

Nevan J Krogan

List of Publications by Year in descending order

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247
papers

40,031
citations

4653

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294
docs citations

294
times ranked

48996
citing authors

#	ARTICLE	IF	CITATIONS
1	A SARS-CoV-2 protein interaction map reveals targets for drug repurposing. <i>Nature</i> , 2020, 583, 459-468.	13.7	3,542
2	Global landscape of protein complexes in the yeast <i>Saccharomyces cerevisiae</i> . <i>Nature</i> , 2006, 440, 637-643.	13.7	2,681
3	Global Mapping of the Yeast Genetic Interaction Network. <i>Science</i> , 2004, 303, 808-813.	6.0	1,908
4	Meta- and Orthogonal Integration of Influenza α OMICs Data Defines a Role for UBR4 in Virus Budding. <i>Cell Host and Microbe</i> , 2015, 18, 723-735.	5.1	868
5	The Global Phosphorylation Landscape of SARS-CoV-2 Infection. <i>Cell</i> , 2020, 182, 685-712.e19.	13.5	825
6	Functional dissection of protein complexes involved in yeast chromosome biology using a genetic interaction map. <i>Nature</i> , 2007, 446, 806-810.	13.7	806
7	Exploration of the Function and Organization of the Yeast Early Secretory Pathway through an Epistatic Miniarray Profile. <i>Cell</i> , 2005, 123, 507-519.	13.5	804
8	Navigating the Chaperone Network: An Integrative Map of Physical and Genetic Interactions Mediated by the Hsp90 Chaperone. <i>Cell</i> , 2005, 120, 715-727.	13.5	729
9	Cotranscriptional Set2 Methylation of Histone H3 Lysine 36 Recruits a Repressive Rpd3 Complex. <i>Cell</i> , 2005, 123, 593-605.	13.5	712
10	Toward a Comprehensive Atlas of the Physical Interactome of <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Proteomics</i> , 2007, 6, 439-450.	2.5	692
11	Differential network biology. <i>Molecular Systems Biology</i> , 2012, 8, 565.	3.2	689
12	Global landscape of HIV-human protein complexes. <i>Nature</i> , 2012, 481, 365-370.	13.7	651
13	The Paf1 Complex Is Required for Histone H3 Methylation by COMPASS and Dot1p: Linking Transcriptional Elongation to Histone Methylation. <i>Molecular Cell</i> , 2003, 11, 721-729.	4.5	642
14	Phenotypic Landscape of a Bacterial Cell. <i>Cell</i> , 2011, 144, 143-156.	13.5	623
15	Methylation of Histone H3 by Set2 in <i>Saccharomyces cerevisiae</i> Is Linked to Transcriptional Elongation by RNA Polymerase II. <i>Molecular and Cellular Biology</i> , 2003, 23, 4207-4218.	1.1	600
16	How many human proteoforms are there?. <i>Nature Chemical Biology</i> , 2018, 14, 206-214.	3.9	580
17	A Snf2 Family ATPase Complex Required for Recruitment of the Histone H2A Variant Htz1. <i>Molecular Cell</i> , 2003, 12, 1565-1576.	4.5	524
18	Comparative host-coronavirus protein interaction networks reveal pan-viral disease mechanisms. <i>Science</i> , 2020, 370, .	6.0	508

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19	A comprehensive strategy enabling high-resolution functional analysis of the yeast genome. Nature Methods, 2008, 5, 711-718.	9.0	473
20	RNA Polymerase II Elongation Factors of <i>Saccharomyces cerevisiae</i> : a Targeted Proteomics Approach. Molecular and Cellular Biology, 2002, 22, 6979-6992.	1.1	462
21	A phosphatase complex that dephosphorylates γ -H2AX regulates DNA damage checkpoint recovery. Nature, 2006, 439, 497-501.	13.7	439
22	SARS-CoV-2 Orf6 hijacks Nup98 to block STAT nuclear import and antagonize interferon signaling. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 28344-28354.	3.3	421
23	CRISPR Interference Efficiently Induces Specific and Reversible Gene Silencing in Human iPSCs. Cell Stem Cell, 2016, 18, 541-553.	5.2	418
24	Inhibition of CRISPR-Cas9 with Bacteriophage Proteins. Cell, 2017, 168, 150-158.e10.	13.5	409
25	Rewiring of Genetic Networks in Response to DNA Damage. Science, 2010, 330, 1385-1389.	6.0	408
26	SNX27 mediates retromer tubule entry and endosome-to-plasma membrane trafficking of signalling receptors. Nature Cell Biology, 2011, 13, 715-721.	4.6	408
27	Critical role of acetylation in tau-mediated neurodegeneration and cognitive deficits. Nature Medicine, 2015, 21, 1154-1162.	15.2	398
28	Host Cell Factors in HIV Replication: Meta-Analysis of Genome-Wide Studies. PLoS Pathogens, 2009, 5, e1000437.	2.1	396
29	Systematic Functional Prioritization of Protein Posttranslational Modifications. Cell, 2012, 150, 413-425.	13.5	375
30	HIV-1 Tat and Host AFF4 Recruit Two Transcription Elongation Factors into a Bifunctional Complex for Coordinated Activation of HIV-1 Transcription. Molecular Cell, 2010, 38, 428-438.	4.5	351
31	High-Definition Macromolecular Composition of Yeast RNA-Processing Complexes. Molecular Cell, 2004, 13, 225-239.	4.5	345
32	An ultrapotent synthetic nanobody neutralizes SARS-CoV-2 by stabilizing inactive Spike. Science, 2020, 370, 1473-1479.	6.0	336
33	Conservation and Rewiring of Functional Modules Revealed by an Epistasis Map in Fission Yeast. Science, 2008, 322, 405-410.	6.0	328
34	An Approach to Spatiotemporally Resolve Protein Interaction Networks in Living Cells. Cell, 2017, 169, 350-360.e12.	13.5	322
35	Genetic Screens Identify Host Factors for SARS-CoV-2 and Common Cold Coronaviruses. Cell, 2021, 184, 106-119.e14.	13.5	320
36	Vif hijacks CBF- β to degrade APOBEC3G and promote HIV-1 infection. Nature, 2012, 481, 371-375.	13.7	312

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37	Evolution and functional cross-talk of protein post-translational modifications. <i>Molecular Systems Biology</i> , 2013, 9, 714.	3.2	294
38	A genome-wide CRISPR screen identifies a restricted set of HIV host dependency factors. <i>Nature Genetics</i> , 2017, 49, 193-203.	9.4	290
39	A strategy for extracting and analyzing large-scale quantitative epistatic interaction data. <i>Genome Biology</i> , 2006, 7, R63.	13.9	287
40	Combinatorial CRISPR-Cas9 screens for de novo mapping of genetic interactions. <i>Nature Methods</i> , 2017, 14, 573-576.	9.0	287
41	The functional landscape of the human phosphoproteome. <i>Nature Biotechnology</i> , 2020, 38, 365-373.	9.4	273
42	The functional landscape of mouse gene expression. <i>Journal of Biology</i> , 2004, 3, 21.	2.7	259
43	Comparative Flavivirus-Host Protein Interaction Mapping Reveals Mechanisms of Dengue and Zika Virus Pathogenesis. <i>Cell</i> , 2018, 175, 1931-1945.e18.	13.5	252
44	Evaluation of SARS-CoV-2 serology assays reveals a range of test performance. <i>Nature Biotechnology</i> , 2020, 38, 1174-1183.	9.4	251
45	Plitidepsin has potent preclinical efficacy against SARS-CoV-2 by targeting the host protein eEF1A. <i>Science</i> , 2021, 371, 926-931.	6.0	247
46	Evolution of enhanced innate immune evasion by SARS-CoV-2. <i>Nature</i> , 2022, 602, 487-495.	13.7	237
47	Functional Organization of the <i>S. cerevisiae</i> Phosphorylation Network. <i>Cell</i> , 2009, 136, 952-963.	13.5	235
48	Regulation of chromosome stability by the histone H2A variant Htz1, the Swr1 chromatin remodeling complex, and the histone acetyltransferase NuA4. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 13513-13518.	3.3	227
49	A Genetic Interaction Map of RNA-Processing Factors Reveals Links between Sem1/Dss1-Containing Complexes and mRNA Export and Splicing. <i>Molecular Cell</i> , 2008, 32, 735-746.	4.5	221
50	High-throughput, quantitative analyses of genetic interactions in <i>E. coli</i> . <i>Nature Methods</i> , 2008, 5, 781-787.	9.0	214
51	Proteasome Involvement in the Repair of DNA Double-Strand Breaks. <i>Molecular Cell</i> , 2004, 16, 1027-1034.	4.5	207
52	H2B Ubiquitylation Acts as a Barrier to Ctk1 Nucleosomal Recruitment Prior to Removal by Ubp8 within a SAGA-Related Complex. <i>Molecular Cell</i> , 2007, 27, 275-288.	4.5	196
53	Hierarchical Modularity and the Evolution of Genetic Interactomes across Species. <i>Molecular Cell</i> , 2012, 46, 691-704.	4.5	185
54	A gene ontology inferred from molecular networks. <i>Nature Biotechnology</i> , 2013, 31, 38-45.	9.4	184

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55	The mTOR Complex Controls HIV Latency. <i>Cell Host and Microbe</i> , 2016, 20, 785-797.	5.1	179
56	NF- κ B-Activating Complex Engaged in Response to EGFR Oncogene Inhibition Drives Tumor Cell Survival and Residual Disease in Lung Cancer. <i>Cell Reports</i> , 2015, 11, 98-110.	2.9	178
57	The Dengue Virus NS5 Protein Intrudes in the Cellular Spliceosome and Modulates Splicing. <i>PLoS Pathogens</i> , 2016, 12, e1005841.	2.1	176
58	Global Mapping of the Inc-Human Interactome Reveals that Retromer Restricts Chlamydia Infection. <i>Cell Host and Microbe</i> , 2015, 18, 109-121.	5.1	174
59	A Cas9 Ribonucleoprotein Platform for Functional Genetic Studies of HIV-Host Interactions in Primary Human T Cells. <i>Cell Reports</i> , 2016, 17, 1438-1452.	2.9	167
60	Global Mapping of Herpesvirus-Host Protein Complexes Reveals a Transcription Strategy for Late Genes. <i>Molecular Cell</i> , 2015, 57, 349-360.	4.5	165
61	Chaperone-mediated autophagy prevents collapse of the neuronal metastable proteome. <i>Cell</i> , 2021, 184, 2696-2714.e25.	13.5	151
62	Drug-induced phospholipidosis confounds drug repurposing for SARS-CoV-2. <i>Science</i> , 2021, 373, 541-547.	6.0	148
63	High-throughput genetic interaction mapping in the fission yeast <i>Schizosaccharomyces pombe</i> . <i>Nature Methods</i> , 2007, 4, 861-866.	9.0	146
64	Cross-species chemogenomic profiling reveals evolutionarily conserved drug mode of action. <i>Molecular Systems Biology</i> , 2010, 6, 451.	3.2	143
65	Genetic interaction mapping in mammalian cells using CRISPR interference. <i>Nature Methods</i> , 2017, 14, 577-580.	9.0	142
66	Quantitative Genetic Interactions Reveal Biological Modularity. <i>Cell</i> , 2010, 141, 739-745.	13.5	140
67	Mutations in SARS-CoV-2 variants of concern link to increased spike cleavage and virus transmission. <i>Cell Host and Microbe</i> , 2022, 30, 373-387.e7.	5.1	138
68	The H3K36me2 Methyltransferase Nsd1 Demarcates PRC2-Mediated H3K27me2 and H3K27me3 Domains in Embryonic Stem Cells. <i>Molecular Cell</i> , 2018, 70, 371-379.e5.	4.5	137
69	From Structure to Systems: High-Resolution, Quantitative Genetic Analysis of RNA Polymerase II. <i>Cell</i> , 2013, 154, 775-788.	13.5	132
70	Functional Maps of Protein Complexes from Quantitative Genetic Interaction Data. <i>PLoS Computational Biology</i> , 2008, 4, e1000065.	1.5	128
71	A Lipid E-MAP Identifies Ubx2 as a Critical Regulator of Lipid Saturation and Lipid Bilayer Stress. <i>Molecular Cell</i> , 2013, 51, 519-530.	4.5	127
72	A Combined Proteomics/Genomics Approach Links Hepatitis C Virus Infection with Nonsense-Mediated mRNA Decay. <i>Molecular Cell</i> , 2015, 57, 329-340.	4.5	124

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73	Functional Overlap and Regulatory Links Shape Genetic Interactions between Signaling Pathways. <i>Cell</i> , 2010, 143, 991-1004.	13.5	123
74	Centriolar satellites assemble centrosomal microcephaly proteins to recruit CDK2 and promote centriole duplication. <i>ELife</i> , 2015, 4, .	2.8	118
75	The Cancer Cell Map Initiative: Defining the Hallmark Networks of Cancer. <i>Molecular Cell</i> , 2015, 58, 690-698.	4.5	117
76	Microcephaly Proteins Wdr62 and Aspm Define a Mother Centriole Complex Regulating Centriole Biogenesis, Apical Complex, and Cell Fate. <i>Neuron</i> , 2016, 92, 813-828.	3.8	116
77	Host Cell Interactome of HIV-1 Rev Includes RNA Helicases Involved in Multiple Facets of Virus Production. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.015313.	2.5	114
78	Tau interactome maps synaptic and mitochondrial processes associated with neurodegeneration. <i>Cell</i> , 2022, 185, 712-728.e14.	13.5	114
79	First-In-Class Small Molecule Inhibitors of the Single-Strand DNA Cytosine Deaminase APOBEC3G. <i>ACS Chemical Biology</i> , 2012, 7, 506-517.	1.6	112
80	Targeting Viral Proteostasis Limits Influenza Virus, HIV, and Dengue Virus Infection. <i>Immunity</i> , 2016, 44, 46-58.	6.6	110
81	CBFÎ² Stabilizes HIV Vif to Counteract APOBEC3 at the Expense of RUNX1 Target Gene Expression. <i>Molecular Cell</i> , 2013, 49, 632-644.	4.5	108
82	Protein Interaction Mapping Identifies RBBP6 as a Negative Regulator of Ebola Virus Replication. <i>Cell</i> , 2018, 175, 1917-1930.e13.	13.5	108
83	The Psychiatric Cell Map Initiative: A Convergent Systems Biological Approach to Illuminating Key Molecular Pathways in Neuropsychiatric Disorders. <i>Cell</i> , 2018, 174, 505-520.	13.5	108
84	Anti-CRISPR-Associated Proteins Are Crucial Repressors of Anti-CRISPR Transcription. <i>Cell</i> , 2019, 178, 1452-1464.e13.	13.5	105
85	Quantitative genetic-interaction mapping in mammalian cells. <i>Nature Methods</i> , 2013, 10, 432-437.	9.0	104
86	An Mtb-Human Protein-Protein Interaction Map Identifies a Switch between Host Antiviral and Antibacterial Responses. <i>Molecular Cell</i> , 2018, 71, 637-648.e5.	4.5	100
87	SIRT1 Deacetylates Tau and Reduces Pathogenic Tau Spread in a Mouse Model of Tauopathy. <i>Journal of Neuroscience</i> , 2018, 38, 3680-3688.	1.7	98
88	CRISPRâ€Cas9 genome engineering of primary CD4+ T cells for the interrogation of HIVâ€™host factor interactions. <i>Nature Protocols</i> , 2019, 14, 1-27.	5.5	98
89	Mass spectrometryâ€based proteinâ€protein interaction networks for the study of human diseases. <i>Molecular Systems Biology</i> , 2021, 17, e8792.	3.2	96
90	A plasma-membrane E-MAP reveals links of the eisosome with sphingolipid metabolism and endosomal trafficking. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 901-908.	3.6	93

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91	Meningioma DNA methylation groups identify biological drivers and therapeutic vulnerabilities. Nature Genetics, 2022, 54, 649-659.	9.4	93
92	High-resolution network biology: connecting sequence with function. Nature Reviews Genetics, 2013, 14, 865-879.	7.7	92
93	Evolutionary Proteomics Uncovers Ancient Associations of Cilia with Signaling Pathways. Developmental Cell, 2017, 43, 744-762.e11.	3.1	92
94	Metabolic reprogramming of human CD8+ memory T cells through loss of SIRT1. Journal of Experimental Medicine, 2018, 215, 51-62.	4.2	91
95	Large dataset enables prediction of repair after CRISPR-Cas9 editing in primary T cells. Nature Biotechnology, 2019, 37, 1034-1037.	9.4	87
96	Envelope protein ubiquitination drives entry and pathogenesis of Zika virus. Nature, 2020, 585, 414-419.	13.7	82
97	A BAG3 chaperone complex maintains cardiomyocyte function during proteotoxic stress. JCI Insight, 2017, 2, .	2.3	81
98	Quantitative Genetic Interaction Mapping Using the E-MAP Approach. Methods in Enzymology, 2010, 470, 205-231.	0.4	80
99	Cullin E3 Ligases and Their Rewiring by Viral Factors. Biomolecules, 2014, 4, 897-930.	1.8	78
100	SMYD2-Mediated Histone Methylation Contributes to HIV-1 Latency. Cell Host and Microbe, 2017, 21, 569-579.e6.	5.1	78
101	UNC93B1 recruits syntenin-1 to dampen TLR7 signalling and prevent autoimmunity. Nature, 2019, 575, 366-370.	13.7	78
102	An acetylated form of histone H2A.Z regulates chromosome architecture in Schizosaccharomyces pombe. Nature Structural and Molecular Biology, 2009, 16, 1286-1293.	3.6	77
103	The AMBRA1 E3 ligase adaptor regulates the stability of cyclin D. Nature, 2021, 592, 794-798.	13.7	76
104	Yeast SREBP Cleavage Activation Requires the Golgi Dsc E3 Ligase Complex. Molecular Cell, 2011, 42, 160-171.	4.5	72
105	Translation of Genotype to Phenotype by a Hierarchy of Cell Subsystems. Cell Systems, 2016, 2, 77-88.	2.9	72
106	A systems approach to infectious disease. Nature Reviews Genetics, 2020, 21, 339-354.	7.7	72
107	Mutations in ANKLE2, a ZIKA Virus Target, Disrupt an Asymmetric Cell Division Pathway in Drosophila Neuroblasts to Cause Microcephaly. Developmental Cell, 2019, 51, 713-729.e6.	3.1	71
108	An ancient viral epidemic involving host coronavirus interacting genes more than 20,000 years ago in East Asia. Current Biology, 2021, 31, 3504-3514.e9.	1.8	71

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109	A scaffold protein connects type IV pili with the Chp chemosensory system to mediate activation of virulence signaling in <i>Pseudomonas aeruginosa</i> . <i>Molecular Microbiology</i> , 2016, 101, 590-605.	1.2	69
110	The Host E3-Ubiquitin Ligase TRIM6 Ubiquitinates the Ebola Virus VP35 Protein and Promotes Virus Replication. <i>Journal of Virology</i> , 2017, 91, .	1.5	68
111	Cyclophilin A Prevents HIV-1 Restriction in Lymphocytes by Blocking Human TRIM5 α Binding to the Viral Core. <i>Cell Reports</i> , 2020, 30, 3766-3777.e6.	2.9	68
112	Multiple Routes to Oncogenesis Are Promoted by the Human Papillomavirus Host Protein Network. <i>Cancer Discovery</i> , 2018, 8, 1474-1489.	7.7	67
113	A Chaperone-Assisted Degradation Pathway Targets Kinetochore Proteins to Ensure Genome Stability. <i>PLoS Genetics</i> , 2014, 10, e1004140.	1.5	66
114	A protein interaction landscape of breast cancer. <i>Science</i> , 2021, 374, eabf3066.	6.0	66
115	Adhesion-mediated mechanosignaling forces mitohormesis. <i>Cell Metabolism</i> , 2021, 33, 1322-1341.e13.	7.2	65
116	Mutations in the X-linked <i>ATP6AP2</i> cause a glycosylation disorder with autophagic defects. <i>Journal of Experimental Medicine</i> , 2017, 214, 3707-3729.	4.2	62
117	Systematic Identification of Host Cell Regulators of <i>Legionella pneumophila</i> Pathogenesis Using a Genome-wide CRISPR Screen. <i>Cell Host and Microbe</i> , 2019, 26, 551-563.e6.	5.1	62
118	Chlamydia interfere with an interaction between the mannose-6-phosphate receptor and sorting nexins to counteract host restriction. <i>ELife</i> , 2017, 6, .	2.8	61
119	The Cellular NMD Pathway Restricts Zika Virus Infection and Is Targeted by the Viral Capsid Protein. <i>MBio</i> , 2018, 9, .	1.8	60
120	Acetylome Profiling Reveals Overlap in the Regulation of Diverse Processes by Sirtuins, Gcn5, and Esa1. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 162-176.	2.5	59
121	Scoring Large-scale Affinity Purification Mass Spectrometry Datasets with MiST. <i>Current Protocols in Bioinformatics</i> , 2015, 49, 8.19.1-8.19.16.	25.8	58
122	Unbiased Proteomic Profiling Uncovers a Targetable GNAS/PKA/PP2A Axis in Small Cell Lung Cancer Stem Cells. <i>Cancer Cell</i> , 2020, 38, 129-143.e7.	7.7	57
123	Purification and characterization of HIV-human protein complexes. <i>Methods</i> , 2011, 53, 13-19.	1.9	56
124	Inhibition of a NEDD8 Cascade Restores Restriction of HIV by APOBEC3G. <i>PLoS Pathogens</i> , 2012, 8, e1003085.	2.1	55
125	CDK11 in TREX/THOC Regulates HIV mRNA 5' End Processing. <i>Cell Host and Microbe</i> , 2015, 18, 560-570.	5.1	53
126	Genome-Wide Association Data Reveal a Global Map of Genetic Interactions among Protein Complexes. <i>PLoS Genetics</i> , 2009, 5, e1000782.	1.5	52

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127	Identification of antiviral roles for the exonâ€‘junction complex and nonsense-mediated decay in flaviviral infection. <i>Nature Microbiology</i> , 2019, 4, 985-995.	5.9	52
128	Enterovirus pathogenesis requires the host methyltransferase SETD3. <i>Nature Microbiology</i> , 2019, 4, 2523-2537.	5.9	51
129	Replication Fork Collapse and Genome Instability in a Deoxycytidylate Deaminase Mutant. <i>Molecular and Cellular Biology</i> , 2012, 32, 4445-4454.	1.1	50
130	SUMO is a pervasive regulator of meiosis. <i>ELife</i> , 2021, 10, .	2.8	50
131	Cyclin-Dependent Kinase 12 Increases 3â€² End Processing of Growth Factor-Induced c-FOS Transcripts. <i>Molecular and Cellular Biology</i> , 2015, 35, 468-478.	1.1	49
132	The RNA Exosome Syncs IAV-RNAPII Transcription to Promote Viral Ribogenesis and Infectivity. <i>Cell</i> , 2017, 169, 679-692.e14.	13.5	48
133	Influenza virus infection causes global RNAPII termination defects. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 885-893.	3.6	48
134	Differential genetic interactions of yeast stress response <scp>MAPK</scp> pathways. <i>Molecular Systems Biology</i> , 2015, 11, 800.	3.2	47
135	From Systems to Structure: Bridging Networks and Mechanism. <i>Molecular Cell</i> , 2013, 49, 222-231.	4.5	46
136	Structural basis of CD4 downregulation by HIV-1 Nef. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 822-828.	3.6	44
137	The Landscape of Human Cancer Proteins Targeted by SARS-CoV-2. <i>Cancer Discovery</i> , 2020, 10, 916-921.	7.7	44
138	Suppression of C9orf72 RNA repeat-induced neurotoxicity by the ALS-associated RNA-binding protein Zfp106. <i>ELife</i> , 2017, 6, .	2.8	44
139	Dynamic post-translational modification profiling of Mycobacterium tuberculosis-infected primary macrophages. <i>ELife</i> , 2020, 9, .	2.8	44
140	Regulation of Sufu activity by p66Î² and Mycbp provides new insight into vertebrate Hedgehog signaling. <i>Genes and Development</i> , 2014, 28, 2547-2563.	2.7	42
141	Lineage-Specific Viral Hijacking of Non-canonical E3Â‘Ubiquitin Ligase Cofactors in the Evolution of Vif Anti-APOBEC3 Activity. <i>Cell Reports</i> , 2015, 11, 1236-1250.	2.9	42
142	The Tyrosine Kinase Inhibitor Gefitinib Restricts <i>Mycobacterium tuberculosis</i> Growth through Increased Lysosomal Biogenesis and Modulation of Cytokine Signaling. <i>ACS Infectious Diseases</i> , 2017, 3, 564-574.	1.8	42
143	ARIH2 Is a Vif-Dependent Regulator of CUL5-Mediated APOBEC3G Degradation in HIV Infection. <i>Cell Host and Microbe</i> , 2019, 26, 86-99.e7.	5.1	42
144	A Herpesvirus Protein Selectively Inhibits Cellular mRNA Nuclear Export. <i>Cell Host and Microbe</i> , 2016, 20, 642-653.	5.1	40

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145	Smoothed transduces Hedgehog signals via activity-dependent sequestration of PKA catalytic subunits. <i>PLoS Biology</i> , 2021, 19, e3001191.	2.6	40
146	Conflicting and ambiguous names of overlapping ORFs in the SARS-CoV-2 genome: A homology-based resolution. <i>Virology</i> , 2021, 558, 145-151.	1.1	40
147	Transcription factor protein interactomes reveal genetic determinants in heart disease. <i>Cell</i> , 2022, 185, 794-814.e30.	13.5	39
148	Thioredoxin-related Protein 32 Is an Arsenite-regulated Thiol Reductase of the Proteasome 19 S Particle. <i>Journal of Biological Chemistry</i> , 2009, 284, 15233-15245.	1.6	38
149	Discovery and functional characterization of a neomorphic PTEN mutation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 13976-13981.	3.3	38
150	Adventures in time and space. <i>RNA Biology</i> , 2014, 11, 313-319.	1.5	37
151	Comparative mapping of hostâ€“pathogen proteinâ€“protein interactions. <i>Current Opinion in Microbiology</i> , 2015, 27, 62-68.	2.3	37
152	A protein network map of head and neck cancer reveals PIK3CA mutant drug sensitivity. <i>Science</i> , 2021, 374, eabf2911.	6.0	37
153	Systematic Triple-Mutant Analysis Uncovers Functional Connectivity between Pathways Involved in Chromosome Regulation. <i>Cell Reports</i> , 2013, 3, 2168-2178.	2.9	36
154	Endosomal cAMP production broadly impacts the cellular phosphoproteome. <i>Journal of Biological Chemistry</i> , 2021, 297, 100907.	1.6	36
155	Proteome Imbalance of Mitochondrial Electron Transport Chain in Brown Adipocytes Leads to Metabolic Benefits. <i>Cell Metabolism</i> , 2018, 27, 616-629.e4.	7.2	34
156	Sympathetic inputs regulate adaptive thermogenesis in brown adipose tissue through cAMP-Salt inducible kinase axis. <i>Scientific Reports</i> , 2018, 8, 11001.	1.6	33
157	Hybrid Gene Origination Creates Human-Virus Chimeric Proteins during Infection. <i>Cell</i> , 2020, 181, 1502-1517.e23.	13.5	33
158	Combined Action of Histone Reader Modules Regulates NuA4 Local Acetyltransferase Function but Not Its Recruitment on the Genome. <i>Molecular and Cellular Biology</i> , 2016, 36, 2768-2781.	1.1	32
159	Two Accessory Proteins Govern MmpL3 Mycolic Acid Transport in Mycobacteria. <i>MBio</i> , 2019, 10, .	1.8	32
160	Chemical Genetics of Rapamycin-Insensitive TORC2 in <i>S.Â cerevisiae</i> . <i>Cell Reports</i> , 2013, 5, 1725-1736.	2.9	31
161	Cross-talk Signaling between HER3 and HPV16 E6 and E7 Mediates Resistance to PI3K Inhibitors in Head and Neck Cancer. <i>Cancer Research</i> , 2018, 78, 2383-2395.	0.4	31
162	Non-degradative Ubiquitination of Protein Kinases. <i>PLoS Computational Biology</i> , 2016, 12, e1004898.	1.5	31

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163	G Protein–Coupled Receptor Endocytosis Confers Uniformity in Responses to Chemically Distinct Ligands. <i>Molecular Pharmacology</i> , 2017, 91, 145-156.	1.0	30
164	PJA2 ubiquitinates the HIV-1 Tat protein with atypical chain linkages to activate viral transcription. <i>Scientific Reports</i> , 2017, 7, 45394.	1.6	30
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