

# Mike Tyers

## List of Publications by Year in Descending Order

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**Version:** 2024-04-28

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

89  
papers

15,851  
citations

43  
h-index

100  
g-index

100  
ext. papers

19,128  
ext. citations

15.9  
avg, IF

6.42  
L-index

#	Paper	IF	Citations
89	The microprotein Nrs1 rewires the G1/S transcriptional machinery during nitrogen limitation in budding yeast.. <i>PLoS Biology</i> , <b>2022</b> , 20, e3001548	9.7	0
88	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> , <b>2022</b> , 33, rp2	3.5	0
87	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> , <b>2021</b> , 433, 167294	6.5	2
86	Identification and optimization of molecular glue compounds that inhibit a noncovalent E2 enzyme-ubiquitin complex. <i>Science Advances</i> , <b>2021</b> , 7, eabi5797	14.3	4
85	A novel p53 regulator, C16ORF72/TAPR1, buffers against telomerase inhibition. <i>Aging Cell</i> , <b>2021</b> , 20, e13331	9.9	3
84	A novel class of inhibitors that target SRSF10 and promote p53-mediated cytotoxicity on human colorectal cancer cells. <i>NAR Cancer</i> , <b>2021</b> , 3, zcab019	5.2	2
83	The BioGRID database: A comprehensive biomedical resource of curated protein, genetic, and chemical interactions. <i>Protein Science</i> , <b>2021</b> , 30, 187-200	6.3	149
82	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> , <b>2021</b> , 28, 48-62.e6	18	11
81	PRMT5 inhibition disrupts splicing and stemness in glioblastoma. <i>Nature Communications</i> , <b>2021</b> , 12, 979	17.4	23
80	Pharmacological inhibition of PRMT7 links arginine monomethylation to the cellular stress response. <i>Nature Communications</i> , <b>2020</b> , 11, 2396	17.4	29
79	Imipridone Anticancer Compounds Ectopically Activate the ClpP Protease and Represent a New Scaffold for Antibiotic Development. <i>Genetics</i> , <b>2020</b> , 214, 1103-1120	4	16
78	G1/S transcription factors assemble in increasing numbers of discrete clusters through G1 phase. <i>Journal of Cell Biology</i> , <b>2020</b> , 219,	7.3	4
77	Metabolic Regulation of the Epigenome Drives Lethal Infantile Ependymoma. <i>Cell</i> , <b>2020</b> , 181, 1329-1345.e24	56.24	40
76	Crippling life support for SARS-CoV-2 and other viruses through synthetic lethality. <i>Journal of Cell Biology</i> , <b>2020</b> , 219,	7.3	9
75	Genome-Wide Screens Reveal that Resveratrol Induces Replicative Stress in Human Cells. <i>Molecular Cell</i> , <b>2020</b> , 79, 846-856.e8	17.6	8
74	Proteome-wide, Structure-Based Prediction of Protein-Protein Interactions/New Molecular Interactions Viewer. <i>Plant Physiology</i> , <b>2019</b> , 179, 1893-1907	6.6	21
73	Drug combinations: a strategy to extend the life of antibiotics in the 21st century. <i>Nature Reviews Microbiology</i> , <b>2019</b> , 17, 141-155	22.2	269

72	Gene Information eXtension (GIX): effortless retrieval of gene product information on any website. <i>Nature Methods</i> , <b>2019</b> , 16, 665-666	21.6	3
71	The p38/HOG stress-activated protein kinase network couples growth to division in <i>Candida albicans</i> . <i>PLoS Genetics</i> , <b>2019</b> , 15, e1008052	6	15
70	Mubritinib Targets the Electron Transport Chain Complex I and Reveals the Landscape of OXPHOS Dependency in Acute Myeloid Leukemia. <i>Cancer Cell</i> , <b>2019</b> , 36, 84-99.e8	24.3	75
69	Robust cullin-RING ligase function is established by a multiplicity of poly-ubiquitylation pathways. <i>ELife</i> , <b>2019</b> , 8,	8.9	20
68	The BioGRID interaction database: 2019 update. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, D529-D541	20.1	626
67	Cdc48/VCP Promotes Chromosome Morphogenesis by Releasing Condensin from Self-Entrapment in Chromatin. <i>Molecular Cell</i> , <b>2018</b> , 69, 664-676.e5	17.6	29
66	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> , <b>2018</b> , 38,	4.8	33
65	Mubritinib Targets the Electron Transport Chain Complex I and Reveals the Landscape of Mitochondrial Vulnerability in Acute Myeloid Leukemia. <i>Blood</i> , <b>2018</b> , 132, 910-910	2.2	0
64	Chemogenomic Approach Unveils the Increased Susceptibility of RUNX1-Mutated AML to Glucocorticoids. <i>Blood</i> , <b>2018</b> , 132, 4675-4675	2.2	
63	Multivalent Interactions with Fbw7 and Pin1 Facilitate Recognition of c-Jun by the SCF Ubiquitin Ligase. <i>Structure</i> , <b>2018</b> , 26, 28-39.e2	5.2	17
62	Real-time tracking of complex ubiquitination cascades using a fluorescent confocal on-bead assay. <i>BMC Biology</i> , <b>2018</b> , 16, 88	7.3	6
61	G1/S Transcription Factor Copy Number Is a Growth-Dependent Determinant of Cell Cycle Commitment in Yeast. <i>Cell Systems</i> , <b>2018</b> , 6, 539-554.e11	10.6	27
60	At Long Last, a C-Terminal Bookend for the Ubiquitin Code. <i>Molecular Cell</i> , <b>2018</b> , 70, 568-571	17.6	7
59	Condensin ATPase motifs contribute differentially to the maintenance of chromosome morphology and genome stability. <i>PLoS Biology</i> , <b>2018</b> , 16, e2003980	9.7	11
58	Synthetic Genomics: Rewriting the Genome Chromosome by Chromosome. <i>Molecular Cell</i> , <b>2017</b> , 66, 441-448	17.4	6
57	CLMSVault: A Software Suite for Protein Cross-Linking Mass-Spectrometry Data Analysis and Visualization. <i>Journal of Proteome Research</i> , <b>2017</b> , 16, 2645-2652	5.6	14
56	The BioGRID interaction database: 2017 update. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, D369-D379	20.1	682
55	An allosteric conduit facilitates dynamic multisite substrate recognition by the SCF ubiquitin ligase. <i>Nature Communications</i> , <b>2017</b> , 8, 13943	17.4	28

54	WD40 repeat domain proteins: a novel target class?. <i>Nature Reviews Drug Discovery</i> , <b>2017</b> , 16, 773-786	64.1	101
53	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> , <b>2017</b> , 2017,	5	23
52	Systematic chemical-genetic and chemical-chemical interaction datasets for prediction of compound synergism. <i>Scientific Data</i> , <b>2016</b> , 3, 160095	8.2	9
51	Discovery of Ibomycin, a Complex Macrolactone that Exerts Antifungal Activity by Impeding Endocytic Trafficking and Membrane Function. <i>Cell Chemical Biology</i> , <b>2016</b> , 23, 1383-1394	8.2	19
50	BioCreative V BioC track overview: collaborative biocurator assistant task for BioGRID. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2016</b> , 2016,	5	23
49	Inhibition of Dopamine Receptor D4 Impedes Autophagic Flux, Proliferation, and Survival of Glioblastoma Stem Cells. <i>Cancer Cell</i> , <b>2016</b> , 29, 859-873	24.3	124
48	Use of the BioGRID Database for Analysis of Yeast Protein and Genetic Interactions. <i>Cold Spring Harbor Protocols</i> , <b>2016</b> , 2016, pdb.prot088880	1.2	19
47	BioGRID: A Resource for Studying Biological Interactions in Yeast. <i>Cold Spring Harbor Protocols</i> , <b>2016</b> , 2016, pdb.top080754	1.2	37
46	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> , <b>2016</b> , 113, 3527-32	11.5	47
45	Data Independent Acquisition analysis in ProHits 4.0. <i>Journal of Proteomics</i> , <b>2016</b> , 149, 64-68	3.9	37
44	The BioGRID interaction database: 2015 update. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, D470-8	20.1	714
43	Caenorhabditis elegans is a useful model for anthelmintic discovery. <i>Nature Communications</i> , <b>2015</b> , 6, 7485	17.4	103
42	An Antifungal Combination Matrix Identifies a Rich Pool of Adjuvant Molecules that Enhance Drug Activity against Diverse Fungal Pathogens. <i>Cell Reports</i> , <b>2015</b> , 13, 1481-1492	10.6	54
41	Prediction of Synergism from Chemical-Genetic Interactions by Machine Learning. <i>Cell Systems</i> , <b>2015</b> , 1, 383-95	10.6	54
40	Panspecies small-molecule disruptors of heterochromatin-mediated transcriptional gene silencing. <i>Molecular and Cellular Biology</i> , <b>2015</b> , 35, 662-74	4.8	2
39	E2 enzyme inhibition by stabilization of a low-affinity interface with ubiquitin. <i>Nature Chemical Biology</i> , <b>2014</b> , 10, 156-163	11.7	58
38	BoxPlotR: a web tool for generation of box plots. <i>Nature Methods</i> , <b>2014</b> , 11, 121-2	21.6	434
37	Targeting the INCENP IN-box-Aurora B interaction to inhibit CPC activity in vivo. <i>Open Biology</i> , <b>2014</b> , 4, 140163	7	20

36	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> , <b>2014</b> , 111, E2831-40	11.5	33
35	A loss of function analysis of host factors influencing Vaccinia virus replication by RNA interference. <i>PLoS ONE</i> , <b>2014</b> , 9, e98431	3.7	22
34	A strategy for modulation of enzymes in the ubiquitin system. <i>Science</i> , <b>2013</b> , 339, 590-5	33.3	199
33	The PhosphoGRID <i>Saccharomyces cerevisiae</i> protein phosphorylation site database: version 2.0 update. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2013</b> , 2013, bat026	5	85
32	Using ProHits to store, annotate, and analyze affinity purification-mass spectrometry (AP-MS) data. <i>Current Protocols in Bioinformatics</i> , <b>2012</b> , Chapter 8, Unit8.16	24.2	17
31	Conserved structural mechanisms for autoinhibition in IpaH ubiquitin ligases. <i>Journal of Biological Chemistry</i> , <b>2012</b> , 287, 268-275	5.4	33
30	PSICQUIC and PSISCORE: accessing and scoring molecular interactions. <i>Nature Methods</i> , <b>2011</b> , 8, 528-9	21.6	227
29	An allosteric inhibitor of the human Cdc34 ubiquitin-conjugating enzyme. <i>Cell</i> , <b>2011</b> , 145, 1075-87	56.2	172
28	The Protein-Protein Interaction tasks of BioCreative III: classification/ranking of articles and linking bio-ontology concepts to full text. <i>BMC Bioinformatics</i> , <b>2011</b> , 12 Suppl 8, S3	3.6	104
27	Sch9 regulates ribosome biogenesis via Stb3, Dot6 and Tod6 and the histone deacetylase complex RPD3L. <i>EMBO Journal</i> , <b>2011</b> , 30, 3052-64	13	119
26	An allosteric inhibitor of substrate recognition by the SCF(Cdc4) ubiquitin ligase. <i>Nature Biotechnology</i> , <b>2010</b> , 28, 733-7	44.5	118
25	A global protein kinase and phosphatase interaction network in yeast. <i>Science</i> , <b>2010</b> , 328, 1043-6	33.3	523
24	A Rab escort protein integrates the secretion system with TOR signaling and ribosome biogenesis. <i>Genes and Development</i> , <b>2009</b> , 23, 1944-58	12.6	43
23	Recurated protein interaction datasets. <i>Nature Methods</i> , <b>2009</b> , 6, 860-1	21.6	48
22	The chemical genomic portrait of yeast: uncovering a phenotype for all genes. <i>Science</i> , <b>2008</b> , 320, 362-5	33.3	769
21	Broadening the horizon--level 2.5 of the HUPO-PSI format for molecular interactions. <i>BMC Biology</i> , <b>2007</b> , 5, 44	7.3	204
20	Size control goes global. <i>Current Opinion in Biotechnology</i> , <b>2007</b> , 18, 341-50	11.4	58
19	The size of the nucleus increases as yeast cells grow. <i>Molecular Biology of the Cell</i> , <b>2007</b> , 18, 3523-32	3.5	265

18	BioGRID: a general repository for interaction datasets. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, D535-9	20.1	2638
17	Comprehensive curation and analysis of global interaction networks in <i>Saccharomyces cerevisiae</i> . <i>Journal of Biology</i> , <b>2006</b> , 5, 11		246
16	A dynamic transcriptional network communicates growth potential to ribosome synthesis and critical cell size. <i>Genes and Development</i> , <b>2004</b> , 18, 2491-505	12.6	472
15	How cells coordinate growth and division. <i>Current Biology</i> , <b>2004</b> , 14, R1014-27	6.3	441
14	Cell cycle goes global. <i>Current Opinion in Cell Biology</i> , <b>2004</b> , 16, 602-13	9	25
13	CDK activity antagonizes Whi5, an inhibitor of G1/S transcription in yeast. <i>Cell</i> , <b>2004</b> , 117, 899-913	56.2	340
12	Functional genomics and proteomics: charting a multidimensional map of the yeast cell. <i>Trends in Cell Biology</i> , <b>2003</b> , 13, 344-56	18.3	102
11	From genomics to proteomics. <i>Nature</i> , <b>2003</b> , 422, 193-7	50.4	734
10	The GRID: the General Repository for Interaction Datasets. <i>Genome Biology</i> , <b>2003</b> , 4, R23	18.3	181
9	Systematic identification of pathways that couple cell growth and division in yeast. <i>Science</i> , <b>2002</b> , 297, 395-400	33.3	607
8	Phosphorylation-Dependent Substrate Recognition in Ubiquitin-Mediated Proteolysis <b>2002</b> , 37-66		
7	Systematic genetic analysis with ordered arrays of yeast deletion mutants. <i>Science</i> , <b>2001</b> , 294, 2364-8	33.3	1676
6	The cell-cycle regulatory protein Cks1 is required for SCF(Skp2)-mediated ubiquitinylation of p27. <i>Nature Cell Biology</i> , <b>2001</b> , 3, 321-4	23.4	415
5	Multisite phosphorylation of a CDK inhibitor sets a threshold for the onset of DNA replication. <i>Nature</i> , <b>2001</b> , 414, 514-21	50.4	639
4	Regulation of cell cycle progression by Swe1p and Hog1p following hypertonic stress. <i>Molecular Biology of the Cell</i> , <b>2001</b> , 12, 53-62	3.5	87
3	Yeast G1 cyclins are unstable in G1 phase. <i>Nature</i> , <b>1998</b> , 395, 86-9	50.4	61
2	Human CPR (cell cycle progression restoration) genes impart a Far- phenotype on yeast cells. <i>Genetics</i> , <b>1997</b> , 147, 1063-76	4	60
1	A nitrogen source-regulated microprotein confers an alternative mechanism of G1/S transcriptional activation in budding yeast		1

