Irene M Ong

List of Publications by Year in Descending Order

40 papers	775 citations	14 h-index	27 g-index
41 ext. papers	1,246 ext. citations	9.3 avg, IF	4.03 L-index

#	Paper	IF	Citations
40	Sex and genetic background define the metabolic, physiologic, and molecular response to protein restriction.. *Cell Metabolism*, **2022**, 34, 209-226.e5	24.6	4
39	Determination of tissue contributions to the circulating lipid pool in cold exposure via systematic assessment of lipid profiles.. *Journal of Lipid Research*, **2022**, 100197	6.3	0
38	BAF155 methylation drives metastasis by hijacking super-enhancers and subverting anti-tumor immunity. *Nucleic Acids Research*, **2021**, 49, 12211-12233	20.1	3
37	The landscape of antibody binding in SARS-CoV-2 infection. *PLoS Biology*, **2021**, 19, e3001265	9.7	17
36	Risk of Late-Onset Breast Cancer in Genetically Predisposed Women. *Journal of Clinical Oncology*, **2021**, 39, 3430-3440	2.2	3
35	Proteomic and Genomic Methylation Signatures of Idiopathic Subglottic Stenosis. *Laryngoscope*, **2021**, 131, E540-E546	3.6	2
34	Systemic Metabolic Alterations Correlate with Islet-Level Prostaglandin E Production and Signaling Mechanisms That Predict ☐Cell Dysfunction in a Mouse Model of Type 2 Diabetes. *Metabolites*, **2021**, 11,	5.6	5
33	MR1 overexpression correlates with poor clinical prognosis in glioma patients. *Neuro-Oncology Advances*, **2021**, 3, vdab034	0.9	0
32	A Population-Based Study of Genes Previously Implicated in Breast Cancer. *New England Journal of Medicine*, **2021**, 384, 440-451	59.2	115
31	SOX17 integrates HOXA and arterial programs in hemogenic endothelium to drive definitive lympho-myeloid hematopoiesis. *Cell Reports*, **2021**, 34, 108758	10.6	6
30	Risk of Breast Cancer Among Carriers of Pathogenic Variants in Breast Cancer Predisposition Genes Varies by Polygenic Risk Score. *Journal of Clinical Oncology*, **2021**, 39, 2564-2573	2.2	12
29	Multiomic analysis reveals decidual-specific transcriptional programing of MAIT cells. *American Journal of Reproductive Immunology*, **2021**, 86, e13495	3.8	0
28	Mediator complex subunit 12 is a gatekeeper of SARS-CoV-2 infection in breast cancer cells. *Genes and Diseases*, **2021**, 9, 5-5	6.6	1
27	PKM2-TMEM33 axis regulates lipid homeostasis in cancer cells by controlling SCAP stability. *EMBO Journal*, **2021**, 40, e108065	13	3
26	Development and characterization of patient-derived xenografts from non-small cell lung cancer brain metastases. *Scientific Reports*, **2021**, 11, 2520	4.9	4
25	Fibroblast Growth Factor Receptors as Targets for Radiosensitization in Head and Neck Squamous Cell Carcinomas. *International Journal of Radiation Oncology Biology Physics*, **2020**, 107, 793-803	4	4
24	Enrichment of melanoma-associated T cells in 6-thioguanine-resistant T cells from metastatic melanoma patients. *Melanoma Research*, **2020**, 30, 52-61	3.3	1

23	Keratin 13 deficiency causes white sponge nevus in mice. *Developmental Biology*, **2020**, 468, 146-153	3.1	2
22	MASH Explorer: A Universal Software Environment for Top-Down Proteomics. *Journal of Proteome Research*, **2020**, 19, 3867-3876	5.6	24
21	Single-cell technologies in reproductive immunology. *American Journal of Reproductive Immunology*, **2019**, 82, e13157	3.8	3
20	SOX17 Is Essential for Integration of Arterial and HOXA Programs in Hemogenic Endothelium. *Blood*, **2019**, 134, 2476-2476	2.2	2
19	Transcriptional and Functional Programming of Decidual Innate Lymphoid Cells. *Frontiers in Immunology*, **2019**, 10, 3065	8.4	9
18	The Metabolic Response to a Low Amino Acid Diet is Independent of Diet-Induced Shifts in the Composition of the Gut Microbiome. *Scientific Reports*, **2019**, 9, 67	4.9	11
17	Caloric Restriction Engages Hepatic RNA Processing Mechanisms in Rhesus Monkeys. *Cell Metabolism*, **2018**, 27, 677-688.e5	24.6	37
16	Polycomb Group Protein YY1 Is an Essential Regulator of Hematopoietic Stem Cell Quiescence. *Cell Reports*, **2018**, 22, 1545-1559	10.6	25
15	Gut microbiome populations are associated with structure-specific changes in white matter architecture. *Translational Psychiatry*, **2018**, 8, 6	8.6	43
14	Tissue factor-factor VIIa complex triggers protease activated receptor 2-dependent growth factor release and migration in ovarian cancer. *Gynecologic Oncology*, **2017**, 145, 167-175	4.9	22
13	Cotargeting mTORC and EGFR Signaling as a Therapeutic Strategy in HNSCC. *Molecular Cancer Therapeutics*, **2017**, 16, 1257-1268	6.1	29
12	Defining the boundaries and expanding the utility of head and neck cancer patient derived xenografts. *Oral Oncology*, **2017**, 64, 65-72	4.4	13
11	PKM2 methylation by CARM1 activates aerobic glycolysis to promote tumorigenesis. *Nature Cell Biology*, **2017**, 19, 1358-1370	23.4	129
10	Integrating Enhancer Mechanisms to Establish a Hierarchical Blood Development Program. *Cell Reports*, **2017**, 20, 2966-2979	10.6	29
9	PP2A-Bδ holoenzyme substrate recognition, regulation and role in cytokinesis. *Cell Discovery*, **2017**, 3, 17027	22.3	44
8	Discriminatory power of common genetic variants in personalized breast cancer diagnosis. *Proceedings of SPIE*, **2016**, 9787,	1.7	2
7	Sex- and tissue-specific changes in mTOR signaling with age in C57BL/6J mice. *Aging Cell*, **2016**, 15, 155-166	9.9	94
6	Ultraviolet radiation-induced differential microRNA expression in the skin of hairless SKH1 mice, a widely used mouse model for dermatology research. *Oncotarget*, **2016**, 7, 84924-84937	3.3	7

5   Structure-Leveraged Methods in Breast Cancer Risk Prediction. *Journal of Machine Learning Research*, **2016**, 17,   28.6   4

4   Ultraviolet radiation-induced tumor necrosis factor alpha, which is linked to the development of cutaneous SCC, modulates differential epidermal microRNAs expression. *Oncotarget*, **2016**, 7, 17945-56   3.3   16

3   GATA Factor-Dependent Positive-Feedback Circuit Controls Acute Myeloid Leukemia Cell Proliferation: Mechanisms and Targets for Therapeutic Intervention. *Blood*, **2016**, 128, 1706-1706   2.2

2   GATA Factor-Dependent Positive-Feedback Circuit in Acute Myeloid Leukemia Cells. *Cell Reports*, **2016**, 16, 2428-41   10.6   45

1   CAMDA 2014: Making sense of RNA-Seq data: From low-level processing to functional analysis. *Systems Biomedicine (Austin, Tex)*, **2014**, 2, 31-40   5