

# Jacques Colinge

## List of Publications by Year in descending order

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116  
papers

11,148  
citations

50276

46  
h-index

31849

101  
g-index

126  
all docs

126  
docs citations

126  
times ranked

21212  
citing authors

#	ARTICLE	IF	CITATIONS
1	Mechanisms underlying the cooperation between loss of epithelial polarity and Notch signaling during neoplastic growth in <i>Drosophila</i> . <i>Development (Cambridge)</i> , 2022, 149, .	2.5	6
2	Application of modular response analysis to medium- to large-size biological systems. <i>PLoS Computational Biology</i> , 2022, 18, e1009312.	3.2	1
3	The immune contexture of primary central nervous system diffuse large B cell lymphoma associates with patient survival and specific cell signaling. <i>Theranostics</i> , 2021, 11, 3565-3579.	10.0	20
4	An R package for generic modular response analysis and its application to estrogen and retinoic acid receptor crosstalk. <i>Scientific Reports</i> , 2021, 11, 7272.	3.3	5
5	MAGI1 inhibits the AMOTL2/p38 stress pathway and prevents luminal breast tumorigenesis. <i>Scientific Reports</i> , 2021, 11, 5752.	3.3	6
6	Transcriptomic and genomic heterogeneity in blastic plasmacytoid dendritic cell neoplasms: from ontogeny to oncogenesis. <i>Blood Advances</i> , 2021, 5, 1540-1551.	5.2	35
7	Machine Learning-Assisted Evaluation of Circulating DNA Quantitative Analysis for Cancer Screening. <i>Advanced Science</i> , 2020, 7, 2000486.	11.2	19
8	SingleCellSignalR: inference of intercellular networks from single-cell transcriptomics. <i>Nucleic Acids Research</i> , 2020, 48, e55-e55.	14.5	257
9	The molecular landscape and microenvironment of salivary duct carcinoma reveal new therapeutic opportunities. <i>Theranostics</i> , 2020, 10, 4383-4394.	10.0	29
10	In Vivo Large-Scale Mapping of Protein Turnover in Human Cerebrospinal Fluid. <i>Analytical Chemistry</i> , 2019, 91, 15500-15508.	6.5	6
11	Distinct oncogenes drive different genome and epigenome alterations in human mammary epithelial cells. <i>International Journal of Cancer</i> , 2019, 145, 1299-1311.	5.1	6
12	The Prognostic Impact of the Aryl Hydrocarbon Receptor (AhR) in Primary Breast Cancer Depends on the Lymph Node Status. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1016.	4.1	24
13	Notch inhibition overcomes resistance to tyrosine kinase inhibitors in EGFR-driven lung adenocarcinoma. <i>Journal of Clinical Investigation</i> , 2019, 130, 612-624.	8.2	27
14	Towards a screening test for cancer by circulating DNA analysis.. <i>Journal of Clinical Oncology</i> , 2019, 37, e13146-e13146.	1.6	2
15	Cell-Cycle Regulation Accounts for Variability in Ki-67 Expression Levels. <i>Cancer Research</i> , 2017, 77, 2722-2734.	0.9	263
16	Artemisinins Target GABAA Receptor Signaling and Impair $\pm$ Cell Identity. <i>Cell</i> , 2017, 168, 86-100.e15.	28.9	330
17	A combinatorial screen of the CLOUD uncovers a synergy targeting the androgen receptor. <i>Nature Chemical Biology</i> , 2017, 13, 771-778.	8.0	39
18	Data-Based Radiation Oncology: Design of Clinical Trials in the Toxicity Biomarkers Era. <i>Frontiers in Oncology</i> , 2017, 7, 83.	2.8	36

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19	Functional analysis of Plasmodium falciparum subpopulations associated with artemisinin resistance in Cambodia. <i>Malaria Journal</i> , 2017, 16, 493.	2.3	17
20	A time-resolved molecular map of the macrophage response to VSV infection. <i>Npj Systems Biology and Applications</i> , 2016, 2, 16027.	3.0	42
21	Germline RBBP6 mutations in familial myeloproliferative neoplasms. <i>Blood</i> , 2016, 127, 362-365.	1.4	49
22	Genome-wide diversity and gene expression profiling of Babesia microti isolates identify polymorphic genes that mediate host-pathogen interactions. <i>Scientific Reports</i> , 2016, 6, 35284.	3.3	74
23	Heme drives hemolysis-induced susceptibility to infection via disruption of phagocyte functions. <i>Nature Immunology</i> , 2016, 17, 1361-1372.	14.5	114
24	A Comprehensive Analysis of the Dynamic Response to Aphidicolin-Mediated Replication Stress Uncovers Targets for ATM and ATMIN. <i>Cell Reports</i> , 2016, 15, 893-908.	6.4	29
25	A Surface Biotinylation Strategy for Reproducible Plasma Membrane Protein Purification and Tracking of Genetic and Drug-Induced Alterations. <i>Journal of Proteome Research</i> , 2016, 15, 647-658.	3.7	39
26	Comparative functional analysis of the molecular network of 7 selected MLL fusion proteins. <i>Experimental Hematology</i> , 2015, 43, S95.	0.4	0
27	Enhancing cognate target elution efficiency in gel-free chemical proteomics. <i>EuPA Open Proteomics</i> , 2015, 9, 43-53.	2.5	2
28	A cellular screen identifies ponatinib and pazopanib as inhibitors of necroptosis. <i>Cell Death and Disease</i> , 2015, 6, e1767-e1767.	6.3	157
29	Superoxide Dismutase 1 Protects Hepatocytes from Type I Interferon-Driven Oxidative Damage. <i>Immunity</i> , 2015, 43, 974-986.	14.3	50
30	The RNA-binding protein HuR/ELAVL1 regulates IFN $\beta$ mRNA abundance and the type I IFN response. <i>European Journal of Immunology</i> , 2015, 45, 1500-1511.	2.9	49
31	Targeting a cell state common to triple-negative breast cancers. <i>Molecular Systems Biology</i> , 2015, 11, 789.	7.2	21
32	The Lipid-Modifying Enzyme SMPDL3B Negatively Regulates Innate Immunity. <i>Cell Reports</i> , 2015, 11, 1919-1928.	6.4	74
33	Target profiling of an antimetastatic RAPTA agent by chemical proteomics: relevance to the mode of action. <i>Chemical Science</i> , 2015, 6, 2449-2456.	7.4	127
34	Proteome-wide drug and metabolite interaction mapping by thermal-stability profiling. <i>Nature Methods</i> , 2015, 12, 1055-1057.	19.0	183
35	Gene essentiality and synthetic lethality in haploid human cells. <i>Science</i> , 2015, 350, 1092-1096.	12.6	773
36	NOTCH1 activation in breast cancer confers sensitivity to inhibition of SUMOylation. <i>Oncogene</i> , 2015, 34, 3780-3790.	5.9	40

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37	Abstract LB-099: A high-throughput screen of approved drugs uncovers a synergistic interaction targeting prostate cancer. , 2015, , .		0
38	The Triggering Receptor Expressed on Myeloid Cells 2 Inhibits Complement Component 1q Effector Mechanisms and Exerts Detrimental Effects during Pneumococcal Pneumonia. PLoS Pathogens, 2014, 10, e1004167.	4.7	46
39	Virulence Factor NSs of Rift Valley Fever Virus Recruits the F-Box Protein FBXO3 To Degrade Subunit p62 of General Transcription Factor TFIIH. Journal of Virology, 2014, 88, 3464-3473.	3.4	65
40	Stereospecific targeting of MTH1 by (S)-crizotinib as an anticancer strategy. Nature, 2014, 508, 222-227.	27.8	336
41	CD4+ T cell lineage integrity is controlled by the histone deacetylases HDAC1 and HDAC2. Nature Immunology, 2014, 15, 439-448.	14.5	70
42	Early-onset inflammatory bowel disease and common variable immunodeficiency-like disease caused by IL-21 deficiency. Journal of Allergy and Clinical Immunology, 2014, 133, 1651-1659.e12.	2.9	124
43	Biallelic loss-of-function mutation in NIK causes a primary immunodeficiency with multifaceted aberrant lymphoid immunity. Nature Communications, 2014, 5, 5360.	12.8	116
44	Identification of Kinase Inhibitor Targets in the Lung Cancer Microenvironment by Chemical and Phosphoproteomics. Molecular Cancer Therapeutics, 2014, 13, 2751-2762.	4.1	21
45	Comprehensive Comparative and Semiquantitative Proteome of a Very Low Number of Native and Matched Epstein-Barr-Virus-Transformed B Lymphocytes Infiltrating Human Melanoma. Journal of Proteome Research, 2014, 13, 2830-2845.	3.7	15
46	Comparative functional analysis of the molecular network of 7 selected MLL fusion proteins. Experimental Hematology, 2014, 42, S60.	0.4	0
47	TOPS: a versatile software tool for statistical analysis and visualization of combinatorial gene-gene and gene-drug interaction screens. BMC Bioinformatics, 2014, 15, 98.	2.6	6
48	A chemical biology approach identifies AMPK as a modulator of melanoma oncogene MITF. Oncogene, 2014, 33, 2531-2539.	5.9	29
49	Building and exploring an integrated human kinase network: Global organization and medical entry points. Journal of Proteomics, 2014, 107, 113-127.	2.4	16
50	Affinity Purification Strategies for Proteomic Analysis of Transcription Factor Complexes. Journal of Proteome Research, 2013, 12, 4018-4027.	3.7	21
51	The CRAPome: a contaminant repository for affinity purification-mass spectrometry data. Nature Methods, 2013, 10, 730-736.	19.0	1,353
52	Quantitative proteomics of aqueous and vitreous fluid from patients with idiopathic epiretinal membranes. Experimental Eye Research, 2013, 108, 48-58.	2.6	58
53	A Miniaturized Chemical Proteomic Approach for Target Profiling of Clinical Kinase Inhibitors in Tumor Biopsies. Journal of Proteome Research, 2013, 12, 4005-4017.	3.7	15
54	A reversible gene trap collection empowers haploid genetics in human cells. Nature Methods, 2013, 10, 965-971.	19.0	90

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55	Interactome of Two Diverse RNA Granules Links mRNA Localization to Translational Repression in Neurons. <i>Cell Reports</i> , 2013, 5, 1749-1762.	6.4	130
56	Experimental characterization of the human non-sequence-specific nucleic acid interactome. <i>Genome Biology</i> , 2013, 14, R81.	9.6	7
57	IsobarPTM: A software tool for the quantitative analysis of post-translationally modified proteins. <i>Journal of Proteomics</i> , 2013, 90, 77-84.	2.4	19
58	Elucidating the molecular mechanism of action of cancer drugs in the second decade of the new millennium. <i>Experimental Hematology</i> , 2013, 41, S9.	0.4	0
59	Interlaboratory reproducibility of large-scale human protein-complex analysis by standardized AP-MS. <i>Nature Methods</i> , 2013, 10, 307-314.	19.0	192
60	Multiple and Sequential Data Acquisition Method: An Improved Method for Fragmentation and Detection of Cross-Linked Peptides on a Hybrid Linear Trap Quadrupole Orbitrap Velos Mass Spectrometer. <i>Analytical Chemistry</i> , 2013, 85, 1454-1461.	6.5	2
61	Perturbation of the mutated EGFR interactome identifies vulnerabilities and resistance mechanisms. <i>Molecular Systems Biology</i> , 2013, 9, 705.	7.2	42
62	Systems Biology Analysis of Kinase Inhibitor Action in Leukemia Treatments. <i>Biomedizinische Technik</i> , 2013, 58 Suppl 1, .	0.8	0
63	A Target-Disease Network Model of Second-Generation BCR-ABL Inhibitor Action in Ph+ ALL. <i>PLoS ONE</i> , 2013, 8, e77155.	2.5	15
64	A Comparative Proteomic Study of Human Skin Suction Blister Fluid from Healthy Individuals Using Immunodepletion and iTRAQ Labeling. <i>Journal of Proteome Research</i> , 2012, 11, 3715-3727.	3.7	62
65	Clinical significance of genetic aberrations in secondary acute myeloid leukemia. <i>American Journal of Hematology</i> , 2012, 87, 1010-1016.	4.1	67
66	Systems-pharmacology dissection of a drug synergy in imatinib-resistant CML. <i>Nature Chemical Biology</i> , 2012, 8, 905-912.	8.0	96
67	Deconvolution of Targeted Protein-Protein Interaction Maps. <i>Journal of Proteome Research</i> , 2012, 11, 4102-4109.	3.7	8
68	Systems biology analysis of protein-drug interactions. <i>Proteomics - Clinical Applications</i> , 2012, 6, 102-116.	1.6	27
69	Viral immune modulators perturb the human molecular network by common and unique strategies. <i>Nature</i> , 2012, 487, 486-490.	27.8	249
70	Analysis of Labeled Quantitative Mass Spectrometry Proteomics Data. , 2012, , 79-91.		0
71	Systems Biology Analysis of Kinase Inhibitor Protein Target Profiles in Leukemia Treatments. <i>Lecture Notes in Computer Science</i> , 2012, , 62-66.	1.3	0
72	Abstract IA2: Network models in oncogene-addicted lung cancer. <i>Clinical Cancer Research</i> , 2012, 18, IA2-IA2.	7.0	0

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73	Using iTRAQ Combined with Tandem Affinity Purification to Enhance Low-Abundance Proteins Associated with Somatic Mutated EGFR Core Complexes in Lung Cancer. <i>Journal of Proteome Research</i> , 2011, 10, 182-190.	3.7	29
74	A chemical-genetic screen reveals a mechanism of resistance to PI3K inhibitors in cancer. <i>Nature Chemical Biology</i> , 2011, 7, 787-793.	8.0	156
75	General Statistical Modeling of Data from Protein Relative Expression Isobaric Tags. <i>Journal of Proteome Research</i> , 2011, 10, 2758-2766.	3.7	120
76	IFIT1 is an antiviral protein that recognizes 5â€²-triphosphate RNA. <i>Nature Immunology</i> , 2011, 12, 624-630.	14.5	422
77	Functional Dissection of the TBK1 Molecular Network. <i>PLoS ONE</i> , 2011, 6, e23971.	2.5	110
78	Initial characterization of the human central proteome. <i>BMC Systems Biology</i> , 2011, 5, 17.	3.0	66
79	Proteomic analysis of human cataract aqueous humour: Comparison of one-dimensional gel LCMS with two-dimensional LCMS of unlabelled and iTRAQ®-labelled specimens. <i>Journal of Proteomics</i> , 2011, 74, 151-166.	2.4	79
80	An Integrated Chemical Biology Approach Identifies Specific Vulnerability of Ewing's Sarcoma to Combined Inhibition of Aurora Kinases A and B. <i>Molecular Cancer Therapeutics</i> , 2011, 10, 1846-1856.	4.1	37
81	TLR 2 and CD14 Mediate Innate Immunity and Lung Inflammation to Staphylococcal Pantoneâ€™Valentine Leukocidin In Vivo. <i>Journal of Immunology</i> , 2011, 186, 1608-1617.	0.8	68
82	MASPECTRAS 2: An integration and analysis platform for proteomic data. <i>Proteomics</i> , 2010, 10, 2719-2722.	2.2	20
83	A comprehensive target selectivity survey of the BCR-ABL kinase inhibitor INNO-406 by kinase profiling and chemical proteomics in chronic myeloid leukemia cells. <i>Leukemia</i> , 2010, 24, 44-50.	7.2	67
84	A chemical and phosphoproteomic characterization of dasatinib action in lung cancer. <i>Nature Chemical Biology</i> , 2010, 6, 291-299.	8.0	254
85	CD14 is a coreceptor of Toll-like receptors 7 and 9. <i>Journal of Experimental Medicine</i> , 2010, 207, 2689-2701.	8.5	181
86	A Computational Approach to Analyze the Mechanism of Action of the Kinase Inhibitor Bafetinib. <i>PLoS Computational Biology</i> , 2010, 6, e1001001.	3.2	23
87	Functional Genomic and Proteomic Characterization of Normal and Oncogenic CEBPA Variants In Myeloid Cells. <i>Blood</i> , 2010, 116, 3873-3873.	1.4	0
88	Charting the molecular network of the drug target Bcr-Abl. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 7414-7419.	7.1	146
89	Global target profile of the kinase inhibitor bosutinib in primary chronic myeloid leukemia cells. <i>Leukemia</i> , 2009, 23, 477-485.	7.2	254
90	An orthogonal proteomic-genomic screen identifies AIM2 as a cytoplasmic DNA sensor for the inflammasome. <i>Nature Immunology</i> , 2009, 10, 266-272.	14.5	935

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91	Acid Elution and One-Dimensional Shotgun Analysis on an Orbitrap Mass Spectrometer: An Application to Drug Affinity Chromatography. <i>Journal of Proteome Research</i> , 2009, 8, 4753-4765.	3.7	27
92	The chemokine interleukin-8 and the surface activation protein CD69 are markers for Bcr-Abl activity in chronic myeloid leukemia. <i>Molecular Oncology</i> , 2008, 2, 272-281.	4.6	27
93	311 Molecular networks in innate immunity. <i>Cytokine</i> , 2008, 43, 317.	3.2	0
94	The Btk tyrosine kinase is a major target of the Bcr-Abl inhibitor dasatinib. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 13283-13288.	7.1	274
95	Introduction to Computational Proteomics. <i>PLoS Computational Biology</i> , 2007, 3, e114.	3.2	56
96	Chemical proteomic profiles of the BCR-ABL inhibitors imatinib, nilotinib, and dasatinib reveal novel kinase and nonkinase targets. <i>Blood</i> , 2007, 110, 4055-4063.	1.4	600
97	Peptide Fragment Intensity Statistical Modeling. <i>Analytical Chemistry</i> , 2007, 79, 7286-7290.	6.5	8
98	Assessing peptide <i>de novo</i> sequencing algorithms performance on large and diverse data sets. <i>Proteomics</i> , 2007, 7, 3051-3054.	2.2	42
99	InSilicoSpectro: An Open-Source Proteomics Library. <i>Journal of Proteome Research</i> , 2006, 5, 619-624.	3.7	24
100	Differential Proteomics via Probabilistic Peptide Identification Scores. <i>Analytical Chemistry</i> , 2005, 77, 596-606.	6.5	102
101	Experiments in Searching Small Proteins in Unannotated Large Eukaryotic Genomes. <i>Journal of Proteome Research</i> , 2005, 4, 167-174.	3.7	15
102	High-performance peptide identification by tandem mass spectrometry allows reliable automatic data processing in proteomics. <i>Proteomics</i> , 2004, 4, 1977-1984.	2.2	74
103	Industrial-scale proteomics: From liters of plasma to chemically synthesized proteins. <i>Proteomics</i> , 2004, 4, 2125-2150.	2.2	103
104	In vitro and in silico processes to identify differentially expressed proteins. <i>Proteomics</i> , 2004, 4, 2333-2351.	2.2	63
105	OLAV-PMF: A Novel Scoring Scheme for High-Throughput Peptide Mass Fingerprinting. <i>Journal of Proteome Research</i> , 2004, 3, 55-60.	3.7	34
106	Mass spectrometry has married statistics: uncle is functionality, children are selectivity and sensitivity. <i>Drug Discovery Today: TARGETS</i> , 2004, 3, 50-55.	0.5	1
107	OLAV: Towards high-throughput tandem mass spectrometry data identification. <i>Proteomics</i> , 2003, 3, 1454-1463.	2.2	291
108	Improved peptide charge state assignment. <i>Proteomics</i> , 2003, 3, 1434-1440.	2.2	23

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109	A Systematic Statistical Analysis of Ion Trap Tandem Mass Spectra in View of Peptide Scoring. Lecture Notes in Computer Science, 2003, , 25-38.	1.3	9
110	MIGâ€“differential gene expression in mouse brain endothelial cells. NeuroReport, 2002, 13, 9-14.	1.2	26
111	Detecting the impact of sequencing errors on SAGE data. Bioinformatics, 2001, 17, 840-842.	4.1	29
112	MetaBlasts: tracing protein tyrosine phosphatase gene family roots from Man to Drosophila melanogaster and Caenorhabditis elegans genomes. Gene, 2000, 253, 137-143.	2.2	23
113	A strongly nonlinear problem arising in glaciology. ESAIM: Mathematical Modelling and Numerical Analysis, 1999, 33, 395-406.	1.9	39
114	Stress and velocity fields in glaciers: Part II. Sliding and basal stress distribution. Journal of Glaciology, 1998, 44, 457-466.	2.2	4
115	Stress and velocity fields in glaciers: Part I. Finite-difference schemes for higher-order glacier models. Journal of Glaciology, 1998, 44, 448-456.	2.2	7
116	Bioinformatics in MS-Based Proteomics. , 0, , 127-139.		0