

# Chi Nam Ignatius Pang

## List of Publications by Year in descending order

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36  
papers

984  
citations

516215

16  
h-index

454577

30  
g-index

36  
all docs

36  
docs citations

36  
times ranked

1901  
citing authors

#	ARTICLE	IF	CITATIONS
1	Dual targeting of the epigenome via FACT complex and histone deacetylase is a potent treatment strategy for DIPG. <i>Cell Reports</i> , 2021, 35, 108994.	2.9	21
2	HGG-09. TARGETING FACILITATES CHROMATIN TRANSCRIPTION (FACT) AS A NOVEL STRATEGY THAT ENHANCES RESPONSE TO HISTONE DEACETYLASE (HDAC) INHIBITION IN DIPG. <i>Neuro-Oncology</i> , 2021, 23, i18-i19.	0.6	0
3	Cross-linking Mass Spectrometry Analysis of the Yeast Nucleus Reveals Extensive Protein-Protein Interactions Not Detected by Systematic Two-Hybrid or Affinity Purification-Mass Spectrometry. <i>Analytical Chemistry</i> , 2020, 92, 1874-1882.	3.2	20
4	Higher frequency of vertebrate-infecting viruses in the gut of infants born to mothers with type 1 diabetes. <i>Pediatric Diabetes</i> , 2020, 21, 271-279.	1.2	10
5	Analytical Guidelines for co-fractionation Mass Spectrometry Obtained through Global Profiling of Gold Standard <i>Saccharomyces cerevisiae</i> Protein Complexes. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1876-1895.	2.5	14
6	Controlling the Controllers: Regulation of Histone Methylation by Phosphosignalling. <i>Trends in Biochemical Sciences</i> , 2020, 45, 1035-1048.	3.7	10
7	DIPG-14. TARGETING POLO-LIKE KINASE 1 IN COMBINATION WITH KEY ONCOGENIC DRIVERS IN DIPG: FROM SINGLE AGENT TO COMBINATION STRATEGIES. <i>Neuro-Oncology</i> , 2020, 22, iii289-iii289.	0.6	0
8	Different Pathways Mediate Amphotericin-Lactoferrin Drug Synergy in <i>Cryptococcus</i> and <i>Saccharomyces</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2195.	1.5	5
9	Distinct Gut Virome Profile of Pregnant Women With Type 1 Diabetes in the ENDIA Study. <i>Open Forum Infectious Diseases</i> , 2019, 6, ofz025.	0.4	32
10	Higher abundance of enterovirus A species in the gut of children with islet autoimmunity. <i>Scientific Reports</i> , 2019, 9, 1749.	1.6	37
11	Visualizing Post-translational Modifications in Protein Interaction Networks Using PTMOracle. <i>Current Protocols in Bioinformatics</i> , 2019, 66, e71.	25.8	3
12	Investigating the Network Basis of Negative Genetic Interactions in <i>Saccharomyces cerevisiae</i> with Integrated Biological Networks and Triplet Motif Analysis. <i>Journal of Proteome Research</i> , 2018, 17, 1014-1030.	1.8	4
13	Knockout of the Hmt1p Arginine Methyltransferase in <i>Saccharomyces cerevisiae</i> Leads to the Dysregulation of Phosphate-associated Genes and Processes. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 2462-2479.	2.5	8
14	Systems-Level Analysis of Bacterial Regulatory Small RNA Networks. <i>RNA Technologies</i> , 2018, , 97-127.	0.2	3
15	Does the primary site really matter? Profiling mucinous ovarian cancers of uncertain primary origin (MO-CUP) to personalise treatment and inform the design of clinical trials. <i>Gynecologic Oncology</i> , 2018, 150, 527-533.	0.6	14
16	Systems-based approaches enable identification of gene targets which improve the flavour profile of low-ethanol wine yeast strains. <i>Metabolic Engineering</i> , 2018, 49, 178-191.	3.6	16
17	Transcriptome and network analyses in <i>Saccharomyces cerevisiae</i> reveal that amphotericin B and lactoferrin synergy disrupt metal homeostasis and stress response. <i>Scientific Reports</i> , 2017, 7, 40232.	1.6	18
18	Small RNA interactome of pathogenic <i>E. coli</i> revealed through crosslinking of RNase E. <i>EMBO Journal</i> , 2017, 36, 374-387.	3.5	153

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19	PTMOracle: A Cytoscape App for Covisualizing and Coanalyzing Post-Translational Modifications in Protein Interaction Networks. <i>Journal of Proteome Research</i> , 2017, 16, 1988-2003.	1.8	17
20	Synergy and antagonism between iron chelators and antifungal drugs in <i>Cryptococcus</i> . <i>International Journal of Antimicrobial Agents</i> , 2016, 48, 388-394.	1.1	54
21	Proteomic Validation of Transcript Isoforms, Including Those Assembled from RNA-Seq Data. <i>Journal of Proteome Research</i> , 2015, 14, 3541-3554.	1.8	13
22	Tools to Covisualize and Coanalyze Proteomic Data with Genomes and Transcriptomes: Validation of Genes and Alternative mRNA Splicing. <i>Journal of Proteome Research</i> , 2014, 13, 84-98.	1.8	40
23	Identification of differentiation-stage specific markers that define the ex vivo osteoblastic phenotype. <i>Bone</i> , 2014, 67, 23-32.	1.4	62
24	Disturbed protein-protein interaction networks in metastatic melanoma are associated with worse prognosis and increased functional mutation burden. <i>Pigment Cell and Melanoma Research</i> , 2013, 26, 708-722.	1.5	12
25	Children With Islet Autoimmunity and Enterovirus Infection Demonstrate a Distinct Cytokine Profile. <i>Diabetes</i> , 2012, 61, 1500-1508.	0.3	37
26	Cytomegalovirus Infection During Pregnancy With Maternofetal Transmission Induces a Proinflammatory Cytokine Bias in Placenta and Amniotic Fluid. <i>Journal of Infectious Diseases</i> , 2012, 205, 1305-1310.	1.9	73
27	A Multidimensional Matrix for Systems Biology Research and Its Application to Interaction Networks. <i>Journal of Proteome Research</i> , 2012, 11, 5204-5220.	1.8	5
28	The methylproteome and the intracellular methylation network. <i>Proteomics</i> , 2012, 12, 564-586.	1.3	73
29	Identification of arginine- and lysine-methylation in the proteome of <i>Saccharomyces cerevisiae</i> and its functional implications. <i>BMC Genomics</i> , 2010, 11, 92.	1.2	78
30	Proteins Deleterious on Overexpression Are Associated with High Intrinsic Disorder, Specific Interaction Domains, and Low Abundance. <i>Journal of Proteome Research</i> , 2010, 9, 1218-1225.	1.8	18
31	The Interactorium: Visualising proteins, complexes and interaction networks in a virtual 3D cell. <i>Proteomics</i> , 2009, 9, 5309-5315.	1.3	8
32	Are protein complexes made of cores, modules and attachments?. <i>Proteomics</i> , 2008, 8, 425-434.	1.3	30
33	High throughput protein-protein interaction data: clues for the architecture of protein complexes. <i>Proteome Science</i> , 2008, 6, 32.	0.7	2
34	Identifying foldable regions in protein sequence from the hydrophobic signal. <i>Nucleic Acids Research</i> , 2007, 36, 578-588.	6.5	15
35	Surface Accessibility of Protein Post-Translational Modifications. <i>Journal of Proteome Research</i> , 2007, 6, 1833-1845.	1.8	68
36	Protein-protein interactions and disease: Use of <i>S. cerevisiae</i> as a model system. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2007, 1774, 838-847.	1.1	11