

Claude Chelala

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3586948/publications.pdf>

Version: 2024-02-01

115
papers

7,648
citations

81889

39
h-index

56717

83
g-index

122
all docs

122
docs citations

122
times ranked

17066
citing authors

#	ARTICLE	IF	CITATIONS
1	The BioMart community portal: an innovative alternative to large, centralized data repositories. <i>Nucleic Acids Research</i> , 2015, 43, W589-W598.	14.5	682
2	Integrated genomic analysis identifies recurrent mutations and evolution patterns driving the initiation and progression of follicular lymphoma. <i>Nature Genetics</i> , 2014, 46, 176-181.	21.4	624
3	Activated Pancreatic Stellate Cells Sequester CD8+ T Cells to Reduce Their Infiltration of the Juxtatumoral Compartment of Pancreatic Ductal Adenocarcinoma. <i>Gastroenterology</i> , 2013, 145, 1121-1132.	1.3	439
4	Mutations in GLIS3 are responsible for a rare syndrome with neonatal diabetes mellitus and congenital hypothyroidism. <i>Nature Genetics</i> , 2006, 38, 682-687.	21.4	327
5	Retinoic Acid-Induced Pancreatic Stellate Cell Quiescence Reduces Paracrine Wnt ² -Catenin Signaling to Slow Tumor Progression. <i>Gastroenterology</i> , 2011, 141, 1486-1497.e14.	1.3	316
6	Integrative Annotation of 21,037 Human Genes Validated by Full-Length cDNA Clones. <i>PLoS Biology</i> , 2004, 2, e162.	5.6	290
7	Yes-associated protein (YAP) functions as a tumor suppressor in breast. <i>Cell Death and Differentiation</i> , 2008, 15, 1752-1759.	11.2	286
8	EZH2 mutations are frequent and represent an early event in follicular lymphoma. <i>Blood</i> , 2013, 122, 3165-3168.	1.4	274
9	Deconstruction of a Metastatic Tumor Microenvironment Reveals a Common Matrix Response in Human Cancers. <i>Cancer Discovery</i> , 2018, 8, 304-319.	9.4	255
10	The genomic landscape of cutaneous SCC reveals drivers and a novel azathioprine associated mutational signature. <i>Nature Communications</i> , 2018, 9, 3667.	12.8	208
11	SNPNexus: a web database for functional annotation of newly discovered and public domain single nucleotide polymorphisms. <i>Bioinformatics</i> , 2009, 25, 655-661.	4.1	187
12	SNPNexus: assessing the functional relevance of genetic variation to facilitate the promise of precision medicine. <i>Nucleic Acids Research</i> , 2018, 46, W109-W113.	14.5	163
13	SNPNexus: a web server for functional annotation of novel and publicly known genetic variants (2012) <i>Tj ETQq1 1 0.784314 rgBT /Overlock 161</i>	14.5	161
14	Recurrent mTORC1-activating RRAC mutations in follicular lymphoma. <i>Nature Genetics</i> , 2016, 48, 183-188.	21.4	160
15	Disease evolution and outcomes in familial AML with germline CEBPA mutations. <i>Blood</i> , 2015, 126, 1214-1223.	1.4	157
16	BioMart Central Portal: an open database network for the biological community. <i>Database: the Journal of Biological Databases and Curation</i> , 2011, 2011, bar041-bar041.	3.0	145
17	SNPNexus: a web server for functional annotation of human genome sequence variation (2020) <i>Tj ETQq1 1 0.784314 rgBT /Overlock 140</i>	14.5	140
18	Therapeutic Targeting of Integrin $\alpha 6$ in Breast Cancer. <i>Journal of the National Cancer Institute</i> , 2014, 106, .	6.3	132

#	ARTICLE	IF	CITATIONS
19	Genome-wide DNA copy number analysis in pancreatic cancer using high-density single nucleotide polymorphism arrays. <i>Oncogene</i> , 2008, 27, 1951-1960.	5.9	131
20	Prognostic and Therapeutic Impact of Argininosuccinate Synthetase 1 Control in Bladder Cancer as Monitored Longitudinally by PET Imaging. <i>Cancer Research</i> , 2014, 74, 896-907.	0.9	122
21	Imbalance of desmoplastic stromal cell numbers drives aggressive cancer processes. <i>Journal of Pathology</i> , 2013, 230, 107-117.	4.5	116
22	S100A4 Contributes to the Suppression of BNIP3 Expression, Chemoresistance, and Inhibition of Apoptosis in Pancreatic Cancer. <i>Cancer Research</i> , 2007, 67, 6786-6795.	0.9	108
23	A multi-gene signature predicts outcome in patients with pancreatic ductal adenocarcinoma. <i>Genome Medicine</i> , 2014, 6, 105.	8.2	106
24	Segmental uniparental disomy is a commonly acquired genetic event in relapsed acute myeloid leukemia. <i>Blood</i> , 2008, 112, 814-821.	1.4	97
25	A practical guide for the functional annotation of genetic variations using SNPnexus. <i>Briefings in Bioinformatics</i> , 2013, 14, 437-447.	6.5	90
26	Genomic profiling reveals spatial intra-tumor heterogeneity in follicular lymphoma. <i>Leukemia</i> , 2018, 32, 1261-1265.	7.2	87
27	Novel regions of acquired uniparental disomy discovered in acute myeloid leukemia. <i>Genes Chromosomes and Cancer</i> , 2008, 47, 729-739.	2.8	83
28	Inactivation of TGF β 2 receptors in stem cells drives cutaneous squamous cell carcinoma. <i>Nature Communications</i> , 2016, 7, 12493.	12.8	81
29	Reduced Expression of Histone Methyltransferases KMT2C and KMT2D Correlates with Improved Outcome in Pancreatic Ductal Adenocarcinoma. <i>Cancer Research</i> , 2016, 76, 4861-4871.	0.9	72
30	Genomic disruption of the histone methyltransferase SETD2 in chronic lymphocytic leukaemia. <i>Leukemia</i> , 2016, 30, 2179-2186.	7.2	69
31	The integrin α 6 β 1 drives pancreatic cancer through diverse mechanisms and represents an effective target for therapy. <i>Journal of Pathology</i> , 2019, 249, 332-342.	4.5	66
32	Tumor microenvironment defines the invasive phenotype of AIP-mutation-positive pituitary tumors. <i>Oncogene</i> , 2019, 38, 5381-5395.	5.9	59
33	PTPN22 R620W Functional Variant in Type 1 Diabetes and Autoimmunity Related Traits. <i>Diabetes</i> , 2007, 56, 522-526.	0.6	57
34	Genome-Wide Analysis of Pancreatic Cancer Using Microarray-Based Techniques. <i>Pancreatology</i> , 2009, 9, 13-24.	1.1	52
35	Therapeutic senescence via GPCR activation in synovial fibroblasts facilitates resolution of arthritis. <i>Nature Communications</i> , 2020, 11, 745.	12.8	49
36	Inhibition of the Polyamine Synthesis Pathway Is Synthetically Lethal with Loss of Argininosuccinate Synthase 1. <i>Cell Reports</i> , 2016, 16, 1604-1613.	6.4	47

#	ARTICLE	IF	CITATIONS
37	Noninvasive urinary miRNA biomarkers for early detection of pancreatic adenocarcinoma. <i>American Journal of Cancer Research</i> , 2015, 5, 3455-66.	1.4	47
38	Molecular Analysis of Precursor Lesions in Familial Pancreatic Cancer. <i>PLoS ONE</i> , 2013, 8, e54830.	2.5	44
39	Identification of ZDHHC14 as a novel human tumour suppressor gene. <i>Journal of Pathology</i> , 2014, 232, 566-577.	4.5	44
40	mTOR-dependent translation amplifies microglia priming in aging mice. <i>Journal of Clinical Investigation</i> , 2021, 131, .	8.2	43
41	S100P is a metastasis-associated gene that facilitates transendothelial migration of pancreatic cancer cells. <i>Clinical and Experimental Metastasis</i> , 2013, 30, 251-264.	3.3	41
42	Gene expression profiling of breast cancer in Lebanese women. <i>Scientific Reports</i> , 2016, 6, 36639.	3.3	41
43	Exosomes derived from embryonal and alveolar rhabdomyosarcoma carry differential miRNA cargo and promote invasion of recipient fibroblasts. <i>Scientific Reports</i> , 2016, 6, 37088.	3.3	39
44	Pancreatic Expression database: a generic model for the organization, integration and mining of complex cancer datasets. <i>BMC Genomics</i> , 2007, 8, 439.	2.8	38
45	A global insight into a cancer transcriptional space using pancreatic data: importance, findings and flaws. <i>Nucleic Acids Research</i> , 2011, 39, 7900-7907.	14.5	38
46	Identification of genetic alterations in pancreatic cancer by the combined use of tissue microdissection and array-based comparative genomic hybridisation. <i>British Journal of Cancer</i> , 2007, 96, 373-382.	6.4	37
47	Longitudinal copy number, whole exome and targeted deep sequencing of 'good risk' IGHV-mutated CLL patients with progressive disease. <i>Leukemia</i> , 2016, 30, 1301-1310.	7.2	37
48	Identification of MAGEA antigens as causal players in the development of tamoxifen-resistant breast cancer. <i>Oncogene</i> , 2014, 33, 4579-4588.	5.9	35
49	Novel Role for p110 β PI 3-Kinase in Male Fertility through Regulation of Androgen Receptor Activity in Sertoli Cells. <i>PLoS Genetics</i> , 2015, 11, e1005304.	3.5	35
50	S100P-Binding Protein, S100BPB, Mediates Adhesion through Regulation of Cathepsin Z in Pancreatic Cancer Cells. <i>American Journal of Pathology</i> , 2012, 180, 1485-1494.	3.8	34
51	Splice variants as novel targets in pancreatic ductal adenocarcinoma. <i>Scientific Reports</i> , 2017, 7, 2980.	3.3	34
52	PHLDA1 Mediates Drug Resistance in Receptor Tyrosine Kinase-Driven Cancer. <i>Cell Reports</i> , 2018, 22, 2469-2481.	6.4	34
53	Clinical and functional significance of α 9 β 1 integrin expression in breast cancer: a novel cell surface marker of the basal phenotype that promotes tumour cell invasion. <i>Journal of Pathology</i> , 2011, 223, 646-658.	4.5	33
54	IW-Scoring: an Integrative Weighted Scoring framework for annotating and prioritizing genetic variations in the noncoding genome. <i>Nucleic Acids Research</i> , 2018, 46, e47-e47.	14.5	30

#	ARTICLE	IF	CITATIONS
55	The Pancreatic Expression database: 2011 update. <i>Nucleic Acids Research</i> , 2011, 39, D1023-D1028.	14.5	29
56	MLH1 deficiency leads to deregulated mitochondrial metabolism. <i>Cell Death and Disease</i> , 2019, 10, 795.	6.3	29
57	CEACAM6 attenuates adenovirus infection by antagonizing viral trafficking in cancer cells. <i>Journal of Clinical Investigation</i> , 2009, 119, 1604-1615.	8.2	28
58	The pancreatic expression database: recent extensions and updates. <i>Nucleic Acids Research</i> , 2014, 42, D944-D949.	14.5	28
59	Transcription-Mediated Chimeric RNAs in Prostate Cancer: Time to Revisit Old Hypothesis?. <i>OMICS A Journal of Integrative Biology</i> , 2014, 18, 615-624.	2.0	28
60	A Virus-Infected, Reprogrammed Somatic Cell-Derived Tumor Cell (VIREST) Vaccination Regime Can Prevent Initiation and Progression of Pancreatic Cancer. <i>Clinical Cancer Research</i> , 2020, 26, 465-476.	7.0	24
61	Online resources of cancer data: barriers, benefits and lessons. <i>Briefings in Bioinformatics</i> , 2011, 12, 52-63.	6.5	20
62	The Sharing Experimental Animal Resources, Coordinating Holdings (SEARCH) Framework: Encouraging Reduction, Replacement, and Refinement in Animal Research. <i>PLoS Biology</i> , 2017, 15, e2000719.	5.6	18
63	A genetic study and meta-analysis of the genetic predisposition of prostate cancer in a Chinese population. <i>Oncotarget</i> , 2016, 7, 21393-21403.	1.8	18
64	A HIF-1 negative feedback mechanism mitigates the pro-tumorigenic effects of hypoxia. <i>EMBO Molecular Medicine</i> , 2018, 10, .	6.9	17
65	p21 promotes oncolytic adenoviral activity in ovarian cancer and is a potential biomarker. <i>Molecular Cancer</i> , 2010, 9, 175.	19.2	16
66	Phosphoproteomic comparison of <i>Pik3ca</i> and <i>Pten</i> signalling identifies the nucleotidase <i>NT5C</i> as a novel AKT substrate. <i>Scientific Reports</i> , 2017, 7, 39985.	3.3	16
67	Field cancerization in breast cancer. <i>Journal of Pathology</i> , 2022, 257, 561-574.	4.5	16
68	MicroRNA and transcriptome analysis in periorbital Sebaceous Gland Carcinoma. <i>Scientific Reports</i> , 2018, 8, 7531.	3.3	15
69	Multi-omic data analysis using O-miner. <i>Briefings in Bioinformatics</i> , 2019, 20, 130-143.	6.5	15
70	Association between <i>CLN3</i> (Neuronal Ceroid Lipofuscinosis, <i>CLN3</i> Type) Gene Expression and Clinical Characteristics of Breast Cancer Patients. <i>Frontiers in Oncology</i> , 2015, 5, 215.	2.8	14
71	Recurrent somatic JAK-STAT pathway variants within a <i>RUNX1</i> -mutated pedigree. <i>European Journal of Human Genetics</i> , 2017, 25, 1020-1024.	2.8	13
72	Crohn's disease associated <i>CARD15</i> (<i>NOD2</i>) variants are not involved in the susceptibility to type 1 diabetes. <i>Molecular Genetics and Metabolism</i> , 2005, 86, 379-383.	1.1	12

#	ARTICLE	IF	CITATIONS
73	The Pancreatic Expression Database: 2018 update. <i>Nucleic Acids Research</i> , 2018, 46, D1107-D1110.	14.5	12
74	Characterization of four subtypes in morphologically normal tissue excised proximal and distal to breast cancer. <i>Npj Breast Cancer</i> , 2020, 6, 38.	5.2	12
75	BCCTBbp: the Breast Cancer Campaign Tissue Bank bioinformatics portal. <i>Nucleic Acids Research</i> , 2015, 43, D831-D836.	14.5	11
76	SEARCHBreast: a new resource to locate and share surplus archival material from breast cancer animal models to help address the 3Rs. <i>Breast Cancer Research and Treatment</i> , 2016, 156, 447-452.	2.5	11
77	O-miner: an integrative platform for automated analysis and mining of -omics data. <i>Nucleic Acids Research</i> , 2012, 40, W560-W568.	14.5	10
78	Using BioMart as a framework to manage and query pancreatic cancer data. <i>Database: the Journal of Biological Databases and Curation</i> , 2011, 2011, bar024-bar024.	3.0	9
79	Pancreatic cancer tissue banks: where are we heading?. <i>Future Oncology</i> , 2016, 12, 2661-2663.	2.4	9
80	COVID-19 in patients with hepatobiliary and pancreatic diseases: a single-centre cross-sectional study in East London. <i>BMJ Open</i> , 2021, 11, e045077.	1.9	9
81	MHC class II molecules on pancreatic cancer cells indicate a potential for neo-antigen-based immunotherapy. <i>Oncolmmunology</i> , 2022, 11, .	4.6	8
82	A Web-Based Platform for Mining Pancreatic Expression Datasets. <i>Pancreatology</i> , 2009, 9, 340-343.	1.1	7
83	SEARCHBreast Workshop Proceedings: 3D Modelling of Breast Cancer. <i>ATLA Alternatives To Laboratory Animals</i> , 2015, 43, 367-375.	1.0	7
84	<i>NKAIN2</i> functions as a novel tumor suppressor in prostate cancer. <i>Oncotarget</i> , 2016, 7, 63793-63803.	1.8	7
85	Longitudinal profiling of circulating tumour DNA for tracking tumour dynamics in pancreatic cancer. <i>BMC Cancer</i> , 2022, 22, 369.	2.6	7
86	The breast cancer oncogene <i>IKK1μ</i> coordinates mitochondrial function and serine metabolism. <i>EMBO Reports</i> , 2020, 21, e48260.	4.5	6
87	Sex-linked recombination variation and distribution of disease-related genes. <i>Gene</i> , 2005, 346, 29-39.	2.2	5
88	BCNTB bioinformatics: the next evolutionary step in the bioinformatics of breast cancer tissue banking. <i>Nucleic Acids Research</i> , 2018, 46, D1055-D1061.	14.5	4
89	SMAC, a computational system to link literature, biomedical and expression data. <i>Scientific Reports</i> , 2019, 9, 10480.	3.3	3
90	INCONSISTENCIES BETWEEN MAPS OF HUMAN CHROMOSOME 22 CORRELATE WITH INCREASED FREQUENCY OF DISEASE-RELATED LOCI. <i>Journal of Biological Systems</i> , 2002, 10, 303-317.	1.4	2

#	ARTICLE	IF	CITATIONS
91	SEARCHBreast: a new online resource to make surplus material from in vivo models of breast cancer visible and accessible to researchers. Breast Cancer Research, 2016, 18, 59.	5.0	2
92	The role of the microenvironment in the invasive phenotype of familial pituitary tumours. Endocrine Abstracts, 0, , .	0.0	2
93	A biobank perspective on use of tissue samples donated by trial participants. Lancet Oncology, The, 2022, 23, e205.	10.7	2
94	Introducing SEARCHBreast: a virtual resource to facilitate sharing of surplus animal material developed for breast cancer research. Npj Breast Cancer, 2016, 2, 16020.	5.2	1
95	A Genome-Wide Map of Acquired Uniparental Disomy in Acute Myeloid Leukemia.. Blood, 2007, 110, 996-996.	1.4	1
96	An Integrated Systems Approach to the Study of Pancreatic Cancer. , 2012, , 83-111.		0
97	Genomic analysis reveals epigenetic "addiction"™ underpinning follicular lymphoma and its transformation " a rationale for targeted epigenetic therapies. Clinical Epigenetics, 2013, 5, .	4.1	0
98	Identification of ZDHHC14 as a novel human tumour suppressor gene. J Pathol 2014; 232: 566-577. Journal of Pathology, 2014, 234, 134-134.	4.5	0
99	SEARCHBreast: An online resource designed to increase the efficiency of using materials derived from breast cancer studies in animals. Journal of Pathology, 2016, 240, 120-120.	4.5	0
100	HiPPO and PANDA: Two Bioinformatics Tools to Support Analysis of Mass Cytometry Data. Journal of Computational Biology, 2020, 27, 1283-1294.	1.6	0
101	Validation of a Novel, Flash-Freezing Method: Aluminum Platform. Current Protocols in Essential Laboratory Techniques, 2020, 21, e46.	2.6	0
102	P020. Defining molecular signatures to personalise management of patients with early breast cancer. European Journal of Surgical Oncology, 2021, 47, e301.	1.0	0
103	Abstract 1537: Role of S100BP in pancreatic adenocarcinoma. , 2011, , .		0
104	Whole Genome Sequencing in Sequential Biopsies Reveals the Genetic Evolution of Follicular Lymphoma to Transformed Follicular Lymphoma. Blood, 2012, 120, 145-145.	1.4	0
105	Invasion signature' revealed by the analysis of AIP positive and AIP mutation negative human pituitary adenomas. Endocrine Abstracts, 0, , 1-1.	0.0	0
106	Gene expression profiling of familial and sporadic pituitary adenomas. Endocrine Abstracts, 0, , .	0.0	0
107	Investigating The Role Of MLL2 (Mll4) In B Cell Development. Blood, 2013, 122, 343-343.	1.4	0
108	Familial AML With Germline CEBPA Mutations: Extended Clinical Outcomes and Analysis Of Secondary Mutations Using Whole Exome Sequencing. Blood, 2013, 122, 740-740.	1.4	0

#	ARTICLE	IF	CITATIONS
109	Abstract 1431: Gene expression analysis of argininosuccinate synthetase loss and the effects of pegylated arginine deiminase in malignant pleural mesothelioma. , 2014, , .		0
110	Potential molecular mechanism of AIP-mediated cellular invasion. Endocrine Abstracts, 0, , .	0.0	0
111	Investigation of the invasive phenotype of AIP-mutated pituitary adenomas. Endocrine Abstracts, 0, , .	0.0	0
112	Genomic Disruption of the Histone Methyltransferase SETD2 in Chronic Lymphocytic Leukemia. Blood, 2015, 126, 365-365.	1.4	0
113	The SEARCHBreast Portal: A Virtual Bioresource to Facilitate the Sharing of Surplus Animal Materials Derived from Breast Cancer Studies. Open Journal of Bioresources, 2016, 3, .	1.5	0
114	The clinical, pathological and molecular differences between sparsely and densely granulated somatotroph adenomas. Endocrine Abstracts, 0, , .	0.0	0
115	Alloresponses of Human T-Cells from Adult Peripheral Blood and Umbilical Cord Blood Are Differentially Impacted By Lenalidomide. Blood, 2016, 128, 5714-5714.	1.4	0