

Nevan J Krogan

List of Publications by Year in Descending Order

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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.

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	Comparative Analysis of T Cell Spatial Proteomics and the Influence of HIV Expression.. <i>Molecular and Cellular Proteomics</i> , 2022 , 100194	7.6	0
256	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
255	SIRT5 is a proviral factor that interacts with SARS-CoV-2 Nsp14 protein. 2022 ,		3
254	Tau interactome maps synaptic and mitochondrial processes associated with neurodegeneration.. <i>Cell</i> , 2022 ,	56.2	11
253	Preclinical and randomized phase I studies of plitidepsin in adults hospitalized with COVID-19.. <i>Life Science Alliance</i> , 2022 , 5,	5.8	6
252	The RNA helicase DHX16 recognizes specific viral RNA to trigger RIG-I-dependent innate antiviral immunity.. <i>Cell Reports</i> , 2022 , 38, 110434	10.6	1
251	Transcription factor protein interactomes reveal genetic determinants in heart disease.. <i>Cell</i> , 2022 ,	56.2	3
250	The E3 ligase TRIM1 ubiquitinates LRRK2 and controls its localization, degradation, and toxicity.. <i>Journal of Cell Biology</i> , 2022 , 221,	7.3	1
249	A functional map of HIV-host interactions in primary human T cells.. <i>Nature Communications</i> , 2022 , 13, 1752	17.4	1
248	Leveraging modeling and simulation to optimize the therapeutic window for epigenetic modifier drugs.. <i>Pharmacology & Therapeutics</i> , 2022 , 108162	13.9	0
247	Global post-translational modification profiling of HIV-1-infected cells reveals mechanisms of host cellular pathway remodeling.. <i>Cell Reports</i> , 2022 , 39, 110690	10.6	1
246	Meningioma DNA methylation groups identify biological drivers and therapeutic vulnerabilities.. <i>Nature Genetics</i> , 2022 , 54, 649-659	36.3	0
245	Viral E Protein Neutralizes BET Protein-Mediated Post-Entry Antagonism of SARS-CoV-2 2021 ,		1
244	Systems-level effects of allosteric perturbations to a model molecular switch. <i>Nature</i> , 2021 , 599, 152-157	30.4	1
243	Phospholipidosis is a shared mechanism underlying the antiviral activity of many repurposed drugs against SARS-CoV-2 2021 ,		1
242	Smoothed transduces Hedgehog signals via activity-dependent sequestration of PKA catalytic subunits. <i>PLoS Biology</i> , 2021 , 19, e3001191	9.7	15
241	Creating collaboration by breaking down scientific barriers. <i>Cell</i> , 2021 , 184, 2271-2275	56.2	3

240	The AMBRA1 E3 ligase adaptor regulates the stability of cyclinD. <i>Nature</i> , 2021 , 592, 794-798	50.4	20
239	CryoEM and AI reveal a structure of SARS-CoV-2 Nsp2, a multifunctional protein involved in key host processes 2021 ,		4
238	Chaperone-mediated autophagy prevents collapse of the neuronal metastable proteome. <i>Cell</i> , 2021 , 184, 2696-2714.e25	56.2	40
237	Chemical-genetic interrogation of RNA polymerase mutants reveals structure-function relationships and physiological tradeoffs. <i>Molecular Cell</i> , 2021 , 81, 2201-2215.e9	17.6	1
236	Efficient generation of isogenic primary human myeloid cells using CRISPR-Cas9 ribonucleoproteins. <i>Cell Reports</i> , 2021 , 35, 109105	10.6	8
235	Plitidepsin has a positive therapeutic index in adult patients with COVID-19 requiring hospitalization 2021 ,		3
234	CryoEM and AI reveal a structure of SARS-CoV-2 Nsp2, a multifunctional protein involved in key host processes 2021 ,		10
233	Evolution of enhanced innate immune evasion by the SARS-CoV-2 B.1.1.7 UK variant 2021 ,		60
232	Conflicting and ambiguous names of overlapping ORFs in the SARS-CoV-2 genome: A homology-based resolution. <i>Virology</i> , 2021 , 558, 145-151	3.6	15
231	Drug-induced phospholipidosis confounds drug repurposing for SARS-CoV-2. <i>Science</i> , 2021 , 373, 541-547	33.3	64
230	Adhesion-mediated mechanosignaling forces mitohormesis. <i>Cell Metabolism</i> , 2021 , 33, 1322-1341.e13	24.6	12
229	Endosomal cAMP production broadly impacts the cellular phosphoproteome. <i>Journal of Biological Chemistry</i> , 2021 , 297, 100907	5.4	9
228	Genetic Screens Identify Host Factors for SARS-CoV-2 and Common Cold Coronaviruses. <i>Cell</i> , 2021 , 184, 106-119.e14	56.2	150
227	Host-directed therapies against early-lineage SARS-CoV-2 retain efficacy against B.1.1.7 variant 2021 ,		14
226	Proteomic Approaches to Study SARS-CoV-2 Biology and COVID-19 Pathology. <i>Journal of Proteome Research</i> , 2021 , 20, 1133-1152	5.6	18
225	Mass spectrometry-based protein-protein interaction networks for the study of human diseases. <i>Molecular Systems Biology</i> , 2021 , 17, e8792	12.2	30
224	Characterization of an A3G-Vif-CRL5-CBF5 structure Using a Cross-linking Mass Spectrometry Pipeline for Integrative Modeling of Host-Pathogen Complexes. <i>Molecular and Cellular Proteomics</i> , 2021 , 20, 100132	7.6	1
223	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

222	A ciliopathy complex builds distal appendages to initiate ciliogenesis. <i>Journal of Cell Biology</i> , 2021 , 220,	7.3	5
221	An ancient viral epidemic involving host coronavirus interacting genes more than 20,000 years ago in East Asia. <i>Current Biology</i> , 2021 , 31, 3504-3514.e9	6.3	15
220	Non-canonical proline-tyrosine interactions with multiple host proteins regulate Ebola virus infection. <i>EMBO Journal</i> , 2021 , 40, e105658	13	4
219	Restriction factor compendium for influenza A virus reveals a mechanism for evasion of autophagy. <i>Nature Microbiology</i> , 2021 , 6, 1319-1333	26.6	7
218	Target Discovery for Host-Directed Antiviral Therapies: Application of Proteomics Approaches. <i>MSystems</i> , 2021 , 6, e0038821	7.6	1
217	Brown adipocyte ATF4 activation improves thermoregulation and systemic metabolism. <i>Cell Reports</i> , 2021 , 36, 109742	10.6	2
216	A protein network map of head and neck cancer reveals PIK3CA mutant drug sensitivity. <i>Science</i> , 2021 , 374, eabf2911	33.3	6
215	A protein interaction landscape of breast cancer. <i>Science</i> , 2021 , 374, eabf3066	33.3	4
214	Interpretation of cancer mutations using a multiscale map of protein systems. <i>Science</i> , 2021 , 374, eabf3067	33.3	3
213	SUMO is a pervasive regulator of meiosis. <i>ELife</i> , 2021 , 10,	8.9	21
212	Evolution of enhanced innate immune evasion by SARS-CoV-2.. <i>Nature</i> , 2021 ,	50.4	30
211	Genetic interaction mapping informs integrative structure determination of protein complexes. <i>Science</i> , 2020 , 370,	33.3	11
210	An ultrapotent synthetic nanobody neutralizes SARS-CoV-2 by stabilizing inactive Spike. <i>Science</i> , 2020 , 370, 1473-1479	33.3	166
209	mRNA display with library of even-distribution reveals cellular interactors of influenza virus NS1. <i>Nature Communications</i> , 2020 , 11, 2449	17.4	3
208	Hybrid Gene Origination Creates Human-Virus Chimeric Proteins during Infection. <i>Cell</i> , 2020 , 181, 1502-1517.e23	56.2	23
207	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
206	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	10.6	32
205	The Global Phosphorylation Landscape of SARS-CoV-2 Infection. <i>Cell</i> , 2020 , 182, 685-712.e19	56.2	439

204	A SARS-CoV-2 protein interaction map reveals targets for drug repurposing. <i>Nature</i> , 2020 , 583, 459-468	50.4	2142
203	Envelope protein ubiquitination drives entry and pathogenesis of Zika virus. <i>Nature</i> , 2020 , 585, 414-419	50.4	31
202	The kinase Isr1 negatively regulates hexosamine biosynthesis in <i>S. cerevisiae</i> . <i>PLoS Genetics</i> , 2020 , 16, e1008840	6	2
201	A Quantitative Genetic Interaction Map of HIV Infection. <i>Molecular Cell</i> , 2020 , 78, 197-209.e7	17.6	9
200	A systems approach to infectious disease. <i>Nature Reviews Genetics</i> , 2020 , 21, 339-354	30.1	44
199	The Landscape of Human Cancer Proteins Targeted by SARS-CoV-2. <i>Cancer Discovery</i> , 2020 , 10, 916-921	24.4	25
198	Dynamic post-translational modification profiling of -infected primary macrophages. <i>ELife</i> , 2020 , 9,	8.9	25
197	A SARS-CoV-2-Human Protein-Protein Interaction Map Reveals Drug Targets and Potential Drug-Repurposing 2020 ,		133
196	An ultra-potent synthetic nanobody neutralizes SARS-CoV-2 by locking Spike into an inactive conformation 2020 ,		20
195	SARS-CoV-2 ORF9c Is a Membrane-Associated Protein that Suppresses Antiviral Responses in Cells 2020 ,		17
194	Functional genomic screens identify human host factors for SARS-CoV-2 and common cold coronaviruses 2020 ,		14
193	The functional landscape of the human phosphoproteome. <i>Nature Biotechnology</i> , 2020 , 38, 365-373	44.5	106
192	Comparative host-coronavirus protein interaction networks reveal pan-viral disease mechanisms. <i>Science</i> , 2020 , 370,	33.3	261
191	Structural basis of CD4 downregulation by HIV-1 Nef. <i>Nature Structural and Molecular Biology</i> , 2020 , 27, 822-828	17.6	18
190	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
189	The E3 Ubiquitin-Protein Ligase Cullin 3 Regulates HIV-1 Transcription. <i>Cells</i> , 2020 , 9,	7.9	1
188	Evaluation of SARS-CoV-2 serology assays reveals a range of test performance. <i>Nature Biotechnology</i> , 2020 , 38, 1174-1183	44.5	166
187	Synthetic Essentiality of Metabolic Regulator PDHK1 in PTEN-Deficient Cells and Cancers. <i>Cell Reports</i> , 2019 , 28, 2317-2330.e8	10.6	7

186	Anti-CRISPR-Associated Proteins Are Crucial Repressors of Anti-CRISPR Transcription. <i>Cell</i> , 2019 , 178, 1452-1464.e13	56.2	56
185	Regulation of Skn7-dependent, oxidative stress-induced genes by the RNA polymerase II-CTD phosphatase, Fcp1, and Mediator kinase subunit, Cdk8, in yeast. <i>Journal of Biological Chemistry</i> , 2019 , 294, 16080-16094	5.4	4
184	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
183	Two Accessory Proteins Govern MmpL3 Mycolic Acid Transport in Mycobacteria. <i>MBio</i> , 2019 , 10,	7.8	19
182	Heart failure drug proscillaridin A targets MYC overexpressing leukemia through global loss of lysine acetylation. <i>Journal of Experimental and Clinical Cancer Research</i> , 2019 , 38, 251	12.8	15
181	SIRT3 controls brown fat thermogenesis by deacetylation regulation of pathways upstream of UCP1. <i>Molecular Metabolism</i> , 2019 , 25, 35-49	8.8	21
180	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
179	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
178	PEAK3/C19orf35 pseudokinase, a new NFK3 kinase family member, inhibits CrkII through dimerization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 15495-15504	11.5	11
177	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
176	Mapping the protein-protein and genetic interactions of cancer to guide precision medicine. <i>Current Opinion in Genetics and Development</i> , 2019 , 54, 110-117	4.9	11
175	UNC93B1 recruits syntenin-1 to dampen TLR7 signalling and prevent autoimmunity. <i>Nature</i> , 2019 , 575, 366-370	50.4	42
174	Mapping genetic interactions in cancer: a road to rational combination therapies. <i>Genome Medicine</i> , 2019 , 11, 62	14.4	12
173	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
172	Enterovirus pathogenesis requires the host methyltransferase SETD3. <i>Nature Microbiology</i> , 2019 , 4, 2523-2537	32	32
171	Virus and host interactions critical for filoviral RNA synthesis as therapeutic targets. <i>Antiviral Research</i> , 2019 , 162, 90-100	10.8	7
170	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
169	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

168	SMARCA2-regulated host cell factors are required for MxA restriction of influenza A viruses. <i>Scientific Reports</i> , 2018 , 8, 2092	4.9	9
167	How many human proteoforms are there?. <i>Nature Chemical Biology</i> , 2018 , 14, 206-214	11.7	324
166	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
165	DNA Preparation from. <i>Cold Spring Harbor Protocols</i> , 2018 , 2018,	1.2	2
164	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
163	Genetic Interaction Mapping in Using the Pombe Epistasis Mapper (PEM) System and a ROTOR HDA Colony Replicating Robot in a 1536 Array Format. <i>Cold Spring Harbor Protocols</i> , 2018 , 2018,	1.2	3
162	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
161	High-Throughput Quantitative Genetic Interaction Mapping in the Fission Yeast. <i>Cold Spring Harbor Protocols</i> , 2018 , 2018,	1.2	2
160	Quantitative Yeast Genetic Interaction Profiling of Bacterial Effector Proteins Uncovers a Role for the Human Retromer in Salmonella Infection. <i>Cell Systems</i> , 2018 , 7, 323-338.e6	10.6	10
159	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
158	Sympathetic inputs regulate adaptive thermogenesis in brown adipose tissue through cAMP-Salt inducible kinase axis. <i>Scientific Reports</i> , 2018 , 8, 11001	4.9	14
157	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
156	Fab-based inhibitors reveal ubiquitin independent functions for HIV Vif neutralization of APOBEC3 restriction factors. <i>PLoS Pathogens</i> , 2018 , 14, e1006830	7.6	14
155	The HIV-1 Tat protein recruits a ubiquitin ligase to reorganize the 7SK snRNP for transcriptional activation. <i>ELife</i> , 2018 , 7,	8.9	19
154	Genetic analysis reveals functions of atypical polyubiquitin chains. <i>ELife</i> , 2018 , 7,	8.9	7
153	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
152	Protein Moonlighting Revealed by Noncatalytic Phenotypes of Yeast Enzymes. <i>Genetics</i> , 2018 , 208, 419-431	15	15
151	Genetic Interaction Score (S-Score) Calculation, Clustering, and Visualization of Genetic Interaction Profiles for Yeast. <i>Cold Spring Harbor Protocols</i> , 2018 , 2018,	1.2	2

150	Transformation of in a 96-Well Format. <i>Cold Spring Harbor Protocols</i> , 2018 , 2018,	1.2	1
149	The Cellular NMD Pathway Restricts Zika Virus Infection and Is Targeted by the Viral Capsid Protein. <i>MBio</i> , 2018 , 9,	7.8	47
148	Protein Interaction Mapping Identifies RBBP6 as a Negative Regulator of Ebola Virus Replication. <i>Cell</i> , 2018 , 175, 1917-1930.e13	56.2	62
147	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
146	The Yeast DNA Damage Checkpoint Kinase Rad53 Targets the Exoribonuclease, Xrn1. <i>G3: Genes, Genomes, Genetics</i> , 2018 , 8, 3931-3944	3.2	12
145	Multiple Routes to Oncogenesis Are Promoted by the Human Papillomavirus-Host Protein Network. <i>Cancer Discovery</i> , 2018 , 8, 1474-1489	24.4	43
144	Influenza virus infection causes global RNAPII termination defects. <i>Nature Structural and Molecular Biology</i> , 2018 , 25, 885-893	17.6	24
143	Mycobacterial Mutagenesis and Drug Resistance Are Controlled by Phosphorylation- and Cardiolipin-Mediated Inhibition of the RecA Coprotease. <i>Molecular Cell</i> , 2018 , 72, 152-161.e7	17.6	10
142	CRL4 targets Elongin C for ubiquitination and degradation to modulate CRL5 signaling. <i>EMBO Journal</i> , 2018 , 37,	13	6
141	G Protein-Coupled Receptor Endocytosis Confers Uniformity in Responses to Chemically Distinct Ligands. <i>Molecular Pharmacology</i> , 2017 , 91, 145-156	4.3	24
140	Systems-based analysis of RIG-I-dependent signalling identifies KHSRP as an inhibitor of RIG-I receptor activation. <i>Nature Microbiology</i> , 2017 , 2, 17022	26.6	18
139	Genetic interaction mapping in mammalian cells using CRISPR interference. <i>Nature Methods</i> , 2017 , 14, 577-580	21.6	108
138	SMYD2-Mediated Histone Methylation Contributes to HIV-1 Latency. <i>Cell Host and Microbe</i> , 2017 , 21, 569-579.e6	23.4	54
137	The RNA Exosome Syncs IAV-RNAPII Transcription to Promote Viral Ribogenesis and Infectivity. <i>Cell</i> , 2017 , 169, 679-692.e14	56.2	35
136	The histone variant H2A.Z promotes splicing of weak introns. <i>Genes and Development</i> , 2017 , 31, 688-701	12.6	17
135	Virus-Like Vesicles of Kaposi's Sarcoma-Associated Herpesvirus Activate Lytic Replication by Triggering Differentiation Signaling. <i>Journal of Virology</i> , 2017 , 91,	6.6	12
134	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
133	An Approach to Spatiotemporally Resolve Protein Interaction Networks in Living Cells. <i>Cell</i> , 2017 , 169, 350-360.e12	56.2	209

132	Combinatorial CRISPR-Cas9 screens for de novo mapping of genetic interactions. <i>Nature Methods</i> , 2017 , 14, 573-576	21.6	209
131	Inhibition of CRISPR-Cas9 with Bacteriophage Proteins. <i>Cell</i> , 2017 , 168, 150-158.e10	56.2	310
130	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
129	PJA2 ubiquitinates the HIV-1 Tat protein with atypical chain linkages to activate viral transcription. <i>Scientific Reports</i> , 2017 , 7, 45394	4.9	18
128	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
127	Evolutionary Proteomics Uncovers Ancient Associations of Cilia with Signaling Pathways. <i>Developmental Cell</i> , 2017 , 43, 744-762.e11	10.2	55
126	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
125	A BAG3 chaperone complex maintains cardiomyocyte function during proteotoxic stress. <i>JCI Insight</i> , 2017 , 2,	9.9	52
124	Suppression of RNA repeat-induced neurotoxicity by the ALS-associated RNA-binding protein Zfp106. <i>ELife</i> , 2017 , 6,	8.9	29
123	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
122	A Herpesvirus Protein Selectively Inhibits Cellular mRNA Nuclear Export. <i>Cell Host and Microbe</i> , 2016 , 20, 642-653	23.4	22
121	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
120	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
119	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
118	Targeting Viral Proteostasis Limits Influenza Virus, HIV, and Dengue Virus Infection. <i>Immunity</i> , 2016 , 44, 46-58	32.3	81
117	Translation of Genotype to Phenotype by a Hierarchy of Cell Subsystems. <i>Cell Systems</i> , 2016 , 2, 77-88	10.6	47
116	CRISPR Interference Efficiently Induces Specific and Reversible Gene Silencing in Human iPSCs. <i>Cell Stem Cell</i> , 2016 , 18, 541-53	18	271
115	Non-degradative Ubiquitination of Protein Kinases. <i>PLoS Computational Biology</i> , 2016 , 12, e1004898	5	23

114	The Dengue Virus NS5 Protein Intrudes in the Cellular Spliceosome and Modulates Splicing. <i>PLoS Pathogens</i> , 2016 , 12, e1005841	7.6	100
113	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
112	The mTOR Complex Controls HIV Latency. <i>Cell Host and Microbe</i> , 2016 , 20, 785-797	23.4	115
111	Nonsense-mediated decay regulates key components of homologous recombination. <i>Nucleic Acids Research</i> , 2016 , 44, 5218-30	20.1	9
110	Prb1 Protease Activity Is Required for Its Recognition by the F-Box Protein Saf1. <i>Biochemistry</i> , 2015 , 54, 4423-6	3.2	3
109	Genetic interaction mapping reveals a role for the SWI/SNF nucleosome remodeler in spliceosome activation in fission yeast. <i>PLoS Genetics</i> , 2015 , 11, e1005074	6	18
108	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
107	Spindle Checkpoint Factors Bub1 and Bub2 Promote DNA Double-Strand Break Repair by Nonhomologous End Joining. <i>Molecular and Cellular Biology</i> , 2015 , 35, 2448-63	4.8	17
106	Genetic Interaction Landscape Reveals Critical Requirements for <i>Schizosaccharomyces pombe</i> Brc1 in DNA Damage Response Mutants. <i>G3: Genes, Genomes, Genetics</i> , 2015 , 5, 953-62	3.2	7
105	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
104	Critical role of acetylation in tau-mediated neurodegeneration and cognitive deficits. <i>Nature Medicine</i> , 2015 , 21, 1154-62	50.5	300
103	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
102	Differential genetic interactions of yeast stress response MAPK pathways. <i>Molecular Systems Biology</i> , 2015 , 11, 800	12.2	31
101	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
100	Comparative mapping of host-pathogen protein-protein interactions. <i>Current Opinion in Microbiology</i> , 2015 , 27, 62-8	7.9	28
99	CDK11 in TREX/THOC Regulates HIV mRNA 3' End Processing. <i>Cell Host and Microbe</i> , 2015 , 18, 560-70	23.4	34
98	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
97	Systems Analyses Reveal Shared and Diverse Attributes of Oct4 Regulation in Pluripotent Cells. <i>Cell Systems</i> , 2015 , 1, 141-51	10.6	11

96	Centriolar satellites assemble centrosomal microcephaly proteins to recruit CDK2 and promote centriole duplication. <i>ELife</i> , 2015 , 4,	8.9	85
95	The cancer cell map initiative: defining the hallmark networks of cancer. <i>Molecular Cell</i> , 2015 , 58, 690-8	17.6	89
94	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
93	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
92	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
91	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
90	Determinants for degradation of SAMHD1, Mus81 and induction of G2 arrest in HIV-1 Vpr and SIVagm Vpr. <i>Virology</i> , 2015 , 477, 10-17	3.6	10
89	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
88	Prediction of Functionally Important Phospho-Regulatory Events in <i>Xenopus laevis</i> Oocytes. <i>PLoS Computational Biology</i> , 2015 , 11, e1004362	5	14
87	Adventures in time and space: splicing efficiency and RNA polymerase II elongation rate. <i>RNA Biology</i> , 2014 , 11, 313-9	4.8	29
86	Regulation of Sufu activity by p66 ^{lck} and Myc ^{bp} provides new insight into vertebrate Hedgehog signaling. <i>Genes and Development</i> , 2014 , 28, 2547-63	12.6	33
85	Quantitative analysis of triple-mutant genetic interactions. <i>Nature Protocols</i> , 2014 , 9, 1867-81	18.8	11
84	Yeast X-chromosome-associated protein 5 (Xap5) functions with H2A.Z to suppress aberrant transcripts. <i>EMBO Reports</i> , 2014 , 15, 894-902	6.5	10
83	Identification of a BET family bromodomain/casein kinase II/TAF-containing complex as a regulator of mitotic condensin function. <i>Cell Reports</i> , 2014 , 6, 892-905	10.6	9
82	Set5 and Set1 cooperate to repress gene expression at telomeres and retrotransposons. <i>Epigenetics</i> , 2014 , 9, 513-22	5.7	23
81	Cullin E3 ligases and their rewiring by viral factors. <i>Biomolecules</i> , 2014 , 4, 897-930	5.9	52
80	A chaperone-assisted degradation pathway targets kinetochore proteins to ensure genome stability. <i>PLoS Genetics</i> , 2014 , 10, e1004140	6	43
79	Genetic interaction analysis of point mutations enables interrogation of gene function at a residue-level resolution: exploring the applications of high-resolution genetic interaction mapping of point mutations. <i>BioEssays</i> , 2014 , 36, 706-13	4.1	3

78	Evolutionarily conserved genetic interactions with budding and fission yeast MutS identify orthologous relationships in mismatch repair-deficient cancer cells. <i>Genome Medicine</i> , 2014 , 6, 68	14.4	10
77	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
76	Conditional genetic interactions of RTT107, SLX4, and HRQ1 reveal dynamic networks upon DNA damage in <i>S. cerevisiae</i> . <i>G3: Genes, Genomes, Genetics</i> , 2014 , 4, 1059-69	3.2	9
75	From structure to systems: high-resolution, quantitative genetic analysis of RNA polymerase II. <i>Cell</i> , 2013 , 154, 775-88	56.2	102
74	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
73	Systematic triple-mutant analysis uncovers functional connectivity between pathways involved in chromosome regulation. <i>Cell Reports</i> , 2013 , 3, 2168-78	10.6	32
72	Chemical genetics of rapamycin-insensitive TORC2 in <i>S. cerevisiae</i> . <i>Cell Reports</i> , 2013 , 5, 1725-36	10.6	27
71	High-resolution network biology: connecting sequence with function. <i>Nature Reviews Genetics</i> , 2013 , 14, 865-79	30.1	65
70	A gene ontology inferred from molecular networks. <i>Nature Biotechnology</i> , 2013 , 31, 38-45	44.5	142
69	Dispersed sites of HIV Vif-dependent polyubiquitination in the DNA deaminase APOBEC3F. <i>Journal of Molecular Biology</i> , 2013 , 425, 1172-82	6.5	18
68	Quantitative genetic-interaction mapping in mammalian cells. <i>Nature Methods</i> , 2013 , 10, 432-7	21.6	84
67	From systems to structure: bridging networks and mechanism. <i>Molecular Cell</i> , 2013 , 49, 222-31	17.6	30
66	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
65	Evolution and functional cross-talk of protein post-translational modifications. <i>Molecular Systems Biology</i> , 2013 , 9, 714	12.2	214
64	Differential network biology. <i>Molecular Systems Biology</i> , 2012 , 8, 565	12.2	538
63	Replication fork collapse and genome instability in a deoxycytidylate deaminase mutant. <i>Molecular and Cellular Biology</i> , 2012 , 32, 4445-54	4.8	33
62	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
61	Hierarchical modularity and the evolution of genetic interactomes across species. <i>Molecular Cell</i> , 2012 , 46, 691-704	17.6	144

60	Systematic functional prioritization of protein posttranslational modifications. <i>Cell</i> , 2012 , 150, 413-25	56.2	296
59	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
58	Inhibition of a NEDD8 Cascade Restores Restriction of HIV by APOBEC3G. <i>PLoS Pathogens</i> , 2012 , 8, e1003085	7.0	50
57	Physical host-pathogen networks. <i>FASEB Journal</i> , 2012 , 26, 89.1	0.9	
56	Vif hijacks CBF- β to degrade APOBEC3G and promote HIV-1 infection. <i>Nature</i> , 2011 , 481, 371-5	50.4	268
55	Global landscape of HIV-human protein complexes. <i>Nature</i> , 2011 , 481, 365-70	50.4	507
54	Phenotypic landscape of a bacterial cell. <i>Cell</i> , 2011 , 144, 143-56	56.2	484
53	Yeast SREBP cleavage activation requires the Golgi Dsc E3 ligase complex. <i>Molecular Cell</i> , 2011 , 42, 160-71	7.6	60
52	Purification and characterization of HIV-human protein complexes. <i>Methods</i> , 2011 , 53, 13-9	4.6	46
51	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
50	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
49	Cross-species chemogenomic profiling reveals evolutionarily conserved drug mode of action. <i>Molecular Systems Biology</i> , 2010 , 6, 451	12.2	108
48	Quantitative genetic interaction mapping using the E-MAP approach. <i>Methods in Enzymology</i> , 2010 , 470, 205-31	1.7	72
47	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
46	Quantitative genetic interactions reveal biological modularity. <i>Cell</i> , 2010 , 141, 739-45	56.2	113
45	Functional overlap and regulatory links shape genetic interactions between signaling pathways. <i>Cell</i> , 2010 , 143, 991-1004	56.2	105
44	Rewiring of genetic networks in response to DNA damage. <i>Science</i> , 2010 , 330, 1385-9	33.3	344
43	The next frontier of systems biology: higher-order and interspecies interactions. <i>Genome Biology</i> , 2010 , 11, 208	18.3	12

42	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
41	Host cell factors in HIV replication: meta-analysis of genome-wide studies. <i>PLoS Pathogens</i> , 2009 , 5, e1000437	10.4	351
40	Genome-wide association data reveal a global map of genetic interactions among protein complexes. <i>PLoS Genetics</i> , 2009 , 5, e1000782	6	51
39	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
38	Functional organization of the <i>S. cerevisiae</i> phosphorylation network. <i>Cell</i> , 2009 , 136, 952-63	56.2	211
37	A comprehensive strategy enabling high-resolution functional analysis of the yeast genome. <i>Nature Methods</i> , 2008 , 5, 711-8	21.6	376
36	High-throughput, quantitative analyses of genetic interactions in <i>E. coli</i> . <i>Nature Methods</i> , 2008 , 5, 781-7	21.6	181
35	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
34	Conservation and rewiring of functional modules revealed by an epistasis map in fission yeast. <i>Science</i> , 2008 , 322, 405-10	33.3	281
33	Functional maps of protein complexes from quantitative genetic interaction data. <i>PLoS Computational Biology</i> , 2008 , 4, e1000065	5	116
32	High-throughput genetic interaction mapping in the fission yeast <i>Schizosaccharomyces pombe</i> . <i>Nature Methods</i> , 2007 , 4, 861-6	21.6	120
31	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
30	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
29	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
28	Genetic Interaction mapping of essential genes in <i>Saccharomyces cerevisiae</i> . <i>FASEB Journal</i> , 2007 , 21, A1004	0.9	
27	A strategy for extracting and analyzing large-scale quantitative epistatic interaction data. <i>Genome Biology</i> , 2006 , 7, R63	18.3	245
26	A phosphatase complex that dephosphorylates gammaH2AX regulates DNA damage checkpoint recovery. <i>Nature</i> , 2006 , 439, 497-501	50.4	387
25	Global landscape of protein complexes in the yeast <i>Saccharomyces cerevisiae</i> . <i>Nature</i> , 2006 , 440, 637-43	50.4	2327

24	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
23	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
22	Cotranscriptional set2 methylation of histone H3 lysine 36 recruits a repressive Rpd3 complex. <i>Cell</i> , 2005 , 123, 593-605	56.2	621
21	Global mapping of the yeast genetic interaction network. <i>Science</i> , 2004 , 303, 808-13	33.3	1700
20	The functional landscape of mouse gene expression. <i>Journal of Biology</i> , 2004 , 3, 21		232
19	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
18	Proteasome involvement in the repair of DNA double-strand breaks. <i>Molecular Cell</i> , 2004 , 16, 1027-34	17.6	178
17	High-definition macromolecular composition of yeast RNA-processing complexes. <i>Molecular Cell</i> , 2004 , 13, 225-39	17.6	321
16	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
15	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
14	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
13	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
12	Ankle2, a Target of Zika Virus, Controls Asymmetric Cell Division of Neuroblasts and Uncovers a Novel Microcephaly Pathway. <i>SSRN Electronic Journal</i> ,	1	2
11	Systematic characterization of genome editing in primary T cells reveals proximal genomic insertions and enables machine learning prediction of CRISPR-Cas9 DNA repair outcomes		4
10	Global post-translational modification profiling of HIV-1-infected cells reveals mechanisms of host cellular pathway remodeling		1
9	Efficient Generation of Isogenic Primary Human Myeloid Cells using CRISPR-Cas9 Ribonucleoproteins		2
8	Zika Virus Infection Prevents Host mRNA Nuclear Export by Disrupting UPF1 Function		1
7	An Mtb-Human Protein-Protein Interaction Map Reveals that Bacterial LpqN Antagonizes CBL, a Host Ubiquitin Ligase that Regulates the Balance Between Anti-Viral and Anti-Bacterial Responses		1

6	Two accessory proteins govern MmpL3 mycolic acid transport in mycobacteria	1
5	Cyclophilin A Prevents HIV-1 Restriction in Lymphocytes by Blocking Human TRIM5 Binding to the viral Core	1
4	Delineation of the SUMO-Modified Proteome Reveals Regulatory Functions Throughout Meiosis	2
3	A CRISPR-Cas9 Genome Engineering Platform in Primary CD4+ T Cells for the Interrogation of HIV Host Factors	2
2	IL-10 driven memory T cell survival and Tfh differentiation promote HIV persistence	2
1	SARS-CoV-2 variants of concern have acquired mutations associated with an increased spike cleavage	8