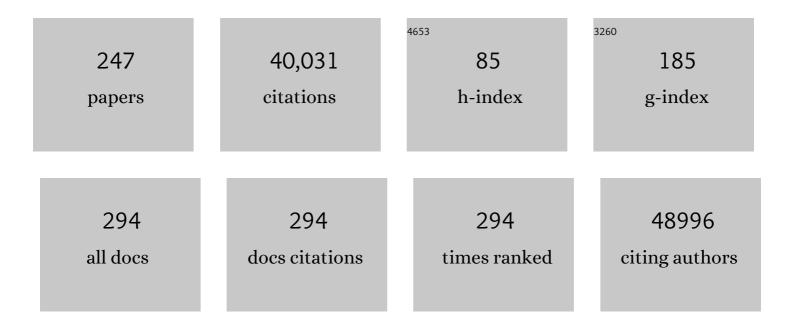
List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/9528101/publications.pdf Version: 2024-02-01



| # | Article | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Integrative structure determination of histones H3 and H4 using genetic interactions. FEBS Journal, 2023, 290, 2565-2575. | 2.2 | 0 |
| 2 | Preclinical and randomized phase I studies of plitidepsin in adults hospitalized with COVID-19. Life Science Alliance, 2022, 5, e202101200. | 1.3 | 26 |
| 3 | Comparative Analysis of T-Cell Spatial Proteomics and the Influence of HIV Expression. Molecular and Cellular Proteomics, 2022, 21, 100194. | 2.5 | 2 |
| 4 | Mutations in SARS-CoV-2 variants of concern link to increased spike cleavage and virus transmission. Cell Host and Microbe, 2022, 30, 373-387.e7. | 5.1 | 138 |
| 5 | From systems to structure — using genetic data to model protein structures. Nature Reviews Genetics, 2022, 23, 342-354. | 7.7 | 14 |
| 6 | Tau interactome maps synaptic and mitochondrial processes associated with neurodegeneration. Cell, 2022, 185, 712-728.e14. | 13.5 | 114 |
| 7 | The RNA helicase DHX16 recognizes specific viral RNA to trigger RIG-I-dependent innate antiviral immunity. Cell Reports, 2022, 38, 110434. | 2.9 | 16 |
| 8 | Transcription factor protein interactomes reveal genetic determinants in heart disease. Cell, 2022, 185, 794-814.e30. | 13.5 | 39 |
| 9 | The E3 ligase TRIM1 ubiquitinates LRRK2 and controls its localization, degradation, and toxicity. Journal of Cell Biology, 2022, 221, . | 2.3 | 8 |
| 10 | A functional map of HIV-host interactions in primary human T cells. Nature Communications, 2022, 13, 1752. | 5.8 | 27 |
| 11 | Leveraging modeling and simulation to optimize the therapeutic window for epigenetic modifier drugs. , 2022, 235, 108162. | | 5 |
| 12 | Evolution of enhanced innate immune evasion by SARS-CoV-2. Nature, 2022, 602, 487-495. | 13.7 | 237 |
| 13 | A Whole-Genome CRISPR Screen Identifies AHR Loss as a Mechanism of Resistance to a PARP7 Inhibitor. Molecular Cancer Therapeutics, 2022, 21, 1076-1089. | 1.9 | 8 |
| 14 | Global post-translational modification profiling of HIV-1-infected cells reveals mechanisms of host cellular pathway remodeling. Cell Reports, 2022, 39, 110690. | 2.9 | 12 |
| 15 | Meningioma DNA methylation groups identify biological drivers and therapeutic vulnerabilities. Nature Genetics, 2022, 54, 649-659. | 9.4 | 93 |
| 16 | Workshop-based learning and networking: a scalable model for research capacity strengthening in low- and middle-income countries. Global Health Action, 2022, 15, . | 0.7 | 0 |
| 17 | DLX1 and the NuRD complex cooperate in enhancer decommissioning and transcriptional repression. Development (Cambridge), 2022, 149, . | 1.2 | 6 |
| 18 | Viral E protein neutralizes BET protein-mediated post-entry antagonism of SARS-CoV-2. Cell Reports, 2022, 40, 111088. | 2.9 | 15 |

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| 19 | Genetic Screens Identify Host Factors for SARS-CoV-2 and Common Cold Coronaviruses. Cell, 2021, 184, 106-119.e14. | 13.5 | 320 |
| 20 | Proteomic Approaches to Study SARS-CoV-2 Biology and COVID-19 Pathology. Journal of Proteome Research, 2021, 20, 1133-1152. | 1.8 | 27 |
| 21 | Mass spectrometryâ€based protein–protein interaction networks for the study of human diseases. Molecular Systems Biology, 2021, 17, e8792. | 3.2 | 96 |
| 22 | Characterization of an A3G-VifHIV-1-CRL5-CBFβ Structure Using a Cross-linking Mass Spectrometry Pipeline for Integrative Modeling of Host–Pathogen Complexes. Molecular and Cellular Proteomics, 2021, 20, 100132. | 2.5 | 4 |
| 23 | Plitidepsin has potent preclinical efficacy against SARS-CoV-2 by targeting the host protein eEF1A. Science, 2021, 371, 926-931. | 6.0 | 247 |
| 24 | Smoothened transduces Hedgehog signals via activity-dependent sequestration of PKA catalytic subunits. PLoS Biology, 2021, 19, e3001191. | 2.6 | 40 |
| 25 | Creating collaboration by breaking down scientific barriers. Cell, 2021, 184, 2271-2275. | 13.5 | 7 |
| 26 | The AMBRA1 E3 ligase adaptor regulates the stability of cyclinÂD. Nature, 2021, 592, 794-798. | 13.7 | 76 |
| 27 | Chaperone-mediated autophagy prevents collapse of the neuronal metastable proteome. Cell, 2021, 184, 2696-2714.e25. | 13.5 | 151 |
| 28 | Chemical-genetic interrogation of RNA polymerase mutants reveals structure-function relationships and physiological tradeoffs. Molecular Cell, 2021, 81, 2201-2215.e9. | 4.5 | 10 |
| 29 | Efficient generation of isogenic primary human myeloid cells using CRISPR-Cas9 ribonucleoproteins. Cell Reports, 2021, 35, 109105. | 2.9 | 29 |
| 30 | Conflicting and ambiguous names of overlapping ORFs in the SARS-CoV-2 genome: A homology-based resolution. Virology, 2021, 558, 145-151. | 1.1 | 40 |
| 31 | Drug-induced phospholipidosis confounds drug repurposing for SARS-CoV-2. Science, 2021, 373, 541-547. | 6.0 | 148 |
| 32 | Adhesion-mediated mechanosignaling forces mitohormesis. Cell Metabolism, 2021, 33, 1322-1341.e13. | 7.2 | 65 |
| 33 | Endosomal cAMP production broadly impacts the cellular phosphoproteome. Journal of Biological Chemistry, 2021, 297, 100907. | 1.6 | 36 |
| 34 | A ciliopathy complex builds distal appendages to initiate ciliogenesis. Journal of Cell Biology, 2021, 220, . | 2.3 | 26 |
| 35 | 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 |
| 36 | Nonâ€canonical prolineâ€tyrosine interactions with multiple host proteins regulate Ebola virus infection. EMBO Journal, 2021, 40, e105658. | 3.5 | 8 |

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| 37 | Restriction factor compendium for influenza A virus reveals a mechanism for evasion of autophagy. Nature Microbiology, 2021, 6, 1319-1333. | 5.9 | 23 |
| 38 | Caveolin-1 and Sox-2 are predictive biomarkers of cetuximab response in head and neck cancer. JCI Insight, 2021, 6, . | 2.3 | 10 |
| 39 | Target Discovery for Host-Directed Antiviral Therapies: Application of Proteomics Approaches. MSystems, 2021, 6, e0038821. | 1.7 | 10 |
| 40 | Brown adipocyte ATF4 activation improves thermoregulation and systemic metabolism. Cell Reports, 2021, 36, 109742. | 2.9 | 15 |
| 41 | A protein network map of head and neck cancer reveals PIK3CA mutant drug sensitivity. Science, 2021, 374, eabf2911. | 6.0 | 37 |
| 42 | A protein interaction landscape of breast cancer. Science, 2021, 374, eabf3066. | 6.0 | 66 |
| 43 | Interpretation of cancer mutations using a multiscale map of protein systems. Science, 2021, 374, eabf3067. | 6.0 | 29 |
| 44 | SUMO is a pervasive regulator of meiosis. ELife, 2021, 10, . | 2.8 | 50 |
| 45 | Systems-level effects of allosteric perturbations to a model molecular switch. Nature, 2021, 599, 152-157. | 13.7 | 13 |
| 46 | Therapeutic implications of activating noncanonical PIK3CA mutations in head and neck squamous cell carcinoma. Journal of Clinical Investigation, 2021, 131, . | 3.9 | 20 |
| 47 | The functional landscape of the human phosphoproteome. Nature Biotechnology, 2020, 38, 365-373. | 9.4 | 273 |
| 48 | Comparative host-coronavirus protein interaction networks reveal pan-viral disease mechanisms. Science, 2020, 370, . | 6.0 | 508 |
| 49 | Structural basis of CD4 downregulation by HIV-1 Nef. Nature Structural and Molecular Biology, 2020, 27, 822-828. | 3.6 | 44 |
| 50 | 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 |
| 51 | The E3 Ubiquitin-Protein Ligase Cullin 3 Regulates HIV-1 Transcription. Cells, 2020, 9, 2010. | 1.8 | 5 |
| 52 | Evaluation of SARS-CoV-2 serology assays reveals a range of test performance. Nature Biotechnology, 2020, 38, 1174-1183. | 9.4 | 251 |
| 53 | Genetic interaction mapping informs integrative structure determination of protein complexes. Science, 2020, 370, . | 6.0 | 24 |
| 54 | An ultrapotent synthetic nanobody neutralizes SARS-CoV-2 by stabilizing inactive Spike. Science, 2020, 370, 1473-1479. | 6.0 | 336 |

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| 55 | mRNA display with library of even-distribution reveals cellular interactors of influenza virus NS1. Nature Communications, 2020, 11, 2449. | 5.8 | 8 |
| 56 | Hybrid Gene Origination Creates Human-Virus Chimeric Proteins during Infection. Cell, 2020, 181, 1502-1517.e23. | 13.5 | 33 |
| 57 | Unbiased Proteomic Profiling Uncovers a Targetable GNAS/PKA/PP2A Axis in Small Cell Lung Cancer Stem Cells. Cancer Cell, 2020, 38, 129-143.e7. | 7.7 | 57 |
| 58 | Cyclophilin A Prevents HIV-1 Restriction in Lymphocytes by Blocking Human TRIM5α Binding to the Viral Core. Cell Reports, 2020, 30, 3766-3777.e6. | 2.9 | 68 |
| 59 | The Global Phosphorylation Landscape of SARS-CoV-2 Infection. Cell, 2020, 182, 685-712.e19. | 13.5 | 825 |
| 60 | A SARS-CoV-2 protein interaction map reveals targets for drug repurposing. Nature, 2020, 583, 459-468. | 13.7 | 3,542 |
| 61 | Envelope protein ubiquitination drives entry and pathogenesis of Zika virus. Nature, 2020, 585, 414-419. | 13.7 | 82 |
| 62 | The kinase Isr1 negatively regulates hexosamine biosynthesis in S. cerevisiae. PLoS Genetics, 2020, 16, e1008840. | 1.5 | 3 |
| 63 | A Quantitative Genetic Interaction Map of HIV Infection. Molecular Cell, 2020, 78, 197-209.e7. | 4.5 | 17 |
| 64 | A systems approach to infectious disease. Nature Reviews Genetics, 2020, 21, 339-354. | 7.7 | 72 |
| 65 | The Landscape of Human Cancer Proteins Targeted by SARS-CoV-2. Cancer Discovery, 2020, 10, 916-921. | 7.7 | 44 |
| 66 | Dynamic post-translational modification profiling of Mycobacterium tuberculosis-infected primary macrophages. ELife, 2020, 9, . | 2.8 | 44 |
| 67 | The kinase Isr1 negatively regulates hexosamine biosynthesis in S. cerevisiae. , 2020, 16, e1008840. | | 0 |
| 68 | The kinase Isr1 negatively regulates hexosamine biosynthesis in S. cerevisiae. , 2020, 16, e1008840. | | 0 |
| 69 | The kinase Isr1 negatively regulates hexosamine biosynthesis in S. cerevisiae. , 2020, 16, e1008840. | | 0 |
| 70 | The kinase Isr1 negatively regulates hexosamine biosynthesis in S. cerevisiae. , 2020, 16, e1008840. | | 0 |
| 71 | Large dataset enables prediction of repair after CRISPR–Cas9 editing in primary T cells. Nature Biotechnology, 2019, 37, 1034-1037. | 9.4 | 87 |
| 72 | PEAK3/C19orf35 pseudokinase, a new NFK3 kinase family member, inhibits CrkII through dimerization. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 15495-15504. | 3.3 | 19 |

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| 73 | ARIH2 Is a Vif-Dependent Regulator of CUL5-Mediated APOBEC3G Degradation in HIV Infection. Cell Host and Microbe, 2019, 26, 86-99.e7. | 5.1 | 42 |
| 74 | Mapping the protein–protein and genetic interactions of cancer to guide precision medicine. Current Opinion in Genetics and Development, 2019, 54, 110-117. | 1.5 | 15 |
| 75 | UNC93B1 recruits syntenin-1 to dampen TLR7 signalling and prevent autoimmunity. Nature, 2019, 575, 366-370. | 13.7 | 78 |
| 76 | Mapping genetic interactions in cancer: a road to rational combination therapies. Genome Medicine, 2019, 11, 62. | 3.6 | 16 |
| 77 | Synthetic Essentiality of Metabolic Regulator PDHK1 in PTEN-Deficient Cells and Cancers. Cell Reports, 2019, 28, 2317-2330.e8. | 2.9 | 12 |
| 78 | Anti-CRISPR-Associated Proteins Are Crucial Repressors of Anti-CRISPR Transcription. Cell, 2019, 178, 1452-1464.e13. | 13.5 | 105 |
| 79 | Regulation of Skn7-dependent, oxidative stress-induced genes by the RNA polymerase II-CTD phosphatase, Fcp1, and Mediator kinase subunit, Cdk8, in yeast. Journal of Biological Chemistry, 2019, 294, 16080-16094. | 1.6 | 9 |
| 80 | Systematic Identification of Host Cell Regulators of Legionella pneumophila Pathogenesis Using a Genome-wide CRISPR Screen. Cell Host and Microbe, 2019, 26, 551-563.e6. | 5.1 | 62 |
| 81 | Two Accessory Proteins Govern MmpL3 Mycolic Acid Transport in Mycobacteria. MBio, 2019, 10, . | 1.8 | 32 |
| 82 | Heart failure drug proscillaridin A targets MYC overexpressing leukemia through global loss of lysine acetylation. Journal of Experimental and Clinical Cancer Research, 2019, 38, 251. | 3.5 | 27 |
| 83 | SIRT3 controls brown fat thermogenesis by deacetylation regulation of pathways upstream of UCP1. Molecular Metabolism, 2019, 25, 35-49. | 3.0 | 30 |
| 84 | Identification of antiviral roles for the exon–junction complex and nonsense-mediated decay in flaviviral infection. Nature Microbiology, 2019, 4, 985-995. | 5.9 | 52 |
| 85 | 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 |
| 86 | Enterovirus pathogenesis requires the host methyltransferase SETD3. Nature Microbiology, 2019, 4, 2523-2537. | 5.9 | 51 |
| 87 | Virus and host interactions critical for filoviral RNA synthesis as therapeutic targets. Antiviral Research, 2019, 162, 90-100. | 1.9 | 12 |
| 88 | CRISPR–Cas9 genome engineering of primary CD4+ T cells for the interrogation of HIV–host factor interactions. Nature Protocols, 2019, 14, 1-27. | 5.5 | 98 |
| 89 | TCO, a Putative Transcriptional Regulator in Arabidopsis, Is a Target of the Protein Kinase CK2. International Journal of Molecular Sciences, 2019, 20, 99. | 1.8 | 0 |
| 90 | Proteome Imbalance of Mitochondrial Electron Transport Chain in Brown Adipocytes Leads to Metabolic Benefits. Cell Metabolism, 2018, 27, 616-629.e4. | 7.2 | 34 |

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| 91 | SMARCA2-regulated host cell factors are required for MxA restriction of influenza A viruses. Scientific Reports, 2018, 8, 2092. | 1.6 | 12 |
| 92 | How many human proteoforms are there?. Nature Chemical Biology, 2018, 14, 206-214. | 3.9 | 580 |
| 93 | Cross-talk Signaling between HER3 and HPV16 E6 and E7 Mediates Resistance to PI3K Inhibitors in Head and Neck Cancer. Cancer Research, 2018, 78, 2383-2395. | 0.4 | 31 |
| 94 | DNA Preparation from Schizosaccharomyces pombe. Cold Spring Harbor Protocols, 2018, 2018, pdb.prot091959. | 0.2 | 2 |
| 95 | The H3K36me2 Methyltransferase Nsd1 Demarcates PRC2-Mediated H3K27me2 and H3K27me3 Domains in Embryonic Stem Cells. Molecular Cell, 2018, 70, 371-379.e5. | 4.5 | 137 |
| 96 | Genetic Interaction Mapping in <i>Schizosaccharomyces pombe</i> Using the Pombe Epistasis Mapper (PEM) System and a ROTOR HDA Colony Replicating Robot in a 1536 Array Format. Cold Spring Harbor Protocols, 2018, 2018, pdb.prot091975. | 0.2 | 4 |
| 97 | SIRT1 Deacetylates Tau and Reduces Pathogenic Tau Spread in a Mouse Model of Tauopathy. Journal of Neuroscience, 2018, 38, 3680-3688. | 1.7 | 98 |
| 98 | High-Throughput Quantitative Genetic Interaction Mapping in the Fission YeastSchizosaccharomyces pombe. Cold Spring Harbor Protocols, 2018, 2018, pdb.top079905. | 0.2 | 5 |
| 99 | Metabolic reprogramming of human CD8+ memory T cells through loss of SIRT1. Journal of Experimental Medicine, 2018, 215, 51-62. | 4.2 | 91 |
| 100 | Protein Moonlighting Revealed by Noncatalytic Phenotypes of Yeast Enzymes. Genetics, 2018, 208, 419-431. | 1.2 | 28 |
| 101 | Genetic Interaction Score (S-Score) Calculation, Clustering, and Visualization of Genetic Interaction Profiles for Yeast. Cold Spring Harbor Protocols, 2018, 2018, pdb.prot091983. | 0.2 | 3 |
| 102 | Transformation of Schizosaccharomyces pombe in a 96-Well Format. Cold Spring Harbor Protocols, 2018, 2018, pdb.prot091942. | 0.2 | 1 |
| 103 | The Cellular NMD Pathway Restricts Zika Virus Infection and Is Targeted by the Viral Capsid Protein. MBio, 2018, 9, . | 1.8 | 60 |
| 104 | Protein Interaction Mapping Identifies RBBP6 as a Negative Regulator of Ebola Virus Replication. Cell, 2018, 175, 1917-1930.e13. | 13.5 | 108 |
| 105 | Comparative Flavivirus-Host Protein Interaction Mapping Reveals Mechanisms of Dengue and Zika Virus Pathogenesis. Cell, 2018, 175, 1931-1945.e18. | 13.5 | 252 |
| 106 | The Yeast DNA Damage Checkpoint Kinase Rad53 Targets the Exoribonuclease, Xrn1. G3: Genes, Genomes, Genetics, 2018, 8, 3931-3944. | 0.8 | 21 |
| 107 | Multiple Routes to Oncogenesis Are Promoted by the Human Papillomavirus–Host Protein Network. Cancer Discovery, 2018, 8, 1474-1489. | 7.7 | 67 |
| 108 | Influenza virus infection causes global RNAPII termination defects. Nature Structural and Molecular Biology, 2018, 25, 885-893. | 3.6 | 48 |

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| 109 | Mycobacterial Mutagenesis and Drug Resistance Are Controlled by Phosphorylation- and Cardiolipin-Mediated Inhibition of the RecA Coprotease. Molecular Cell, 2018, 72, 152-161.e7. | 4.5 | 23 |
| 110 | CRL4 ^{AMBRA1} targets Elongin C for ubiquitination and degradation to modulate CRL5 signaling. EMBO Journal, 2018, 37, . | 3.5 | 13 |
| 111 | Quantitative Yeast Genetic Interaction Profiling of Bacterial Effector Proteins Uncovers a Role for the Human Retromer in Salmonella Infection. Cell Systems, 2018, 7, 323-338.e6. | 2.9 | 15 |
| 112 | The Psychiatric Cell Map Initiative: A Convergent Systems Biological Approach to Illuminating Key Molecular Pathways in Neuropsychiatric Disorders. Cell, 2018, 174, 505-520. | 13.5 | 108 |
| 113 | Sympathetic inputs regulate adaptive thermogenesis in brown adipose tissue through cAMP-Salt inducible kinase axis. Scientific Reports, 2018, 8, 11001. | 1.6 | 33 |
| 114 | An Mtb-Human Protein-Protein Interaction Map Identifies a Switch between Host Antiviral and Antibacterial Responses. Molecular Cell, 2018, 71, 637-648.e5. | 4.5 | 100 |
| 115 | Fab-based inhibitors reveal ubiquitin independent functions for HIV Vif neutralization of APOBEC3 restriction factors. PLoS Pathogens, 2018, 14, e1006830. | 2.1 | 17 |
| 116 | The HIV-1 Tat protein recruits a ubiquitin ligase to reorganize the 7SK snRNP for transcriptional activation. ELife, 2018, 7, . | 2.8 | 29 |
| 117 | Genetic analysis reveals functions of atypical polyubiquitin chains. ELife, 2018, 7, . | 2.8 | 12 |
| 118 | G Protein–Coupled Receptor Endocytosis Confers Uniformity in Responses to Chemically Distinct Ligands. Molecular Pharmacology, 2017, 91, 145-156. | 1.0 | 30 |
| 119 | Systems-based analysis of RIG-I-dependent signalling identifies KHSRP as an inhibitor of RIG-I receptor activation. Nature Microbiology, 2017, 2, 17022. | 5.9 | 25 |
| 120 | Genetic interaction mapping in mammalian cells using CRISPR interference. Nature Methods, 2017, 14, 577-580. | 9.0 | 142 |
| 121 | SMYD2-Mediated Histone Methylation Contributes to HIV-1 Latency. Cell Host and Microbe, 2017, 21, 569-579.e6. | 5.1 | 78 |
| 122 | The RNA Exosome Syncs IAV-RNAPII Transcription to Promote Viral Ribogenesis and Infectivity. Cell, 2017, 169, 679-692.e14. | 13.5 | 48 |
| 123 | The histone variant H2A.Z promotes splicing of weak introns. Genes and Development, 2017, 31, 688-701. | 2.7 | 22 |
| 124 | Virus-Like Vesicles of Kaposi's Sarcoma-Associated Herpesvirus Activate Lytic Replication by Triggering Differentiation Signaling. Journal of Virology, 2017, 91, . | 1.5 | 17 |
| 125 | The Tyrosine Kinase Inhibitor Gefitinib Restricts <i>Mycobacterium tuberculosis</i> Growth through Increased Lysosomal Biogenesis and Modulation of Cytokine Signaling. ACS Infectious Diseases, 2017, 3, 564-574. | 1.8 | 42 |
| 126 | An Approach to Spatiotemporally Resolve Protein Interaction Networks in Living Cells. Cell, 2017, 169, 350-360.e12. | 13.5 | 322 |

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| 127 | Combinatorial CRISPR–Cas9 screens for de novo mapping of genetic interactions. Nature Methods, 2017, 14, 573-576. | 9.0 | 287 |
| 128 | Inhibition of CRISPR-Cas9 with Bacteriophage Proteins. Cell, 2017, 168, 150-158.e10. | 13.5 | 409 |
| 129 | A genome-wide CRISPR screen identifies a restricted set of HIV host dependency factors. Nature Genetics, 2017, 49, 193-203. | 9.4 | 290 |
| 130 | PJA2 ubiquitinates the HIV-1 Tat protein with atypical chain linkages to activate viral transcription. Scientific Reports, 2017, 7, 45394. | 1.6 | 30 |
| 131 | The Host E3-Ubiquitin Ligase TRIM6 Ubiquitinates the Ebola Virus VP35 Protein and Promotes Virus Replication. Journal of Virology, 2017, 91, . | 1.5 | 68 |
| 132 | Evolutionary Proteomics Uncovers Ancient Associations of Cilia with Signaling Pathways. Developmental Cell, 2017, 43, 744-762.e11. | 3.1 | 92 |
| 133 | Mutations in the X-linked <i>ATP6AP2</i> cause a glycosylation disorder with autophagic defects. Journal of Experimental Medicine, 2017, 214, 3707-3729. | 4.2 | 62 |
| 134 | A BAG3 chaperone complex maintains cardiomyocyte function during proteotoxic stress. JCI Insight, 2017, 2, . | 2.3 | 81 |
| 135 | Suppression of C9orf72 RNA repeat-induced neurotoxicity by the ALS-associated RNA-binding protein Zfp106. ELife, 2017, 6, . | 2.8 | 44 |
| 136 | Chlamydia interfere with an interaction between the mannose-6-phosphate receptor and sorting nexins to counteract host restriction. ELife, 2017, 6, . | 2.8 | 61 |
| 137 | The Dengue Virus NS5 Protein Intrudes in the Cellular Spliceosome and Modulates Splicing. PLoS Pathogens, 2016, 12, e1005841. | 2.1 | 176 |
| 138 | A scaffold protein connects type IV pili with the Chp chemosensory system to mediate activation of virulence signaling in <i>Pseudomonas aeruginosa</i> . Molecular Microbiology, 2016, 101, 590-605. | 1.2 | 69 |
| 139 | The mTOR Complex Controls HIV Latency. Cell Host and Microbe, 2016, 20, 785-797. | 5.1 | 179 |
| 140 | Nonsense-mediated decay regulates key components of homologous recombination. Nucleic Acids Research, 2016, 44, 5218-5230. | 6.5 | 18 |
| 141 | A Herpesvirus Protein Selectively Inhibits Cellular mRNA Nuclear Export. Cell Host and Microbe, 2016, 20, 642-653. | 5.1 | 40 |
| 142 | A Cas9 Ribonucleoprotein Platform for Functional Genetic Studies of HIV-Host Interactions in Primary Human T Cells. Cell Reports, 2016, 17, 1438-1452. | 2.9 | 167 |
| 143 | Microcephaly Proteins Wdr62 and Aspm Define a Mother Centriole Complex Regulating Centriole Biogenesis, Apical Complex, and Cell Fate. Neuron, 2016, 92, 813-828. | 3.8 | 116 |
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| 146 | Translation of Genotype to Phenotype by a Hierarchy of Cell Subsystems. Cell Systems, 2016, 2, 77-88. | 2.9 | 72 |
| 147 | CRISPR Interference Efficiently Induces Specific and Reversible Gene Silencing in Human iPSCs. Cell Stem Cell, 2016, 18, 541-553. | 5.2 | 418 |
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| 150 | Centriolar satellites assemble centrosomal microcephaly proteins to recruit CDK2 and promote centriole duplication. ELife, 2015, 4, . | 2.8 | 118 |
| 151 | The Cancer Cell Map Initiative: Defining the Hallmark Networks of Cancer. Molecular Cell, 2015, 58, 690-698. | 4.5 | 117 |
| 152 | Scoring Large cale Affinity Purification Mass Spectrometry Datasets with MiST. Current Protocols in Bioinformatics, 2015, 49, 8.19.1-8.19.16. | 25.8 | 58 |
| 153 | Meta- and Orthogonal Integration of Influenza "OMICs―Data Defines a Role for UBR4 in Virus Budding. Cell Host and Microbe, 2015, 18, 723-735. | 5.1 | 868 |
| 154 | Acetylome Profiling Reveals Overlap in the Regulation of Diverse Processes by Sirtuins, Gcn5, and Esa1. Molecular and Cellular Proteomics, 2015, 14, 162-176. | 2.5 | 59 |
| 155 | Clobal Mapping of Herpesvirus-Host Protein Complexes Reveals a Transcription Strategy for Late Genes. Molecular Cell, 2015, 57, 349-360. | 4.5 | 165 |
| 156 | Determinants for degradation of SAMHD1, Mus81 and induction of G 2 arrest in HIV-1 Vpr and SIVagm Vpr. Virology, 2015, 477, 10-17. | 1.1 | 11 |
| 157 | A Combined Proteomics/Genomics Approach Links Hepatitis C Virus Infection with Nonsense-Mediated mRNA Decay. Molecular Cell, 2015, 57, 329-340. | 4.5 | 124 |
| 158 | Prb1 Protease Activity Is Required for Its Recognition by the F-Box Protein Saf1. Biochemistry, 2015, 54, 4423-4426. | 1.2 | 6 |
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| 160 | Global Mapping of the Inc-Human Interactome Reveals that Retromer Restricts Chlamydia Infection. Cell Host and Microbe, 2015, 18, 109-121. | 5.1 | 174 |
| 161 | Spindle Checkpoint Factors Bub1 and Bub2 Promote DNA Double-Strand Break Repair by Nonhomologous End Joining. Molecular and Cellular Biology, 2015, 35, 2448-2463. | 1.1 | 21 |
| 162 | Genetic Interaction Landscape Reveals Critical Requirements for <i>Schizosaccharomyces pombe</i> Brc1 in DNA Damage Response Mutants. G3: Genes, Genomes, Genetics, 2015, 5, 953-962. | 0.8 | 11 |

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| 164 | Critical role of acetylation in tau-mediated neurodegeneration and cognitive deficits. Nature Medicine, 2015, 21, 1154-1162. | 15.2 | 398 |
| 165 | Discovery and functional characterization of a neomorphic PTEN mutation. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 13976-13981. | 3.3 | 38 |
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| 167 | Lineage-Specific Viral Hijacking of Non-canonical E3ÂUbiquitin Ligase Cofactors in the Evolution of Vif Anti-APOBEC3 Activity. Cell Reports, 2015, 11, 1236-1250. | 2.9 | 42 |
| 168 | Comparative mapping of host–pathogen protein–protein interactions. Current Opinion in Microbiology, 2015, 27, 62-68. | 2.3 | 37 |
| 169 | CDK11 in TREX/THOC Regulates HIV mRNA 3′ End Processing. Cell Host and Microbe, 2015, 18, 560-570. | 5.1 | 53 |
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