

Mike Tyers

List of Publications by Year in descending order

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92
papers

21,112
citations

47004

47
h-index

43886

91
g-index

100
all docs

100
docs citations

100
times ranked

28604
citing authors

#	ARTICLE	IF	CITATIONS
1	BioGRID: a general repository for interaction datasets. <i>Nucleic Acids Research</i> , 2006, 34, D535-D539.	14.5	3,407
2	Systematic Genetic Analysis with Ordered Arrays of Yeast Deletion Mutants. <i>Science</i> , 2001, 294, 2364-2368.	12.6	1,946
3	The BioGRID interaction database: 2019 update. <i>Nucleic Acids Research</i> , 2019, 47, D529-D541.	14.5	1,096
4	The BioGRID interaction database: 2017 update. <i>Nucleic Acids Research</i> , 2017, 45, D369-D379.	14.5	920
5	The Chemical Genomic Portrait of Yeast: Uncovering a Phenotype for All Genes. <i>Science</i> , 2008, 320, 362-365.	12.6	892
6	From genomics to proteomics. <i>Nature</i> , 2003, 422, 193-197.	27.8	886
7	The BioGRID interaction database: 2015 update. <i>Nucleic Acids Research</i> , 2015, 43, D470-D478.	14.5	868
8	The <scp>BioGRID</scp> database: A comprehensive biomedical resource of curated protein, genetic, and chemical interactions. <i>Protein Science</i> , 2021, 30, 187-200.	7.6	769
9	Systematic Identification of Pathways That Couple Cell Growth and Division in Yeast. <i>Science</i> , 2002, 297, 395-400.	12.6	719
10	Multisite phosphorylation of a CDK inhibitor sets a threshold for the onset of DNA replication. <i>Nature</i> , 2001, 414, 514-521.	27.8	710
11	BoxPlotR: a web tool for generation of box plots. <i>Nature Methods</i> , 2014, 11, 121-122.	19.0	665
12	A Global Protein Kinase and Phosphatase Interaction Network in Yeast. <i>Science</i> , 2010, 328, 1043-1046.	12.6	608
13	A dynamic transcriptional network communicates growth potential to ribosome synthesis and critical cell size. <i>Genes and Development</i> , 2004, 18, 2491-2505.	5.9	553
14	Drug combinations: a strategy to extend the life of antibiotics in the 21st century. <i>Nature Reviews Microbiology</i> , 2019, 17, 141-155.	28.6	526
15	How Cells Coordinate Growth and Division. <i>Current Biology</i> , 2004, 14, R1014-R1027.	3.9	515
16	The cell-cycle regulatory protein Cks1 is required for SCF ^{Skp2} -mediated ubiquitinylation of p27. <i>Nature Cell Biology</i> , 2001, 3, 321-324.	10.3	444
17	CDK Activity Antagonizes Whi5, an Inhibitor of G1/S Transcription in Yeast. <i>Cell</i> , 2004, 117, 899-913.	28.9	414
18	The Size of the Nucleus Increases as Yeast Cells Grow. <i>Molecular Biology of the Cell</i> , 2007, 18, 3523-3532.	2.1	354

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19	Comprehensive curation and analysis of global interaction networks in <i>Saccharomyces cerevisiae</i> . <i>Journal of Biology</i> , 2006, 5, 11.	2.7	276
20	PSICQUIC and PSIScore: accessing and scoring molecular interactions. <i>Nature Methods</i> , 2011, 8, 528-529.	19.0	274
21	A Strategy for Modulation of Enzymes in the Ubiquitin System. <i>Science</i> , 2013, 339, 590-595.	12.6	257
22	The GRID: the General Repository for Interaction Datasets. <i>Genome Biology</i> , 2003, 4, R23.	9.6	238
23	Broadening the horizon – level 2.5 of the HUPO-PSI format for molecular interactions. <i>BMC Biology</i> , 2007, 5, 44.	3.8	237
24	An Allosteric Inhibitor of the Human Cdc34 Ubiquitin-Conjugating Enzyme. <i>Cell</i> , 2011, 145, 1075-1087.	28.9	203
25	WD40 repeat domain proteins: a novel target class?. <i>Nature Reviews Drug Discovery</i> , 2017, 16, 773-786.	46.4	202
26	Inhibition of Dopamine Receptor D4 Impedes Autophagic Flux, Proliferation, and Survival of Glioblastoma Stem Cells. <i>Cancer Cell</i> , 2016, 29, 859-873.	16.8	169
27	<i>Caenorhabditis elegans</i> is a useful model for anthelmintic discovery. <i>Nature Communications</i> , 2015, 6, 7485.	12.8	163
28	Mubritinib Targets the Electron Transport Chain Complex I and Reveals the Landscape of OXPHOS Dependency in Acute Myeloid Leukemia. <i>Cancer Cell</i> , 2019, 36, 84-99.e8.	16.8	163
29	Sch9 regulates ribosome biogenesis via Stb3, Dot6 and Tod6 and the histone deacetylase complex RPD3L. <i>EMBO Journal</i> , 2011, 30, 3052-3064.	7.8	154
30	An allosteric inhibitor of substrate recognition by the SCFCdc4 ubiquitin ligase. <i>Nature Biotechnology</i> , 2010, 28, 733-737.	17.5	136
31	Functional genomics and proteomics: charting a multidimensional map of the yeast cell. <i>Trends in Cell Biology</i> , 2003, 13, 344-356.	7.9	126
32	The Protein-Protein Interaction tasks of BioCreative III: classification/ranking of articles and linking bio-ontology concepts to full text. <i>BMC Bioinformatics</i> , 2011, 12, S3.	2.6	121
33	Regulation of Cell Cycle Progression by Swe1p and Hog1p Following Hypertonic Stress. <i>Molecular Biology of the Cell</i> , 2001, 12, 53-62.	2.1	98
34	The PhosphoGRID <i>Saccharomyces cerevisiae</i> protein phosphorylation site database: version 2.0 update. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat026-bat026.	3.0	96
35	Prediction of Synergism from Chemical-Genetic Interactions by Machine Learning. <i>Cell Systems</i> , 2015, 1, 383-395.	6.2	89
36	E2 enzyme inhibition by stabilization of a low-affinity interface with ubiquitin. <i>Nature Chemical Biology</i> , 2014, 10, 156-163.	8.0	81

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37	Metabolic Regulation of the Epigenome Drives Lethal Infantile Ependymoma. <i>Cell</i> , 2020, 181, 1329-1345.e24.	28.9	79
38	PRMT5 inhibition disrupts splicing and stemness in glioblastoma. <i>Nature Communications</i> , 2021, 12, 979.	12.8	77
39	Human <i>CPR</i> (Cell Cycle Progression Restoration) Genes Impart a " Phenotype on Yeast Cells. <i>Genetics</i> , 1997, 147, 1063-1076.	2.9	72
40	An Antifungal Combination Matrix Identifies a Rich Pool of Adjuvant Molecules that Enhance Drug Activity against Diverse Fungal Pathogens. <i>Cell Reports</i> , 2015, 13, 1481-1492.	6.4	68
41	Yeast G1 cyclins are unstable in G1 phase. <i>Nature</i> , 1998, 395, 86-89.	27.8	67
42	Size control goes global. <i>Current Opinion in Biotechnology</i> , 2007, 18, 341-350.	6.6	67
43	Data Independent Acquisition analysis in ProHits 4.0. <i>Journal of Proteomics</i> , 2016, 149, 64-68.	2.4	66
44	A High-Resolution Genome-Wide CRISPR/Cas9 Viability Screen Reveals Structural Features and Contextual Diversity of the Human Cell-Essential Proteome. <i>Molecular and Cellular Biology</i> , 2018, 38, .	2.3	66
45	Inhibition of SCF ubiquitin ligases by engineered ubiquitin variants that target the Cul1 binding site on the Skp1 "F-box interface. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 3527-3532.	7.1	61
46	Pharmacological inhibition of PRMT7 links arginine monomethylation to the cellular stress response. <i>Nature Communications</i> , 2020, 11, 2396.	12.8	59
47	Recurated protein interaction datasets. <i>Nature Methods</i> , 2009, 6, 860-861.	19.0	58
48	A Rab escort protein integrates the secretion system with TOR signaling and ribosome biogenesis. <i>Genes and Development</i> , 2009, 23, 1944-1958.	5.9	55
49	Cdc48/VCP Promotes Chromosome Morphogenesis by Releasing Condensin from Self-Entrapment in Chromatin. <i>Molecular Cell</i> , 2018, 69, 664-676.e5.	9.7	53
50	G1/S Transcription Factor Copy Number Is a Growth-Dependent Determinant of Cell Cycle Commitment in Yeast. <i>Cell Systems</i> , 2018, 6, 539-554.e11.	6.2	52
51	BioGRID: A Resource for Studying Biological Interactions in Yeast. <i>Cold Spring Harbor Protocols</i> , 2016, 2016, pdb.top080754.	0.3	50
52	UM171 Preserves Epigenetic Marks that Are Reduced in Ex Vivo Culture of Human HSCs via Potentiation of the CLR3-KBTBD4 Complex. <i>Cell Stem Cell</i> , 2021, 28, 48-62.e6.	11.1	44
53	Structural basis for the recruitment of glycogen synthase by glycogenin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E2831-40.	7.1	43
54	Conserved Structural Mechanisms for Autoinhibition in IpaH Ubiquitin Ligases. <i>Journal of Biological Chemistry</i> , 2012, 287, 268-275.	3.4	39

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55	Imipridone Anticancer Compounds Ectopically Activate the ClpP Protease and Represent a New Scaffold for Antibiotic Development. <i>Genetics</i> , 2020, 214, 1103-1120.	2.9	36
56	Robust cullin-RING ligase function is established by a multiplicity of poly-ubiquitylation pathways. <i>ELife</i> , 2019, 8, .	6.0	36
57	Proteome-wide, Structure-Based Prediction of Protein-Protein Interactions/New Molecular Interactions Viewer. <i>Plant Physiology</i> , 2019, 179, 1893-1907.	4.8	34
58	A Loss of Function Analysis of Host Factors Influencing Vaccinia virus Replication by RNA Interference. <i>PLoS ONE</i> , 2014, 9, e98431.	2.5	34
59	An allosteric conduit facilitates dynamic multisite substrate recognition by the SCFCdc4 ubiquitin ligase. <i>Nature Communications</i> , 2017, 8, 13943.	12.8	33
60	Cell cycle goes global. <i>Current Opinion in Cell Biology</i> , 2004, 16, 602-613.	5.4	32
61	Multivalent Interactions with Fbw7 and Pin1 Facilitate Recognition of c-Jun by the SCFFbw7 Ubiquitin Ligase. <i>Structure</i> , 2018, 26, 28-39.e2.	3.3	29
62	BioCreative V BioC track overview: collaborative biocurator assistant task for BioGRID. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw121.	3.0	28
63	The p38/HOG stress-activated protein kinase network couples growth to division in <i>Candida albicans</i> . <i>PLoS Genetics</i> , 2019, 15, e1008052.	3.5	28
64	Discovery of Ibomycin, a Complex Macrolactone that Exerts Antifungal Activity by Impeding Endocytic Trafficking and Membrane Function. <i>Cell Chemical Biology</i> , 2016, 23, 1383-1394.	5.2	27
65	The BioC-BioGRID corpus: full text articles annotated for curation of protein-protein and genetic interactions. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, baw147.	3.0	24
66	Targeting the INCENP IN-box-Aurora B interaction to inhibit CPC activity <i>in vivo</i> . <i>Open Biology</i> , 2014, 4, 140163.	3.6	23
67	Use of the BioGRID Database for Analysis of Yeast Protein and Genetic Interactions. <i>Cold Spring Harbor Protocols</i> , 2016, 2016, pdb.prot088880.	0.3	23
68	Archipelago of destruction. <i>Nature</i> , 2001, 413, 268-269.	27.8	20
69	A novel p53 regulator, C16ORF72/TAPR1, buffers against telomerase inhibition. <i>Aging Cell</i> , 2021, 20, e13331.	6.7	20
70	Crippling life support for SARS-CoV-2 and other viruses through synthetic lethality. <i>Journal of Cell Biology</i> , 2020, 219, .	5.2	20
71	Using ProHits to Store, Annotate, and Analyze Affinity Purification-Mass Spectrometry (AP-MS) Data. <i>Current Protocols in Bioinformatics</i> , 2012, 39, Unit8.16.	25.8	19
72	Condensin ATPase motifs contribute differentially to the maintenance of chromosome morphology and genome stability. <i>PLoS Biology</i> , 2018, 16, e2003980.	5.6	19

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73	Genome-Wide Screens Reveal that Resveratrol Induces Replicative Stress in Human Cells. <i>Molecular Cell</i> , 2020, 79, 846-856.e8.	9.7	18
74	A novel class of inhibitors that target SRSF10 and promote p53-mediated cytotoxicity on human colorectal cancer cells. <i>NAR Cancer</i> , 2021, 3, zcab019.	3.1	17
75	Identification and optimization of molecular glue compounds that inhibit a noncovalent E2 enzyme-ubiquitin complex. <i>Science Advances</i> , 2021, 7, eabi5797.	10.3	17
76	CLMSVault: A Software Suite for Protein Cross-Linking Mass-Spectrometry Data Analysis and Visualization. <i>Journal of Proteome Research</i> , 2017, 16, 2645-2652.	3.7	16
77	Systematic chemical-genetic and chemical-chemical interaction datasets for prediction of compound synergism. <i>Scientific Data</i> , 2016, 3, 160095.	5.3	12
78	Chemical Interrogation of Nuclear Size Identifies Compounds with Cancer Cell Line-Specific Effects on Migration and Invasion. <i>ACS Chemical Biology</i> , 2022, 17, 680-700.	3.4	12
79	At Long Last, a C-Terminal Bookend for the Ubiquitin Code. <i>Molecular Cell</i> , 2018, 70, 568-571.	9.7	11
80	The microprotein Nrs1 rewires the G1/S transcriptional machinery during nitrogen limitation in budding yeast. <i>PLoS Biology</i> , 2022, 20, e3001548.	5.6	10
81	Real-time tracking of complex ubiquitination cascades using a fluorescent confocal on-bead assay. <i>BMC Biology</i> , 2018, 16, 88.	3.8	9
82	The timing of Start is determined primarily by increased synthesis of the Cln3 activator rather than dilution of the Whi5 inhibitor. <i>Molecular Biology of the Cell</i> , 2022, 33, rp2.	2.1	9
83	G1/S transcription factors assemble in increasing numbers of discrete clusters through G1 phase. <i>Journal of Cell Biology</i> , 2020, 219, .	5.2	8
84	Synthetic Genomics: Rewriting the Genome Chromosome by Chromosome. <i>Molecular Cell</i> , 2017, 66, 441-443.	9.7	7
85	Chemical Genetics Screen Identifies COPB2 Tool Compounds That Alters ER Stress Response and Induces RTK Dysregulation in Lung Cancer Cells. <i>Journal of Molecular Biology</i> , 2021, 433, 167294.	4.2	4
86	Vesicular trafficking is a key determinant of the statin response in acute myeloid leukemia. <i>Blood Advances</i> , 2022, 6, 509-514.	5.2	4
87	Panspecies Small-Molecule Disruptors of Heterochromatin-Mediated Transcriptional Gene Silencing. <i>Molecular and Cellular Biology</i> , 2015, 35, 662-674.	2.3	3
88	Gene Information eXtension (GIX): effortless retrieval of gene product information on any website. <i>Nature Methods</i> , 2019, 16, 665-666.	19.0	3
89	Head-to-tail cyclization of side chain-protected linear peptides to recapitulate genetically encoded cyclized peptides. <i>Peptide Science</i> , 2022, 114, .	1.8	3
90	Mubritinib Targets the Electron Transport Chain Complex I and Reveals the Landscape of Mitochondrial Vulnerability in Acute Myeloid Leukemia. <i>Blood</i> , 2018, 132, 910-910.	1.4	1

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91	Phosphorylation-Dependent Substrate Recognition in Ubiquitin-Mediated Proteolysis. , 2002, , 37-66.		0
92	Chemogenomic Approach Unveils the Increased Susceptibility of RUNX1-Mutated AML to Glucocorticoids. Blood, 2018, 132, 4675-4675.	1.4	0