

# Jason Wong

## List of Publications by Year in descending order

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103  
papers

4,745  
citations

94381

37  
h-index

110317

64  
g-index

114  
all docs

114  
docs citations

114  
times ranked

8825  
citing authors

#	ARTICLE	IF	CITATIONS
1	Gene expression is a poor predictor of steady-state metabolite abundance in cancer cells. <i>FASEB Journal</i> , 2022, 36, e22296.	0.2	6
2	Induction of muscle-regenerative multipotent stem cells from human adipocytes by PDGF-AB and 5-azacytidine. <i>Science Advances</i> , 2021, 7, .	4.7	3
3	Poor mobilization of autologous CD34 <sup>+</sup> peripheral blood stem cells in haematology patients undergoing autologous stem cell transplantation is associated with the presence of variants in genes implicated in clonal haematopoiesis of indeterminant potential. <i>British Journal of Haematology</i> , 2021, 193, 841-844.	1.2	6
4	A tumor microenvironment-specific gene expression signature predicts chemotherapy resistance in colorectal cancer patients. <i>Npj Precision Oncology</i> , 2021, 5, 7.	2.3	29
5	Proteogenomic interrogation of cancer cell lines: an overview of the field. <i>Expert Review of Proteomics</i> , 2021, 18, 1-12.	1.3	1
6	Disruption of a GATA2-TAL1-ERG regulatory circuit promotes erythroid transition in healthy and leukemic stem cells. <i>Blood</i> , 2021, 138, 1441-1455.	0.6	26
7	Repurposing sodium-glucose co-transporter 2 inhibitors (SGLT2i) for cancer treatment – A Review. <i>Reviews in Endocrine and Metabolic Disorders</i> , 2021, 22, 1121-1136.	2.6	17
8	Overexpression of transposable elements is associated with immune evasion and poor outcome in colorectal cancer. <i>European Journal of Cancer</i> , 2021, 157, 94-107.	1.3	12
9	Deficiency of replication-independent DNA mismatch repair drives a 5-methylcytosine deamination mutational signature in cancer. <i>Science Advances</i> , 2021, 7, eabg4398.	4.7	11
10	RNA Splicing Alterations Induce a Cellular Stress Response Associated with Poor Prognosis in Acute Myeloid Leukemia. <i>Clinical Cancer Research</i> , 2020, 26, 3597-3607.	3.2	26
11	Organoid cultures of early-onset colorectal cancers reveal distinct and rare genetic profiles. <i>Gut</i> , 2020, 69, 2165-2179.	6.1	47
12	Mutational processes of distinct POLE exonuclease domain mutants drive an enrichment of a specific TP53 mutation in colorectal cancer. <i>PLoS Genetics</i> , 2020, 16, e1008572.	1.5	27
13	Title is missing!. , 2020, 16, e1008572.		0
14	Title is missing!. , 2020, 16, e1008572.		0
15	Title is missing!. , 2020, 16, e1008572.		0
16	Title is missing!. , 2020, 16, e1008572.		0
17	JMJD6 is a tumorigenic factor and therapeutic target in neuroblastoma. <i>Nature Communications</i> , 2019, 10, 3319.	5.8	63
18	Glutarylation of Histone H4 Lysine 91 Regulates Chromatin Dynamics. <i>Molecular Cell</i> , 2019, 76, 660-675.e9.	4.5	112

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19	Assessing the Evolutionary Conservation of Protein Disulphide Bonds. <i>Methods in Molecular Biology</i> , 2019, 1967, 9-19.	0.4	1
20	Finding cancer driver mutations in the era of big data research. <i>Biophysical Reviews</i> , 2019, 11, 21-29.	1.5	20
21	Dysregulation of Cis-Regulatory Elements in Cancer. , 2019, , 173-192.		1
22	Analysis of 7,815 cancer exomes reveals associations between mutational processes and somatic driver mutations. <i>PLoS Genetics</i> , 2018, 14, e1007779.	1.5	44
23	Identification of allosteric disulfides from labile bonds in X-ray structures. <i>Royal Society Open Science</i> , 2018, 5, 171058.	1.1	17
24	Lymphocyte-Specific Chromatin Accessibility Pre-determines Glucocorticoid Resistance in Acute Lymphoblastic Leukemia. <i>Cancer Cell</i> , 2018, 34, 906-921.e8.	7.7	51
25	Dual roles of different redox forms of complement factor H in protecting against age related macular degeneration. <i>Free Radical Biology and Medicine</i> , 2018, 129, 237-246.	1.3	10
26	A Comprehensive Human Gastric Cancer Organoid Biobank Captures Tumor Subtype Heterogeneity and Enables Therapeutic Screening. <i>Cell Stem Cell</i> , 2018, 23, 882-897.e11.	5.2	445
27	Disruption of a 35 kb Enhancer Impairs CTCF Binding and <i>MLH1</i> Expression in Colorectal Cells. <i>Clinical Cancer Research</i> , 2018, 24, 4602-4611.	3.2	12
28	The Histone Methyltransferase DOT1L Promotes Neuroblastoma by Regulating Gene Transcription. <i>Cancer Research</i> , 2017, 77, 2522-2533.	0.4	59
29	The interaction between cytosine methylation and processes of DNA replication and repair shape the mutational landscape of cancer genomes. <i>Nucleic Acids Research</i> , 2017, 45, 7786-7795.	6.5	78
30	Cancer-associated noncoding mutations affect RNA G-quadruplex-mediated regulation of gene expression. <i>Scientific Reports</i> , 2017, 7, 708.	1.6	37
31	The non-coding RNA landscape of human hematopoiesis and leukemia. <i>Nature Communications</i> , 2017, 8, 218.	5.8	131
32	Integrative Genomics Identifies the Molecular Basis of Resistance to Azacitidine Therapy in Myelodysplastic Syndromes. <i>Cell Reports</i> , 2017, 20, 572-585.	2.9	99
33	Phylogenetic Analysis Using Protein Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2017, 1549, 135-146.	0.4	5
34	Nitration of tyrosines in complement factor H domains alters its immunological activity and mediates a pathogenic role in age related macular degeneration. <i>Oncotarget</i> , 2017, 8, 49016-49032.	0.8	16
35	Proteogenomic analysis prioritises functional single nucleotide variants in cancer samples. <i>Oncotarget</i> , 2017, 8, 95841-95852.	0.8	12
36	Identification of novel regulators of developmental hematopoiesis using Endoglin regulatory elements as molecular probes. <i>Blood</i> , 2016, 128, 1928-1939.	0.6	6

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37	Functional Mutations Form at CTCF-Cohesin Binding Sites in Melanoma Due to Uneven Nucleotide Excision Repair across the Motif. <i>Cell Reports</i> , 2016, 17, 2865-2872.	2.9	61
38	PDGF-AB and 5-Azacytidine induce conversion of somatic cells into tissue-regenerative multipotent stem cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E2306-15.	3.3	40
39	MAPK/ERK2 phosphorylates ERG at serine 283 in leukemic cells and promotes stem cell signatures and cell proliferation. <i>Leukemia</i> , 2016, 30, 1552-1561.	3.3	18
40	An investigation of the potential for epigenetic inactivation by transcription read-through in a sporadic colorectal cancer. <i>Gene</i> , 2016, 585, 154-158.	1.0	4
41	Differential DNA repair underlies mutation hotspots at active promoters in cancer genomes. <i>Nature</i> , 2016, 532, 259-263.	13.7	195
42	A quantitative proteomics approach identifies ETV6 and IKZF1 as new regulators of an <i>ERG</i> -driven transcriptional network. <i>Nucleic Acids Research</i> , 2016, 44, 10644-10661.	6.5	17
43	Integrated Genetic, Epigenetic, and Transcriptional Profiling Identifies Molecular Pathways in the Development of Laterally Spreading Tumors. <i>Molecular Cancer Research</i> , 2016, 14, 1217-1228.	1.5	20
44	Arrested Hematopoiesis and Vascular Relaxation Defects in Mice with a Mutation in <i>Dhfr</i> . <i>Molecular and Cellular Biology</i> , 2016, 36, 1222-1236.	1.1	6
45	Mutation hotspots in cis-regulatory regions in cancer. <i>Oncoscience</i> , 2016, 3, 318-319.	0.9	1
46	Opposing regulation of BIM and BCL2 controls glucocorticoid-induced apoptosis of pediatric acute lymphoblastic leukemia cells. <i>Blood</i> , 2015, 125, 273-283.	0.6	107
47	Single nucleotide polymorphism array profiling identifies distinct chromosomal aberration patterns across colorectal adenomas and carcinomas. <i>Genes Chromosomes and Cancer</i> , 2015, 54, 303-314.	1.5	14
48	FluClass: A novel algorithm and approach to score and visualize the phylogeny of the influenza virus using mass spectrometry. <i>Analytica Chimica Acta</i> , 2015, 895, 54-61.	2.6	7
49	Lynch Syndrome Associated with Two <i>MLH1</i> Promoter Variants and Allelic Imbalance of <i>MLH1</i> Expression. <i>Human Mutation</i> , 2015, 36, 622-630.	1.1	26
50	Systematic Screening of Promoter Regions Pinpoints Functional <i>Cis</i> -Regulatory Mutations in a Cutaneous Melanoma Genome. <i>Molecular Cancer Research</i> , 2015, 13, 1218-1226.	1.5	29
51	Overexpression of ERG in cord blood progenitors promotes expansion and recapitulates molecular signatures of high ERG leukemias. <i>Leukemia</i> , 2015, 29, 819-827.	3.3	24
52	WDR5 Supports an N-Myc Transcriptional Complex That Drives a Protumorigenic Gene Expression Signature in Neuroblastoma. <i>Cancer Research</i> , 2015, 75, 5143-5154.	0.4	88
53	Bioorthogonal labelling of 3-nitrotyrosine in peptides and proteins through diazotisation mediated azidation. <i>Organic and Biomolecular Chemistry</i> , 2015, 13, 374-378.	1.5	2
54	The search for <i>cis</i> -regulatory driver mutations in cancer genomes. <i>Oncotarget</i> , 2015, 6, 32509-32525.	0.8	18

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55	Epigenetic inactivation of the candidate tumor suppressor <i>USP44</i> is a frequent and early event in colorectal neoplasia. <i>Epigenetics</i> , 2014, 9, 1092-1100.	1.3	42
56	Altered promoter nucleosome positioning is an early event in gene silencing. <i>Epigenetics</i> , 2014, 9, 1422-1430.	1.3	25
57	OncoCis: annotation of cis-regulatory mutations in cancer. <i>Genome Biology</i> , 2014, 15, 485.	3.8	22
58	Redox Regulation of Methionine Aminopeptidase 2 Activity. <i>Journal of Biological Chemistry</i> , 2014, 289, 15035-15043.	1.6	20
59	BloodChIP: a database of comparative genome-wide transcription factor binding profiles in human blood cells. <i>Nucleic Acids Research</i> , 2014, 42, D172-D177.	6.5	43
60	Mechanism of Dimerization of a Recombinant Mature Vascular Endothelial Growth Factor C. <i>Biochemistry</i> , 2014, 53, 7-9.	1.2	19
61	Control of blood proteins by functional disulfide bonds. <i>Blood</i> , 2014, 123, 2000-2007.	0.6	83
62	Orchestrated Intron Retention Regulates Normal Granulocyte Differentiation. <i>Cell</i> , 2013, 154, 583-595.	13.5	408
63	Genome-wide analysis of transcriptional regulators in human HSPCs reveals a densely interconnected network of coding and noncoding genes. <i>Blood</i> , 2013, 122, e12-e22.	0.6	123
64	Tyrosine nitration moderates the peptidase activity of human methionyl aminopeptidase 2. <i>Biochemical and Biophysical Research Communications</i> , 2013, 440, 37-42.	1.0	6
65	Mass Trees: A New Phylogenetic Approach and Algorithm to Chart Evolutionary History with Mass Spectrometry. <i>Analytical Chemistry</i> , 2013, 85, 5475-5482.	3.2	24
66	Bioinformatics analysis reveals biophysical and evolutionary insights into the 3-nitrotyrosine post-translational modification in the human proteome. <i>Open Biology</i> , 2013, 3, 120148.	1.5	22
67	Activity of a heptad of transcription factors is associated with stem cell programs and clinical outcome in acute myeloid leukemia. <i>Blood</i> , 2013, 121, 2289-2300.	0.6	72
68	Signal analysis for genome-wide maps of histone modifications measured by ChIP-seq. <i>Bioinformatics</i> , 2012, 28, 1062-1069.	1.8	12
69	Factor XI is a substrate for oxidoreductases: Enhanced activation of reduced FXI and its role in antiphospholipid syndrome thrombosis. <i>Journal of Autoimmunity</i> , 2012, 39, 121-129.	3.0	41
70	<i>MMSAT</i> : Automated Quantification of Metabolites in Selected Reaction Monitoring Experiments. <i>Analytical Chemistry</i> , 2012, 84, 470-474.	3.2	23
71	FluShuffle and FluResort: new algorithms to identify reassorted strains of the influenza virus by mass spectrometry. <i>BMC Bioinformatics</i> , 2012, 13, 208.	1.2	20
72	Activity of a Heptad of Transcription Factors Is Associated with Stem Cell Programs and Clinical Outcome in Acute Myeloid Leukaemia. <i>Blood</i> , 2012, 120, 3525-3525.	0.6	0

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73	Noninvasive Imaging of Cell Death Using an Hsp90 Ligand. <i>Journal of the American Chemical Society</i> , 2011, 133, 2832-2835.	6.6	56
74	Disulfide Bond Acquisition through Eukaryotic Protein Evolution. <i>Molecular Biology and Evolution</i> , 2011, 28, 327-334.	3.5	83
75	Control of Mature Protein Function by Allosteric Disulfide Bonds. <i>Antioxidants and Redox Signaling</i> , 2011, 14, 113-126.	2.5	40
76	Mass and relative elution time profiling: two-dimensional analysis of sphingolipids in Alzheimer's disease brains. <i>Biochemical Journal</i> , 2011, 438, 165-175.	1.7	45
77	ERG promotes T-acute lymphoblastic leukemia and is transcriptionally regulated in leukemic cells by a stem cell enhancer. <i>Blood</i> , 2011, 117, 7079-7089.	0.6	81
78	Lateral self-association of VWF involves the Cys2431-Cys2453 disulfide/dithiol in the C2 domain. <i>Blood</i> , 2011, 118, 5312-5318.	0.6	47
79	Allosteric Disulfide Bonds. , 2011, , 151-182.		3
80	Beta 2 glycoprotein I is a substrate of thiol oxidoreductases. <i>Blood</i> , 2010, 116, 1995-1997.	0.6	60
81	Rapid Typing and Subtyping of Vaccine Strains of the Influenza Virus with High Resolution Mass Spectrometry. <i>European Journal of Mass Spectrometry</i> , 2010, 16, 321-329.	0.5	18
82	Typing of human and animal strains of influenza virus with conserved signature peptides of matrix M1 protein by high resolution mass spectrometry. <i>Journal of Virological Methods</i> , 2010, 165, 178-185.	1.0	32
83	FluTyper-an algorithm for automated typing and subtyping of the influenza virus from high resolution mass spectral data. <i>BMC Bioinformatics</i> , 2010, 11, 266.	1.2	16
84	Redox control of Î²2â€“glycoproteinÎ” von Willebrand factor interaction by thioredoxinâ€“. <i>Journal of Thrombosis and Haemostasis</i> , 2010, 8, 1754-1762.	1.9	52
85	Direct and Coordinate Regulation of ATP-binding Cassette Transporter Genes by Myc Factors Generates Specific Transcription Signatures That Significantly Affect the Chemoresistance Phenotype of Cancer Cells. <i>Journal of Biological Chemistry</i> , 2010, 285, 19532-19543.	1.6	96
86	Disulfide Bond That Constrains the HIV-1 gp120 V3 Domain Is Cleaved by Thioredoxin. <i>Journal of Biological Chemistry</i> , 2010, 285, 40072-40080.	1.6	31
87	An Overview of Label-Free Quantitation Methods in Proteomics by Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2010, 604, 273-283.	0.4	99
88	Rapid Differentiation of Seasonal and Pandemic H1N1 Influenza through Proteotyping of Viral Neuraminidase with Mass Spectrometry. <i>Analytical Chemistry</i> , 2010, 82, 4584-4590.	3.2	32
89	ETISEQ â€“ an algorithm for automated elution time ion sequencing of concurrently fragmented peptides for mass spectrometry-based proteomics. <i>BMC Bioinformatics</i> , 2009, 10, 244.	1.2	11
90	Activity profiling of platelets by chemical proteomics. <i>Proteomics</i> , 2009, 9, 40-50.	1.3	21

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91	Subtyping of the Influenza Virus by High Resolution Mass Spectrometry. <i>Analytical Chemistry</i> , 2009, 81, 3500-3506.	3.2	56
92	Signature peptides of influenza nucleoprotein for the typing and subtyping of the virus by high resolution mass spectrometry. <i>Analyst, The</i> , 2009, 134, 2253.	1.7	33
93	Computational methods for the comparative quantification of proteins in label-free LCn-MS experiments. <i>Briefings in Bioinformatics</i> , 2007, 9, 156-165.	3.2	68
94	msmsEval: tandem mass spectral quality assignment for high-throughput proteomics. <i>BMC Bioinformatics</i> , 2007, 8, 51.	1.2	41
95	Hydroxyl radical probe of the calmodulin-melittin complex interface by electrospray ionization mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2005, 16, 225-233.	1.2	58
96	Deterministic projection by growing cell structure networks for visualization of high-dimensionality datasets. <i>Journal of Biomedical Informatics</i> , 2005, 38, 322-330.	2.5	6
97	Performance of the computer algorithm COMPLX for the detection of protein complexes in the mass spectra of simulated biological mixtures. <i>Journal of Mass Spectrometry</i> , 2005, 40, 1187-1196.	0.7	3
98	SpecAlign-processing and alignment of mass spectra datasets. <i>Bioinformatics</i> , 2005, 21, 2088-2090.	1.8	168
99	Application of Fast Fourier Transform Cross-Correlation for the Alignment of Large Chromatographic and Spectral Datasets. <i>Analytical Chemistry</i> , 2005, 77, 5655-5661.	3.2	162
100	Grouping of visual objects by honeybees. <i>Journal of Experimental Biology</i> , 2004, 207, 3289-3298.	0.8	80
101	Photochemical and electrophysical production of radicals on millisecond timescales to probe the structure, dynamics and interactions of proteins. <i>Photochemical and Photobiological Sciences</i> , 2004, 3, 741.	1.6	61
102	COMPLX: a computer algorithm for the detection of protein-ligand and other macromolecular complexes in mass spectra. <i>Journal of Mass Spectrometry</i> , 2003, 38, 573-581.	0.7	6
103	Study of the Ribonuclease <sup>s</sup> -Protein <sup>a</sup> -Peptide Complex Using a Radical Probe and Electrospray Ionization Mass Spectrometry. <i>Analytical Chemistry</i> , 2003, 75, 1557-1563.	3.2	60