Biochemical and Biophysical Research Communications*, **2012**, 417, 462-7	3.4	26

38	Aberrant expression of tumor suppressors CADM1 and 4.1B in invasive lesions of primary breast cancer. *Breast Cancer*, **2012**, 19, 242-52	3.4	64
37	Adhesion molecule CADM1 contributes to gap junctional communication among pancreatic islet β-cells and prevents their excessive secretion of glucagon. *Islets*, **2012**, 4, 49-55	2	20
36	Transcriptional regulation of the CADM1 gene by retinoic acid during the neural differentiation of murine embryonal carcinoma P19 cells. *Genes To Cells*, **2011**, 16, 791-802	2.3	11
35	CADM1 interacts with Tiam1 and promotes invasive phenotype of human T-cell leukemia virus type I-transformed cells and adult T-cell leukemia cells. *Journal of Biological Chemistry*, **2010**, 285, 15511-15522	5.4	53
34	Tumor suppressor CADM1 is involved in epithelial cell structure. *Biochemical and Biophysical Research Communications*, **2009**, 390, 977-82	3.4	51
33	Expression of a soluble isoform of cell adhesion molecule 1 in the brain and its involvement in directional neurite outgrowth. *American Journal of Pathology*, **2009**, 174, 2278-89	5.8	24
32	Expression of TSLC1, a candidate tumor suppressor gene mapped to chromosome 11q23, is downregulated in unfavorable neuroblastoma without promoter hypermethylation. *International Journal of Cancer*, **2008**, 123, 2087-94	7.5	45
31	Involvement of the SgIGSF/Necl-2 adhesion molecule in degranulation of mesenteric mast cells. *Journal of Neuroimmunology*, **2007**, 184, 209-13	3.5	14
30	Hypermethylation of the TSLC1/IGSF4 promoter is associated with tobacco smoking and a poor prognosis in primary nonsmall cell lung carcinoma. *Cancer*, **2006**, 106, 1751-8	6.4	72
29	Promoter hypermethylation of the potential tumor suppressor DAL-1/4.1B gene in renal clear cell carcinoma. *International Journal of Cancer*, **2006**, 118, 916-23	7.5	68
28	Disruption of spermatogenic cell adhesion and male infertility in mice lacking TSLC1/IGSF4, an immunoglobulin superfamily cell adhesion molecule. *Molecular and Cellular Biology*, **2006**, 26, 3610-24	4.8	79
27	Overexpression of a cell adhesion molecule, TSLC1, as a possible molecular marker for acute-type adult T-cell leukemia. *Blood*, **2005**, 105, 1204-13	2.2	139
26	Loss of TSLC1 expression in lung adenocarcinoma: relationships with histological subtypes, sex and prognostic significance. *Cancer Science*, **2005**, 96, 480-6	6.9	38
25	Involvement of a cell adhesion molecule, TSLC1/IGSF4, in human oncogenesis. *Cancer Science*, **2005**, 96, 543-52	6.9	136
24	Promoter methylation of DAL-1/4.1B predicts poor prognosis in non-small cell lung cancer. *Clinical Cancer Research*, **2005**, 11, 2954-61	12.9	64
23	Tumor suppressor in lung cancer (TSLC)1 suppresses epithelial cell scattering and tubulogenesis. *Journal of Biological Chemistry*, **2005**, 280, 42164-71	5.4	33
22	Loss of tumor suppressor in lung cancer-1 (TSLC1) expression in meningioma correlates with increased malignancy grade and reduced patient survival. *Journal of Neuropathology and Experimental Neurology*, **2004**, 63, 1015-27	3.1	52
21	Fine mapping of the 11q22-23 tumor suppressive region and involvement of TSLC1 in nasopharyngeal carcinoma. *International Journal of Cancer*, **2004**, 112, 628-35	7.5	37

20	Association of a lung tumor suppressor TSLC1 with MPP3, a human homologue of Drosophila tumor suppressor Dlg. *Oncogene*, **2003**, 22, 6160-5	9.2	68
19	Promoter methylation of the TSLC1 gene in advanced lung tumors and various cancer cell lines. *International Journal of Cancer*, **2003**, 107, 53-9	7.5	93
18	Involvement of TSLC1 in progression of esophageal squamous cell carcinoma. *Cancer Research*, **2003**, 63, 6320-6	10.1	76
17	The cytoplasmic domain is critical to the tumor suppressor activity of TSLC1 in non-small cell lung cancer. *Cancer Research*, **2003**, 63, 7979-85	10.1	39
16	Promoter methylation of TSLC1 and tumor suppression by its gene product in human prostate cancer. *Japanese Journal of Cancer Research*, **2002**, 93, 605-9		89
15	Hypermethylation of the TSLC1 gene promoter in primary gastric cancers and gastric cancer cell lines. *Japanese Journal of Cancer Research*, **2002**, 93, 857-60		61
14	Functional cloning of a tumor suppressor gene, TSLC1, in human non-small cell lung cancer. *Oncogene*, **2002**, 21, 6936-48	9.2	48
13	The tumor suppressor protein TSLC1 is involved in cell-cell adhesion. *Journal of Biological Chemistry* , **2002**, 277, 31014-9	5.4	132
12	Direct association of TSLC1 and DAL-1, two distinct tumor suppressor proteins in lung cancer. *Cancer Research*, **2002**, 62, 5129-33	10.1	133
11	TSLC1 is a tumor-suppressor gene in human non-small-cell lung cancer. *Nature Genetics*, **2001**, 27, 427-30	36.3	369
10	Isolation of the TSLL1 and TSLL2 genes, members of the tumor suppressor TSLC1 gene family encoding transmembrane proteins. *Oncogene*, **2001**, 20, 5401-7	9.2	59
9	A 2-Mb sequence-ready contig map and a novel immunoglobulin superfamily gene IGSF4 in the LOH region of chromosome 11q23.2. *Genomics*, **1999**, 62, 139-46	4.3	106
8	Accumulation of genetic alterations and their significance in each primary human cancer and cell line. *Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis*, **1998**, 400, 421-37	3.3	16
7	Genetic alterations in human pancreatic cancer. *Journal of Hepato-Biliary-Pancreatic Surgery*, **1997**, 4, 283-290		4
6	Random segregation of DNA strands in epidermal basal cells. *Japanese Journal of Cancer Research*, **1989**, 80, 637-42		24
5	Family trees representing the finitely proliferative nature of cultured rat liver cells. *Cell Structure and Function*, **1983**, 8, 293-301	2.2	3
4	Global biobank analyses provide lessons for computing polygenic risk scores across diverse cohorts		3
3	In silico integration of thousands of epigenetic datasets into 707 cell type regulatory annotations improves the trans-ethnic portability of polygenic risk scores		1

List of Publications

2	A global atlas of genetic associations of 220 deep phenotypes	14
1	Genetic predisposition to mosaic Y chromosome loss in blood is associated with genomic instability in other tissues and susceptibility to non-haematological cancers	5