

Jacques Colinge

List of Publications by Year in descending order

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116
papers

11,148
citations

50244

46
h-index

31818

101
g-index

126
all docs

126
docs citations

126
times ranked

21212
citing authors

#	ARTICLE	IF	CITATIONS
1	The CRAPome: a contaminant repository for affinity purification-mass spectrometry data. <i>Nature Methods</i> , 2013, 10, 730-736.	9.0	1,353
2	An orthogonal proteomic-genomic screen identifies AIM2 as a cytoplasmic DNA sensor for the inflammasome. <i>Nature Immunology</i> , 2009, 10, 266-272.	7.0	935
3	Gene essentiality and synthetic lethality in haploid human cells. <i>Science</i> , 2015, 350, 1092-1096.	6.0	773
4	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.	0.6	600
5	IFIT1 is an antiviral protein that recognizes 5'-triphosphate RNA. <i>Nature Immunology</i> , 2011, 12, 624-630.	7.0	422
6	Stereospecific targeting of MTH1 by (S)-crizotinib as an anticancer strategy. <i>Nature</i> , 2014, 508, 222-227.	13.7	336
7	Artemisinins Target GABAA Receptor Signaling and Impair \pm Cell Identity. <i>Cell</i> , 2017, 168, 86-100.e15.	13.5	330
8	OLAV: Towards high-throughput tandem mass spectrometry data identification. <i>Proteomics</i> , 2003, 3, 1454-1463.	1.3	291
9	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.	3.3	274
10	Cell-Cycle Regulation Accounts for Variability in Ki-67 Expression Levels. <i>Cancer Research</i> , 2017, 77, 2722-2734.	0.4	263
11	SingleCellSignalR: inference of intercellular networks from single-cell transcriptomics. <i>Nucleic Acids Research</i> , 2020, 48, e55-e55.	6.5	257
12	Global target profile of the kinase inhibitor bosutinib in primary chronic myeloid leukemia cells. <i>Leukemia</i> , 2009, 23, 477-485.	3.3	254
13	A chemical and phosphoproteomic characterization of dasatinib action in lung cancer. <i>Nature Chemical Biology</i> , 2010, 6, 291-299.	3.9	254
14	Viral immune modulators perturb the human molecular network by common and unique strategies. <i>Nature</i> , 2012, 487, 486-490.	13.7	249
15	Interlaboratory reproducibility of large-scale human protein-complex analysis by standardized AP-MS. <i>Nature Methods</i> , 2013, 10, 307-314.	9.0	192
16	Proteome-wide drug and metabolite interaction mapping by thermal-stability profiling. <i>Nature Methods</i> , 2015, 12, 1055-1057.	9.0	183
17	CD14 is a coreceptor of Toll-like receptors 7 and 9. <i>Journal of Experimental Medicine</i> , 2010, 207, 2689-2701.	4.2	181
18	A cellular screen identifies ponatinib and pazopanib as inhibitors of necroptosis. <i>Cell Death and Disease</i> , 2015, 6, e1767-e1767.	2.7	157

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19	A chemical-genetic screen reveals a mechanism of resistance to PI3K inhibitors in cancer. <i>Nature Chemical Biology</i> , 2011, 7, 787-793.	3.9	156
20	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.	3.3	146
21	Interactome of Two Diverse RNA Granules Links mRNA Localization to Translational Repression in Neurons. <i>Cell Reports</i> , 2013, 5, 1749-1762.	2.9	130
22	Target profiling of an antimetastatic RAPT agent by chemical proteomics: relevance to the mode of action. <i>Chemical Science</i> , 2015, 6, 2449-2456.	3.7	127
23	Early-onset inflammatory bowel disease and common variable immunodeficiency-like disease caused by IL-21 deficiency. <i>Journal of Allergy and Clinical Immunology</i> , 2014, 133, 1651-1659.e12.	1.5	124
24	General Statistical Modeling of Data from Protein Relative Expression Isobaric Tags. <i>Journal of Proteome Research</i> , 2011, 10, 2758-2766.	1.8	120
25	Biallelic loss-of-function mutation in NIK causes a primary immunodeficiency with multifaceted aberrant lymphoid immunity. <i>Nature Communications</i> , 2014, 5, 5360.	5.8	116
26	Heme drives hemolysis-induced susceptibility to infection via disruption of phagocyte functions. <i>Nature Immunology</i> , 2016, 17, 1361-1372.	7.0	114
27	Functional Dissection of the TBK1 Molecular Network. <i>PLoS ONE</i> , 2011, 6, e23971.	1.1	110
28	Industrial-scale proteomics: From liters of plasma to chemically synthesized proteins. <i>Proteomics</i> , 2004, 4, 2125-2150.	1.3	103
29	Differential Proteomics via Probabilistic Peptide Identification Scores. <i>Analytical Chemistry</i> , 2005, 77, 596-606.	3.2	102
30	Systems-pharmacology dissection of a drug synergy in imatinib-resistant CML. <i>Nature Chemical Biology</i> , 2012, 8, 905-912.	3.9	96
31	A reversible gene trap collection empowers haploid genetics in human cells. <i>Nature Methods</i> , 2013, 10, 965-971.	9.0	90
32	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.	1.2	79
33	High-performance peptide identification by tandem mass spectrometry allows reliable automatic data processing in proteomics. <i>Proteomics</i> , 2004, 4, 1977-1984.	1.3	74
34	The Lipid-Modifying Enzyme SMPDL3B Negatively Regulates Innate Immunity. <i>Cell Reports</i> , 2015, 11, 1919-1928.	2.9	74
35	Genome-wide diversity and gene expression profiling of <i>Babesia microti</i> isolates identify polymorphic genes that mediate host-pathogen interactions. <i>Scientific Reports</i> , 2016, 6, 35284.	1.6	74
36	CD4+ T cell lineage integrity is controlled by the histone deacetylases HDAC1 and HDAC2. <i>Nature Immunology</i> , 2014, 15, 439-448.	7.0	70

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37	TLR 2 and CD14 Mediate Innate Immunity and Lung Inflammation to Staphylococcal Pantone's Valentine Leukocidin In Vivo. <i>Journal of Immunology</i> , 2011, 186, 1608-1617.	0.4	68
38	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.	3.3	67
39	Clinical significance of genetic aberrations in secondary acute myeloid leukemia. <i>American Journal of Hematology</i> , 2012, 87, 1010-1016.	2.0	67
40	Initial characterization of the human central proteome. <i>BMC Systems Biology</i> , 2011, 5, 17.	3.0	66
41	Virulence Factor NSs of Rift Valley Fever Virus Recruits the F-Box Protein FBXO3 To Degrade Subunit p62 of General Transcription Factor TFIIF. <i>Journal of Virology</i> , 2014, 88, 3464-3473.	1.5	65
42	In vitro and in silico processes to identify differentially expressed proteins. <i>Proteomics</i> , 2004, 4, 2333-2351.	1.3	63
43	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.	1.8	62
44	Quantitative proteomics of aqueous and vitreous fluid from patients with idiopathic epiretinal membranes. <i>Experimental Eye Research</i> , 2013, 108, 48-58.	1.2	58
45	Introduction to Computational Proteomics. <i>PLoS Computational Biology</i> , 2007, 3, e114.	1.5	56
46	Superoxide Dismutase 1 Protects Hepatocytes from Type I Interferon-Driven Oxidative Damage. <i>Immunity</i> , 2015, 43, 974-986.	6.6	50
47	The RNA-binding protein HuR/ELAVL1 regulates IFN β mRNA abundance and the type I IFN response. <i>European Journal of Immunology</i> , 2015, 45, 1500-1511.	1.6	49
48	Germline RBBP6 mutations in familial myeloproliferative neoplasms. <i>Blood</i> , 2016, 127, 362-365.	0.6	49
49	The Triggering Receptor Expressed on Myeloid Cells 2 Inhibits Complement Component 1q Effector Mechanisms and Exerts Detrimental Effects during Pneumococcal Pneumonia. <i>PLoS Pathogens</i> , 2014, 10, e1004167.	2.1	46
50	Assessing peptide <i>de novo</i> sequencing algorithms performance on large and diverse data sets. <i>Proteomics</i> , 2007, 7, 3051-3054.	1.3	42
51	Perturbation of the mutated EGFR interactome identifies vulnerabilities and resistance mechanisms. <i>Molecular Systems Biology</i> , 2013, 9, 705.	3.2	42
52	A time-resolved molecular map of the macrophage response to VSV infection. <i>Npj Systems Biology and Applications</i> , 2016, 2, 16027.	1.4	42
53	NOTCH1 activation in breast cancer confers sensitivity to inhibition of SUMOylation. <i>Oncogene</i> , 2015, 34, 3780-3790.	2.6	40
54	A strongly nonlinear problem arising in glaciology. <i>ESAIM: Mathematical Modelling and Numerical Analysis</i> , 1999, 33, 395-406.	0.8	39

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55	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.	1.8	39
56	A combinatorial screen of the CLOUD uncovers a synergy targeting the androgen receptor. <i>Nature Chemical Biology</i> , 2017, 13, 771-778.	3.9	39
57	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.	1.9	37
58	Data-Based Radiation Oncology: Design of Clinical Trials in the Toxicity Biomarkers Era. <i>Frontiers in Oncology</i> , 2017, 7, 83.	1.3	36
59	Transcriptomic and genomic heterogeneity in blastic plasmacytoid dendritic cell neoplasms: from ontogeny to oncogenesis. <i>Blood Advances</i> , 2021, 5, 1540-1551.	2.5	35
60	OLAV-PMF: A Novel Scoring Scheme for High-Throughput Peptide Mass Fingerprinting. <i>Journal of Proteome Research</i> , 2004, 3, 55-60.	1.8	34
61	Detecting the impact of sequencing errors on SAGE data. <i>Bioinformatics</i> , 2001, 17, 840-842.	1.8	29
62	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.	1.8	29
63	A chemical biology approach identifies AMPK as a modulator of melanoma oncogene MITF. <i>Oncogene</i> , 2014, 33, 2531-2539.	2.6	29
64	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.	2.9	29
65	The molecular landscape and microenvironment of salivary duct carcinoma reveal new therapeutic opportunities. <i>Theranostics</i> , 2020, 10, 4383-4394.	4.6	29
66	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.	2.1	27
67	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.	1.8	27
68	Systems biology analysis of protein-drug interactions. <i>Proteomics - Clinical Applications</i> , 2012, 6, 102-116.	0.8	27
69	Notch inhibition overcomes resistance to tyrosine kinase inhibitors in EGFR-driven lung adenocarcinoma. <i>Journal of Clinical Investigation</i> , 2019, 130, 612-624.	3.9	27
70	MIC-differential gene expression in mouse brain endothelial cells. <i>NeuroReport</i> , 2002, 13, 9-14.	0.6	26
71	InSilicoSpectro: An Open-Source Proteomics Library. <i>Journal of Proteome Research</i> , 2006, 5, 619-624.	1.8	24
72	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.	1.8	24

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73	MetaBlasts: tracing protein tyrosine phosphatase gene family roots from Man to <i>Drosophila melanogaster</i> and <i>Caenorhabditis elegans</i> genomes. <i>Gene</i> , 2000, 253, 137-143.	1.0	23
74	Improved peptide charge state assignment. <i>Proteomics</i> , 2003, 3, 1434-1440.	1.3	23
75	A Computational Approach to Analyze the Mechanism of Action of the Kinase Inhibitor Bafetinib. <i>PLoS Computational Biology</i> , 2010, 6, e1001001.	1.5	23
76	Affinity Purification Strategies for Proteomic Analysis of Transcription Factor Complexes. <i>Journal of Proteome Research</i> , 2013, 12, 4018-4027.	1.8	21
77	Identification of Kinase Inhibitor Targets in the Lung Cancer Microenvironment by Chemical and Phosphoproteomics. <i>Molecular Cancer Therapeutics</i> , 2014, 13, 2751-2762.	1.9	21
78	Targeting a cell state common to triple-negative breast cancers. <i>Molecular Systems Biology</i> , 2015, 11, 789.	3.2	21
79	MASPECTRAS 2: An integration and analysis platform for proteomic data. <i>Proteomics</i> , 2010, 10, 2719-2722.	1.3	20
80	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.	4.6	20
81	IsobarPTM: A software tool for the quantitative analysis of post-translationally modified proteins. <i>Journal of Proteomics</i> , 2013, 90, 77-84.	1.2	19
82	Machine Learning-Assisted Evaluation of Circulating DNA Quantitative Analysis for Cancer Screening. <i>Advanced Science</i> , 2020, 7, 2000486.	5.6	19
83	Functional analysis of <i>Plasmodium falciparum</i> subpopulations associated with artemisinin resistance in Cambodia. <i>Malaria Journal</i> , 2017, 16, 493.	0.8	17
84	Building and exploring an integrated human kinase network: Global organization and medical entry points. <i>Journal of Proteomics</i> , 2014, 107, 113-127.	1.2	16
85	Experiments in Searching Small Proteins in Unannotated Large Eukaryotic Genomes. <i>Journal of Proteome Research</i> , 2005, 4, 167-174.	1.8	15
86	A Miniaturized Chemical Proteomic Approach for Target Profiling of Clinical Kinase Inhibitors in Tumor Biopsies. <i>Journal of Proteome Research</i> , 2013, 12, 4005-4017.	1.8	15
87	A Target-Disease Network Model of Second-Generation BCR-ABL Inhibitor Action in Ph+ ALL. <i>PLoS ONE</i> , 2013, 8, e77155.	1.1	15
88	Comprehensive Comparative and Semiquantitative Proteome of a Very Low Number of Native and Matched Epstein-Barr-Virus-Transformed B Lymphocytes Infiltrating Human Melanoma. <i>Journal of Proteome Research</i> , 2014, 13, 2830-2845.	1.8	15
89	A Systematic Statistical Analysis of Ion Trap Tandem Mass Spectra in View of Peptide Scoring. <i>Lecture Notes in Computer Science</i> , 2003, , 25-38.	1.0	9
90	Peptide Fragment Intensity Statistical Modeling. <i>Analytical Chemistry</i> , 2007, 79, 7286-7290.	3.2	8

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91	Deconvolution of Targeted Protein-Protein Interaction Maps. <i>Journal of Proteome Research</i> , 2012, 11, 4102-4109.	1.8	8
92	Experimental characterization of the human non-sequence-specific nucleic acid interactome. <i>Genome Biology</i> , 2013, 14, R81.	13.9	7
93	Stress and velocity fields in glaciers: Part I. Finite-difference schemes for higher-order glacier models. <i>Journal of Glaciology</i> , 1998, 44, 448-456.	1.1	7
94	TOPS: a versatile software tool for statistical analysis and visualization of combinatorial gene-gene and gene-drug interaction screens. <i>BMC Bioinformatics</i> , 2014, 15, 98.	1.2	6
95	In Vivo Large-Scale Mapping of Protein Turnover in Human Cerebrospinal Fluid. <i>Analytical Chemistry</i> , 2019, 91, 15500-15508.	3.2	6
96	Distinct oncogenes drive different genome and epigenome alterations in human mammary epithelial cells. <i>International Journal of Cancer</i> , 2019, 145, 1299-1311.	2.3	6
97	MAG11 inhibits the AMOTL2/p38 stress pathway and prevents luminal breast tumorigenesis. <i>Scientific Reports</i> , 2021, 11, 5752.	1.6	6
98	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, .	1.2	6
99	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.	1.6	5
100	Stress and velocity fields in glaciers: Part II. Sliding and basal stress distribution. <i>Journal of Glaciology</i> , 1998, 44, 457-466.	1.1	4
101	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.	3.2	2
102	Enhancing cognate target elution efficiency in gel-free chemical proteomics. <i>EuPA Open Proteomics</i> , 2015, 9, 43-53.	2.5	2
103	Towards a screening test for cancer by circulating DNA analysis.. <i>Journal of Clinical Oncology</i> , 2019, 37, e13146-e13146.	0.8	2
104	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
105	Application of modular response analysis to medium- to large-size biological systems. <i>PLoS Computational Biology</i> , 2022, 18, e1009312.	1.5	1
106	Bioinformatics in MS-Based Proteomics. , 0, , 127-139.		0
107	311 Molecular networks in innate immunity. <i>Cytokine</i> , 2008, 43, 317.	1.4	0
108	Elucidating the molecular mechanism of action of cancer drugs in the second decade of the new millennium. <i>Experimental Hematology</i> , 2013, 41, S9.	0.2	0

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109	Systems Biology Analysis of Kinase Inhibitor Action in Leukemia Treatments. Biomedizinische Technik, 2013, 58 Suppl 1, .	0.9	0
110	Comparative functional analysis of the molecular network of 7 selected MLL fusion proteins. Experimental Hematology, 2014, 42, S60.	0.2	0
111	Comparative functional analysis of the molecular network of 7 selected MLL fusion proteins. Experimental Hematology, 2015, 43, S95.	0.2	0
112	Functional Genomic and Proteomic Characterization of Normal and Oncogenic CEBPA Variants In Myeloid Cells. Blood, 2010, 116, 3873-3873.	0.6	0
113	Analysis of Labeled Quantitative Mass Spectrometry Proteomics Data. , 2012, , 79-91.		0
114	Systems Biology Analysis of Kinase Inhibitor Protein Target Profiles in Leukemia Treatments. Lecture Notes in Computer Science, 2012, , 62-66.	1.0	0
115	Abstract IA2: Network models in oncogene-addicted lung cancer. Clinical Cancer Research, 2012, 18, IA2-IA2.	3.2	0
116	Abstract LB-099: A high-throughput screen of approved drugs uncovers a synergistic interaction targeting prostate cancer. , 2015, , .		0