

Gerald Goh

List of Publications by Year in descending order

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Version: 2024-02-01

28
papers

6,784
citations

304743

22
h-index

501196

28
g-index

29
all docs

29
docs citations

29
times ranked

14252
citing authors

#	ARTICLE	IF	CITATIONS
1	Computational Methods for Analysis of Tumor Clonality and Evolutionary History. <i>Methods in Molecular Biology</i> , 2019, 1878, 217-226.	0.9	5
2	Fc-Optimized Anti-CD25 Depletes Tumor-Infiltrating Regulatory T Cells and Synergizes with PD-1 Blockade to Eradicate Established Tumors. <i>Immunity</i> , 2017, 46, 577-586.	14.3	323
3	Phylogenetic ctDNA analysis depicts early-stage lung cancer evolution. <i>Nature</i> , 2017, 545, 446-451.	27.8	1,287
4	Intratumoural evolutionary landscape of high-risk prostate cancer: the PROGENY study of genomic and immune parameters. <i>Annals of Oncology</i> , 2017, 28, 2472-2480.	1.2	45
5	Mutational landscape of MCPyV-positive and MCPyV-negative Merkel cell carcinomas with implications for immunotherapy. <i>Oncotarget</i> , 2016, 7, 3403-3415.	1.8	306
6	Shifting patterns of genomic variation in the somatic evolution of papillary thyroid carcinoma. <i>BMC Cancer</i> , 2016, 16, 646.	2.6	5
7	Clonal Evolutionary Analysis during HER2 Blockade in HER2-Positive Inflammatory Breast Cancer: A Phase II Open-Label Clinical Trial of Afatinib +/- Vinorelbine. <i>PLoS Medicine</i> , 2016, 13, e1002136.	8.4	28
8	Identification of a gain-of-function STAT3 mutation (p.Y640F) in lymphocytic variant hypereosinophilic syndrome. <i>Blood</i> , 2016, 127, 948-951.	1.4	52
9	DNA replication stress mediates APOBEC3 family mutagenesis in breast cancer. <i>Genome Biology</i> , 2016, 17, 185.	8.8	140
10	Absence of <i>KMT2D</i> / <i>MLL2</i> mutations in abdominal paraganglioma. <i>Clinical Endocrinology</i> , 2016, 84, 632-634.	2.4	3
11	Chromosome 19 amplification correlates with advanced disease in adrenocortical carcinoma. <i>Surgery</i> , 2016, 159, 296-301.	1.9	9
12	Whole-exome sequencing defines the mutational landscape of pheochromocytoma and identifies <i>KMT2D</i> as a recurrently mutated gene. <i>Genes Chromosomes and Cancer</i> , 2015, 54, 542-554.	2.8	57
13	Novel somatic mutations in primary hyperaldosteronism are related to the clinical, radiological and pathological phenotype. <i>Clinical Endocrinology</i> , 2015, 83, 779-789.	2.4	115
14	Recurrent gain of function mutation in calcium channel <i>CACNA1H</i> causes early-onset hypertension with primary aldosteronism. <i>ELife</i> , 2015, 4, e06315.	6.0	271
15	Increased Levels of Macrophage Inflammatory Proteins Result in Resistance to R5-Tropic HIV-1 in a Subset of Elite Controllers. <i>Journal of Virology</i> , 2015, 89, 5502-5514.	3.4	68
16	Characterization of the mutational landscape of anaplastic thyroid cancer via whole-exome sequencing. <i>Human Molecular Genetics</i> , 2015, 24, 2318-2329.	2.9	290
17	<i>PRKACA</i> mutations in cortisol-producing adenomas and adrenal hyperplasia: a single-center study of 60 cases. <i>European Journal of Endocrinology</i> , 2015, 172, 677-685.	3.7	64
18	Genomic landscape of cutaneous T cell lymphoma. <i>Nature Genetics</i> , 2015, 47, 1011-1019.	21.4	347

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19	Whole-Exome Sequencing Characterizes the Landscape of Somatic Mutations and Copy Number Alterations in Adrenocortical Carcinoma. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2015, 100, E493-E502.	3.6	131
20	Genetic landscape of metastatic and recurrent head and neck squamous cell carcinoma. <i>Journal of Clinical Investigation</i> , 2015, 126, 169-180.	8.2	156
21	Recurrent activating mutation in PRKACA in cortisol-producing adrenal tumors. <i>Nature Genetics</i> , 2014, 46, 613-617.	21.4	211
22	Abstract 985: The mutational landscape of LN metastasis and recurrence in HNSCC. , 2014, , .		0
23	Somatic and germline CACNA1D calcium channel mutations in aldosterone-producing adenomas and primary aldosteronism. <i>Nature Genetics</i> , 2013, 45, 1050-1054.	21.4	519
24	Exome sequencing identifies recurrent somatic RAC1 mutations in melanoma. <i>Nature Genetics</i> , 2012, 44, 1006-1014.	21.4	1,052
25	Effector CD4+ T Cell Expression Signatures and Immune-Mediated Disease Associated Genes. <i>PLoS ONE</i> , 2012, 7, e38510.	2.5	16
26	Application of Whole Exome Sequencing to Identify Disease-Causing Variants in Inherited Human Diseases. <i>Genomics and Informatics</i> , 2012, 10, 214.	0.8	56
27	Multiple Recurrent De Novo CNVs, Including Duplications of the 7q11.23 Williams Syndrome Region, Are Strongly Associated with Autism. <i>Neuron</i> , 2011, 70, 863-885.	8.1	1,146
28	Association and Mutation Analyses of 16p11.2 Autism Candidate Genes. <i>PLoS ONE</i> , 2009, 4, e4582.	2.5	80