

Nevan J Krogan

List of Publications by Citations

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257
papers

28,918
citations

78
h-index

168
g-index

293
ext. papers

35,769
ext. citations

19.2
avg, IF

6.65
L-index

| # | Paper | IF | Citations |
|-----|--|------|-----------|
| 257 | Global landscape of protein complexes in the yeast <i>Saccharomyces cerevisiae</i> . <i>Nature</i> , 2006 , 440, 637-43 | 50.4 | 2327 |
| 256 | A SARS-CoV-2 protein interaction map reveals targets for drug repurposing. <i>Nature</i> , 2020 , 583, 459-468 | 50.4 | 2142 |
| 255 | Global mapping of the yeast genetic interaction network. <i>Science</i> , 2004 , 303, 808-13 | 33.3 | 1700 |
| 254 | Functional dissection of protein complexes involved in yeast chromosome biology using a genetic interaction map. <i>Nature</i> , 2007 , 446, 806-10 | 50.4 | 731 |
| 253 | Exploration of the function and organization of the yeast early secretory pathway through an epistatic miniarray profile. <i>Cell</i> , 2005 , 123, 507-19 | 56.2 | 706 |
| 252 | Meta- and Orthogonal Integration of Influenza "OMICs" Data Defines a Role for UBR4 in Virus Budding. <i>Cell Host and Microbe</i> , 2015 , 18, 723-35 | 23.4 | 647 |
| 251 | Navigating the chaperone network: an integrative map of physical and genetic interactions mediated by the hsp90 chaperone. <i>Cell</i> , 2005 , 120, 715-27 | 56.2 | 642 |
| 250 | Cotranscriptional set2 methylation of histone H3 lysine 36 recruits a repressive Rpd3 complex. <i>Cell</i> , 2005 , 123, 593-605 | 56.2 | 621 |
| 249 | Toward a comprehensive atlas of the physical interactome of <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Proteomics</i> , 2007 , 6, 439-50 | 7.6 | 610 |
| 248 | 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, 721-9 | 17.6 | 566 |
| 247 | Differential network biology. <i>Molecular Systems Biology</i> , 2012 , 8, 565 | 12.2 | 538 |
| 246 | 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, 4207-18 | 4.8 | 533 |
| 245 | Global landscape of HIV-human protein complexes. <i>Nature</i> , 2011 , 481, 365-70 | 50.4 | 507 |
| 244 | Phenotypic landscape of a bacterial cell. <i>Cell</i> , 2011 , 144, 143-56 | 56.2 | 484 |
| 243 | A Snf2 family ATPase complex required for recruitment of the histone H2A variant Htz1. <i>Molecular Cell</i> , 2003 , 12, 1565-76 | 17.6 | 471 |
| 242 | The Global Phosphorylation Landscape of SARS-CoV-2 Infection. <i>Cell</i> , 2020 , 182, 685-712.e19 | 56.2 | 439 |
| 241 | RNA polymerase II elongation factors of <i>Saccharomyces cerevisiae</i> : a targeted proteomics approach. <i>Molecular and Cellular Biology</i> , 2002 , 22, 6979-92 | 4.8 | 413 |

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| 240 | A phosphatase complex that dephosphorylates gammaH2AX regulates DNA damage checkpoint recovery. <i>Nature</i> , 2006 , 439, 497-501 | 50.4 | 387 |
| 239 | A comprehensive strategy enabling high-resolution functional analysis of the yeast genome. <i>Nature Methods</i> , 2008 , 5, 711-8 | 21.6 | 376 |
| 238 | Host cell factors in HIV replication: meta-analysis of genome-wide studies. <i>PLoS Pathogens</i> , 2009 , 5, e1000437 | 10.4 | 351 |
| 237 | Rewiring of genetic networks in response to DNA damage. <i>Science</i> , 2010 , 330, 1385-9 | 33.3 | 344 |
| 236 | SNX27 mediates retromer tubule entry and endosome-to-plasma membrane trafficking of signalling receptors. <i>Nature Cell Biology</i> , 2011 , 13, 715-21 | 23.4 | 340 |
| 235 | How many human proteoforms are there?. <i>Nature Chemical Biology</i> , 2018 , 14, 206-214 | 11.7 | 324 |
| 234 | High-definition macromolecular composition of yeast RNA-processing complexes. <i>Molecular Cell</i> , 2004 , 13, 225-39 | 17.6 | 321 |
| 233 | Inhibition of CRISPR-Cas9 with Bacteriophage Proteins. <i>Cell</i> , 2017 , 168, 150-158.e10 | 56.2 | 310 |
| 232 | Critical role of acetylation in tau-mediated neurodegeneration and cognitive deficits. <i>Nature Medicine</i> , 2015 , 21, 1154-62 | 50.5 | 300 |
| 231 | Systematic functional prioritization of protein posttranslational modifications. <i>Cell</i> , 2012 , 150, 413-25 | 56.2 | 296 |
| 230 | HIV-1 Tat and host AFF4 recruit two transcription elongation factors into a bifunctional complex for coordinated activation of HIV-1 transcription. <i>Molecular Cell</i> , 2010 , 38, 428-38 | 17.6 | 285 |
| 229 | Conservation and rewiring of functional modules revealed by an epistasis map in fission yeast. <i>Science</i> , 2008 , 322, 405-10 | 33.3 | 281 |
| 228 | CRISPR Interference Efficiently Induces Specific and Reversible Gene Silencing in Human iPSCs. <i>Cell Stem Cell</i> , 2016 , 18, 541-53 | 18 | 271 |
| 227 | Vif hijacks CBF- β to degrade APOBEC3G and promote HIV-1 infection. <i>Nature</i> , 2011 , 481, 371-5 | 50.4 | 268 |
| 226 | Comparative host-coronavirus protein interaction networks reveal pan-viral disease mechanisms. <i>Science</i> , 2020 , 370, | 33.3 | 261 |
| 225 | A strategy for extracting and analyzing large-scale quantitative epistatic interaction data. <i>Genome Biology</i> , 2006 , 7, R63 | 18.3 | 245 |
| 224 | The functional landscape of mouse gene expression. <i>Journal of Biology</i> , 2004 , 3, 21 | | 232 |
| 223 | Evolution and functional cross-talk of protein post-translational modifications. <i>Molecular Systems Biology</i> , 2013 , 9, 714 | 12.2 | 214 |

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| 222 | Functional organization of the <i>S. cerevisiae</i> phosphorylation network. <i>Cell</i> , 2009 , 136, 952-63 | 56.2 | 211 |
| 221 | An Approach to Spatiotemporally Resolve Protein Interaction Networks in Living Cells. <i>Cell</i> , 2017 , 169, 350-360.e12 | 56.2 | 209 |
| 220 | Combinatorial CRISPR-Cas9 screens for de novo mapping of genetic interactions. <i>Nature Methods</i> , 2017 , 14, 573-576 | 21.6 | 209 |
| 219 | 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, 735-46 | 17.6 | 205 |
| 218 | 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, 13513-8 | 11.5 | 202 |
| 217 | SARS-CoV-2 Orf6 hijacks Nup98 to block STAT nuclear import and antagonize interferon signaling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 28344-28354 | 11.5 | 201 |
| 216 | A genome-wide CRISPR screen identifies a restricted set of HIV host dependency factors. <i>Nature Genetics</i> , 2017 , 49, 193-203 | 36.3 | 197 |
| 215 | High-throughput, quantitative analyses of genetic interactions in <i>E. coli</i> . <i>Nature Methods</i> , 2008 , 5, 781-7 | 21.6 | 181 |
| 214 | Proteasome involvement in the repair of DNA double-strand breaks. <i>Molecular Cell</i> , 2004 , 16, 1027-34 | 17.6 | 178 |
| 213 | 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 | 17.6 | 175 |
| 212 | An ultrapotent synthetic nanobody neutralizes SARS-CoV-2 by stabilizing inactive Spike. <i>Science</i> , 2020 , 370, 1473-1479 | 33.3 | 166 |
| 211 | Evaluation of SARS-CoV-2 serology assays reveals a range of test performance. <i>Nature Biotechnology</i> , 2020 , 38, 1174-1183 | 44.5 | 166 |
| 210 | Genetic Screens Identify Host Factors for SARS-CoV-2 and Common Cold Coronaviruses. <i>Cell</i> , 2021 , 184, 106-119.e14 | 56.2 | 150 |
| 209 | Comparative Flavivirus-Host Protein Interaction Mapping Reveals Mechanisms of Dengue and Zika Virus Pathogenesis. <i>Cell</i> , 2018 , 175, 1931-1945.e18 | 56.2 | 148 |
| 208 | Hierarchical modularity and the evolution of genetic interactomes across species. <i>Molecular Cell</i> , 2012 , 46, 691-704 | 17.6 | 144 |
| 207 | A gene ontology inferred from molecular networks. <i>Nature Biotechnology</i> , 2013 , 31, 38-45 | 44.5 | 142 |
| 206 | A SARS-CoV-2-Human Protein-Protein Interaction Map Reveals Drug Targets and Potential Drug-Repurposing 2020 , | | 133 |
| 205 | Global mapping of herpesvirus-host protein complexes reveals a transcription strategy for late genes. <i>Molecular Cell</i> , 2015 , 57, 349-60 | 17.6 | 125 |

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| 204 | Global Mapping of the Inc-Human Interactome Reveals that Retromer Restricts Chlamydia Infection. <i>Cell Host and Microbe</i> , 2015 , 18, 109-21 | 23.4 | 124 |
| 203 | High-throughput genetic interaction mapping in the fission yeast <i>Schizosaccharomyces pombe</i> . <i>Nature Methods</i> , 2007 , 4, 861-6 | 21.6 | 120 |
| 202 | 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 | 10.6 | 118 |
| 201 | Plitidepsin has potent preclinical efficacy against SARS-CoV-2 by targeting the host protein eEF1A. <i>Science</i> , 2021 , 371, 926-931 | 33.3 | 117 |
| 200 | Functional maps of protein complexes from quantitative genetic interaction data. <i>PLoS Computational Biology</i> , 2008 , 4, e1000065 | 5 | 116 |
| 199 | The mTOR Complex Controls HIV Latency. <i>Cell Host and Microbe</i> , 2016 , 20, 785-797 | 23.4 | 115 |
| 198 | Quantitative genetic interactions reveal biological modularity. <i>Cell</i> , 2010 , 141, 739-45 | 56.2 | 113 |
| 197 | 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 | 10.6 | 110 |
| 196 | Genetic interaction mapping in mammalian cells using CRISPR interference. <i>Nature Methods</i> , 2017 , 14, 577-580 | 21.6 | 108 |
| 195 | Cross-species chemogenomic profiling reveals evolutionarily conserved drug mode of action. <i>Molecular Systems Biology</i> , 2010 , 6, 451 | 12.2 | 108 |
| 194 | The functional landscape of the human phosphoproteome. <i>Nature Biotechnology</i> , 2020 , 38, 365-373 | 44.5 | 106 |
| 193 | Functional overlap and regulatory links shape genetic interactions between signaling pathways. <i>Cell</i> , 2010 , 143, 991-1004 | 56.2 | 105 |
| 192 | From structure to systems: high-resolution, quantitative genetic analysis of RNA polymerase II. <i>Cell</i> , 2013 , 154, 775-88 | 56.2 | 102 |
| 191 | A lipid E-MAP identifies Ubx2 as a critical regulator of lipid saturation and lipid bilayer stress. <i>Molecular Cell</i> , 2013 , 51, 519-30 | 17.6 | 100 |
| 190 | The Dengue Virus NS5 Protein Intrudes in the Cellular Spliceosome and Modulates Splicing. <i>PLoS Pathogens</i> , 2016 , 12, e1005841 | 7.6 | 100 |
| 189 | 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 | 7.6 | 94 |
| 188 | A combined proteomics/genomics approach links hepatitis C virus infection with nonsense-mediated mRNA decay. <i>Molecular Cell</i> , 2015 , 57, 329-340 | 17.6 | 93 |
| 187 | First-in-class small molecule inhibitors of the single-strand DNA cytosine deaminase APOBEC3G. <i>ACS Chemical Biology</i> , 2012 , 7, 506-17 | 4.9 | 90 |

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| 186 | The cancer cell map initiative: defining the hallmark networks of cancer. <i>Molecular Cell</i> , 2015 , 58, 690-8 | 17.6 | 89 |
| 185 | CBF β stabilizes HIV Vif to counteract APOBEC3 at the expense of RUNX1 target gene expression. <i>Molecular Cell</i> , 2013 , 49, 632-44 | 17.6 | 87 |
| 184 | Centriolar satellites assemble centrosomal microcephaly proteins to recruit CDK2 and promote centriole duplication. <i>ELife</i> , 2015 , 4, | 8.9 | 85 |
| 183 | Quantitative genetic-interaction mapping in mammalian cells. <i>Nature Methods</i> , 2013 , 10, 432-7 | 21.6 | 84 |
| 182 | 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 | 13.9 | 82 |
| 181 | Targeting Viral Proteostasis Limits Influenza Virus, HIV, and Dengue Virus Infection. <i>Immunity</i> , 2016 , 44, 46-58 | 32.3 | 81 |
| 180 | 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, 901-8 | 17.6 | 79 |
| 179 | Quantitative genetic interaction mapping using the E-MAP approach. <i>Methods in Enzymology</i> , 2010 , 470, 205-31 | 1.7 | 72 |
| 178 | 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 | 56.2 | 69 |
| 177 | An acetylated form of histone H2A.Z regulates chromosome architecture in <i>Schizosaccharomyces pombe</i> . <i>Nature Structural and Molecular Biology</i> , 2009 , 16, 1286-93 | 17.6 | 68 |
| 176 | SIRT1 Deacetylates Tau and Reduces Pathogenic Tau Spread in a Mouse Model of Tauopathy. <i>Journal of Neuroscience</i> , 2018 , 38, 3680-3688 | 6.6 | 66 |
| 175 | High-resolution network biology: connecting sequence with function. <i>Nature Reviews Genetics</i> , 2013 , 14, 865-79 | 30.1 | 65 |
| 174 | The H3K36me2 Methyltransferase Nsd1 Demarcates PRC2-Mediated H3K27me2 and H3K27me3 Domains in Embryonic Stem Cells. <i>Molecular Cell</i> , 2018 , 70, 371-379.e5 | 17.6 | 64 |
| 173 | Drug-induced phospholipidosis confounds drug repurposing for SARS-CoV-2. <i>Science</i> , 2021 , 373, 541-547 | 33.3 | 64 |
| 172 | Protein Interaction Mapping Identifies RBBP6 as a Negative Regulator of Ebola Virus Replication. <i>Cell</i> , 2018 , 175, 1917-1930.e13 | 56.2 | 62 |
| 171 | Yeast SREBP cleavage activation requires the Golgi Dsc E3 ligase complex. <i>Molecular Cell</i> , 2011 , 42, 160-171 | 17.6 | 60 |
| 170 | Evolution of enhanced innate immune evasion by the SARS-CoV-2 B.1.1.7 UK variant 2021 , | | 60 |
| 169 | CRISPR-Cas9 genome engineering of primary CD4 T cells for the interrogation of HIV-host factor interactions. <i>Nature Protocols</i> , 2019 , 14, 1-27 | 18.8 | 58 |

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| 168 | Anti-CRISPR-Associated Proteins Are Crucial Repressors of Anti-CRISPR Transcription. <i>Cell</i> , 2019 , 178, 1452-1464.e13 | 56.2 | 56 |
| 167 | Metabolic reprogramming of human CD8 memory T cells through loss of SIRT1. <i>Journal of Experimental Medicine</i> , 2018 , 215, 51-62 | 16.6 | 56 |
| 166 | Evolutionary Proteomics Uncovers Ancient Associations of Cilia with Signaling Pathways. <i>Developmental Cell</i> , 2017 , 43, 744-762.e11 | 10.2 | 55 |
| 165 | SMYD2-Mediated Histone Methylation Contributes to HIV-1 Latency. <i>Cell Host and Microbe</i> , 2017 , 21, 569-579.e6 | 23.4 | 54 |
| 164 | Large dataset enables prediction of repair after CRISPR-Cas9 editing in primary T cells. <i>Nature Biotechnology</i> , 2019 , 37, 1034-1037 | 44.5 | 52 |
| 163 | Cullin E3 ligases and their rewiring by viral factors. <i>Biomolecules</i> , 2014 , 4, 897-930 | 5.9 | 52 |
| 162 | A BAG3 chaperone complex maintains cardiomyocyte function during proteotoxic stress. <i>JCI Insight</i> , 2017 , 2, | 9.9 | 52 |
| 161 | The Host E3-Ubiquitin Ligase TRIM6 Ubiquitinates the Ebola Virus VP35 Protein and Promotes Virus Replication. <i>Journal of Virology</i> , 2017 , 91, | 6.6 | 51 |
| 160 | Genome-wide association data reveal a global map of genetic interactions among protein complexes. <i>PLoS Genetics</i> , 2009 , 5, e1000782 | 6 | 51 |
| 159 | Inhibition of a NEDD8 Cascade Restores Restriction of HIV by APOBEC3G. <i>PLoS Pathogens</i> , 2012 , 8, e1002085 | 7.085 | 50 |
| 158 | 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 | 17.6 | 48 |
| 157 | interfere with an interaction between the mannose-6-phosphate receptor and sorting nexins to counteract host restriction. <i>ELife</i> , 2017 , 6, | 8.9 | 48 |
| 156 | Translation of Genotype to Phenotype by a Hierarchy of Cell Subsystems. <i>Cell Systems</i> , 2016 , 2, 77-88 | 10.6 | 47 |
| 155 | The Cellular NMD Pathway Restricts Zika Virus Infection and Is Targeted by the Viral Capsid Protein. <i>MBio</i> , 2018 , 9, | 7.8 | 47 |
| 154 | Purification and characterization of HIV-human protein complexes. <i>Methods</i> , 2011 , 53, 13-9 | 4.6 | 46 |
| 153 | A systems approach to infectious disease. <i>Nature Reviews Genetics</i> , 2020 , 21, 339-354 | 30.1 | 44 |
| 152 | Mutations in the X-linked cause a glycosylation disorder with autophagic defects. <i>Journal of Experimental Medicine</i> , 2017 , 214, 3707-3729 | 16.6 | 43 |
| 151 | A chaperone-assisted degradation pathway targets kinetochore proteins to ensure genome stability. <i>PLoS Genetics</i> , 2014 , 10, e1004140 | 6 | 43 |

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| 150 | Multiple Routes to Oncogenesis Are Promoted by the Human Papillomavirus-Host Protein Network. <i>Cancer Discovery</i> , 2018 , 8, 1474-1489 | 24.4 | 43 |
| 149 | UNC93B1 recruits syntenin-1 to dampen TLR7 signalling and prevent autoimmunity. <i>Nature</i> , 2019 , 575, 366-370 | 50.4 | 42 |
| 148 | Acetylome profiling reveals overlap in the regulation of diverse processes by sirtuins, gcn5, and esa1. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 162-76 | 7.6 | 42 |
| 147 | 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 | 4.1 | 42 |
| 146 | Chaperone-mediated autophagy prevents collapse of the neuronal metastable proteome. <i>Cell</i> , 2021 , 184, 2696-2714.e25 | 56.2 | 40 |
| 145 | Cyclin-dependent kinase 12 increases 3' end processing of growth factor-induced c-FOS transcripts. <i>Molecular and Cellular Biology</i> , 2015 , 35, 468-78 | 4.8 | 39 |
| 144 | Lineage-Specific Viral Hijacking of Non-canonical E3 Ubiquitin Ligase Cofactors in the Evolution of Vif Anti-APOBEC3 Activity. <i>Cell Reports</i> , 2015 , 11, 1236-50 | 10.6 | 38 |
| 143 | Scoring Large-Scale Affinity Purification Mass Spectrometry Datasets with MiST. <i>Current Protocols in Bioinformatics</i> , 2015 , 49, 8.19.1-8.19.16 | 24.2 | 38 |
| 142 | The RNA Exosome Syncs IAV-RNAPII Transcription to Promote Viral Ribogenesis and Infectivity. <i>Cell</i> , 2017 , 169, 679-692.e14 | 56.2 | 35 |
| 141 | Identification of antiviral roles for the exon-junction complex and nonsense-mediated decay in flaviviral infection. <i>Nature Microbiology</i> , 2019 , 4, 985-995 | 26.6 | 34 |
| 140 | CDK11 in TREX/THOC Regulates HIV mRNA 3' End Processing. <i>Cell Host and Microbe</i> , 2015 , 18, 560-70 | 23.4 | 34 |
| 139 | Regulation of Sufu activity by p66 and MycBP provides new insight into vertebrate Hedgehog signaling. <i>Genes and Development</i> , 2014 , 28, 2547-63 | 12.6 | 33 |
| 138 | Replication fork collapse and genome instability in a deoxycytidylate deaminase mutant. <i>Molecular and Cellular Biology</i> , 2012 , 32, 4445-54 | 4.8 | 33 |
| 137 | Cyclophilin A Prevents HIV-1 Restriction in Lymphocytes by Blocking Human TRIM5 Binding to the Viral Core. <i>Cell Reports</i> , 2020 , 30, 3766-3777.e6 | 10.6 | 32 |
| 136 | Systematic triple-mutant analysis uncovers functional connectivity between pathways involved in chromosome regulation. <i>Cell Reports</i> , 2013 , 3, 2168-78 | 10.6 | 32 |
| 135 | Enterovirus pathogenesis requires the host methyltransferase SETD3. <i>Nature Microbiology</i> , 2019 , 4, 2523-2537 | 32 | |
| 134 | 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, 13976-81 | 11.5 | 31 |
| 133 | Differential genetic interactions of yeast stress response MAPK pathways. <i>Molecular Systems Biology</i> , 2015 , 11, 800 | 12.2 | 31 |

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|-----|--|------|----|
| 132 | Envelope protein ubiquitination drives entry and pathogenesis of Zika virus. <i>Nature</i> , 2020 , 585, 414-419 | 50.4 | 31 |
| 131 | Thioredoxin-related Protein 32 is an arsenite-regulated Thiol Reductase of the proteasome 19 S particle. <i>Journal of Biological Chemistry</i> , 2009 , 284, 15233-45 | 5.4 | 31 |
| 130 | From systems to structure: bridging networks and mechanism. <i>Molecular Cell</i> , 2013 , 49, 222-31 | 17.6 | 30 |
| 129 | Mass spectrometry-based protein-protein interaction networks for the study of human diseases. <i>Molecular Systems Biology</i> , 2021 , 17, e8792 | 12.2 | 30 |
| 128 | Evolution of enhanced innate immune evasion by SARS-CoV-2.. <i>Nature</i> , 2021 , | 50.4 | 30 |
| 127 | Adventures in time and space: splicing efficiency and RNA polymerase II elongation rate. <i>RNA Biology</i> , 2014 , 11, 313-9 | 4.8 | 29 |
| 126 | Suppression of RNA repeat-induced neurotoxicity by the ALS-associated RNA-binding protein Zfp106. <i>ELife</i> , 2017 , 6, | 8.9 | 29 |
| 125 | Comparative mapping of host-pathogen protein-protein interactions. <i>Current Opinion in Microbiology</i> , 2015 , 27, 62-8 | 7.9 | 28 |
| 124 | Mutations in ANKLE2, a ZIKA Virus Target, Disrupt an Asymmetric Cell Division Pathway in Drosophila Neuroblasts to Cause Microcephaly. <i>Developmental Cell</i> , 2019 , 51, 713-729.e6 | 10.2 | 28 |
| 123 | Chemical genetics of rapamycin-insensitive TORC2 in <i>S. cerevisiae</i> . <i>Cell Reports</i> , 2013 , 5, 1725-36 | 10.6 | 27 |
| 122 | Systematic Identification of Host Cell Regulators of Legionella pneumophila Pathogenesis Using a Genome-wide CRISPR Screen. <i>Cell Host and Microbe</i> , 2019 , 26, 551-563.e6 | 23.4 | 26 |
| 121 | The Tyrosine Kinase Inhibitor Gefitinib Restricts Mycobacterium tuberculosis Growth through Increased Lysosomal Biogenesis and Modulation of Cytokine Signaling. <i>ACS Infectious Diseases</i> , 2017 , 3, 564-574 | 5.5 | 25 |
| 120 | The Landscape of Human Cancer Proteins Targeted by SARS-CoV-2. <i>Cancer Discovery</i> , 2020 , 10, 916-921 | 24.4 | 25 |
| 119 | Dynamic post-translational modification profiling of -infected primary macrophages. <i>ELife</i> , 2020 , 9, | 8.9 | 25 |
| 118 | G Protein-Coupled Receptor Endocytosis Confers Uniformity in Responses to Chemically Distinct Ligands. <i>Molecular Pharmacology</i> , 2017 , 91, 145-156 | 4.3 | 24 |
| 117 | Influenza virus infection causes global RNAPII termination defects. <i>Nature Structural and Molecular Biology</i> , 2018 , 25, 885-893 | 17.6 | 24 |
| 116 | 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 | 23.4 | 23 |
| 115 | Set5 and Set1 cooperate to repress gene expression at telomeres and retrotransposons. <i>Epigenetics</i> , 2014 , 9, 513-22 | 5.7 | 23 |

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|-----|--|------|----|
| 114 | A Pil1-Sle1-Syj1-Tax4 functional pathway links eisosomes with PI(4,5)P2 regulation. <i>Journal of Cell Science</i> , 2014 , 127, 1318-26 | 5.3 | 23 |
| 113 | Mutations in SARS-CoV-2 variants of concern link to increased spike cleavage and virus transmission.. <i>Cell Host and Microbe</i> , 2022 , | 23.4 | 23 |
| 112 | Non-degradative Ubiquitination of Protein Kinases. <i>PLoS Computational Biology</i> , 2016 , 12, e1004898 | 5 | 23 |
| 111 | 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 | 24.3 | 22 |
| 110 | Proteome Imbalance of Mitochondrial Electron Transport Chain in Brown Adipocytes Leads to Metabolic Benefits. <i>Cell Metabolism</i> , 2018 , 27, 616-629.e4 | 24.6 | 22 |
| 109 | A Herpesvirus Protein Selectively Inhibits Cellular mRNA Nuclear Export. <i>Cell Host and Microbe</i> , 2016 , 20, 642-653 | 23.4 | 22 |
| 108 | SIRT3 controls brown fat thermogenesis by deacetylation regulation of pathways upstream of UCP1. <i>Molecular Metabolism</i> , 2019 , 25, 35-49 | 8.8 | 21 |
| 107 | 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 | 4.8 | 21 |
| 106 | SUMO is a pervasive regulator of meiosis. <i>ELife</i> , 2021 , 10, | 8.9 | 21 |
| 105 | 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 | 10.1 | 20 |
| 104 | An ultra-potent synthetic nanobody neutralizes SARS-CoV-2 by locking Spike into an inactive conformation 2020 , | | 20 |
| 103 | The AMBRA1 E3 ligase adaptor regulates the stability of cyclinD. <i>Nature</i> , 2021 , 592, 794-798 | 50.4 | 20 |
| 102 | Two Accessory Proteins Govern MmpL3 Mycolic Acid Transport in Mycobacteria. <i>MBio</i> , 2019 , 10, | 7.8 | 19 |
| 101 | Hybrid Gene Origination Creates Human-Virus Chimeric Proteins during Infection. <i>Cell</i> , 2020 , 181, 1502-1517.e23 | 56.7 | 23 |
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