

Stephen J Elledge

List of Publications by Year in descending order

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124
papers

32,268
citations

22099

59
h-index

18606

119
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140
all docs

140
docs citations

140
times ranked

43272
citing authors

#	ARTICLE	IF	CITATIONS
1	The DNA Damage Response: Making It Safe to Play with Knives. <i>Molecular Cell</i> , 2010, 40, 179-204.	4.5	3,563
2	The DNA damage response: putting checkpoints in perspective. <i>Nature</i> , 2000, 408, 433-439.	13.7	2,922
3	ATM and ATR Substrate Analysis Reveals Extensive Protein Networks Responsive to DNA Damage. <i>Science</i> , 2007, 316, 1160-1166.	6.0	2,689
4	Conservation of the Chk1 Checkpoint Pathway in Mammals: Linkage of DNA Damage to Cdk Regulation Through Cdc25. <i>Science</i> , 1997, 277, 1497-1501.	6.0	1,214
5	The IFITM Proteins Mediate Cellular Resistance to Influenza A H1N1 Virus, West Nile Virus, and Dengue Virus. <i>Cell</i> , 2009, 139, 1243-1254.	13.5	1,111
6	Tumor aneuploidy correlates with markers of immune evasion and with reduced response to immunotherapy. <i>Science</i> , 2017, 355, .	6.0	988
7	Requirement of ATM-Dependent Phosphorylation of Brca1 in the DNA Damage Response to Double-Strand Breaks. <i>Science</i> , 1999, 286, 1162-1166.	6.0	941
8	Longitudinal analysis reveals high prevalence of Epstein-Barr virus associated with multiple sclerosis. <i>Science</i> , 2022, 375, 296-301.	6.0	892
9	Meta- and Orthogonal Integration of Influenza A "OMICs" Data Defines a Role for UBR4 in Virus Budding. <i>Cell Host and Microbe</i> , 2015, 18, 723-735.	5.1	868
10	Altered cell differentiation and proliferation in mice lacking p57KIP2 indicates a role in Beckwith-Wiedemann syndrome. <i>Nature</i> , 1997, 387, 151-158.	13.7	721
11	Phosphorylation-Dependent Ubiquitination of Cyclin E by the SCFFbw7 Ubiquitin Ligase. <i>Science</i> , 2001, 294, 173-177.	6.0	718
12	Cumulative Haploinsufficiency and Triplosensitivity Drive Aneuploidy Patterns and Shape the Cancer Genome. <i>Cell</i> , 2013, 155, 948-962.	13.5	695
13	The DNA damage response induces inflammation and senescence by inhibiting autophagy of GATA4. <i>Science</i> , 2015, 349, aaa5612.	6.0	693
14	Homologous-recombination-deficient tumours are dependent on Pol η -mediated repair. <i>Nature</i> , 2015, 518, 258-262.	13.7	671
15	Cyclin D2 is an FSH-responsive gene involved in gonadal cell proliferation and oncogenesis. <i>Nature</i> , 1996, 384, 470-474.	13.7	668
16	Identification of the FANCI Protein, a Monoubiquitinated FANCD2 Paralog Required for DNA Repair. <i>Cell</i> , 2007, 129, 289-301.	13.5	608
17	Second-generation shRNA libraries covering the mouse and human genomes. <i>Nature Genetics</i> , 2005, 37, 1281-1288.	9.4	582
18	The pINDUCER lentiviral toolkit for inducible RNA interference in vitro and in vivo. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 3665-3670.	3.3	570

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19	Control of the DNA Damage Checkpoint by Chk1 and Rad53 Protein Kinases Through Distinct Mechanisms. <i>Science</i> , 1999, 286, 1166-1171.	6.0	517
20	Viral epitope profiling of COVID-19 patients reveals cross-reactivity and correlates of severity. <i>Science</i> , 2020, 370, .	6.0	511
21	Mrc1 transduces signals of DNA replication stress to activate Rad53. <i>Nature Cell Biology</i> , 2001, 3, 958-965.	4.6	474
22	Transcriptional regulation and function during the human cell cycle. <i>Nature Genetics</i> , 2001, 27, 48-54.	9.4	399
23	Global Protein Stability Profiling in Mammalian Cells. <i>Science</i> , 2008, 322, 918-923.	6.0	397
24	A SUMOylation-Dependent Transcriptional Subprogram Is Required for Myc-Driven Tumorigenesis. <i>Science</i> , 2012, 335, 348-353.	6.0	374
25	Global Identification of Modular Cullin-RING Ligase Substrates. <i>Cell</i> , 2011, 147, 459-474.	13.5	370
26	Mutations in TGIF cause holoprosencephaly and link NODAL signalling to human neural axis determination. <i>Nature Genetics</i> , 2000, 25, 205-208.	9.4	368
27	Reconstitution of G1 Cyclin Ubiquitination with Complexes Containing SCFGrr1 and Rbx1. <i>Science</i> , 1999, 284, 662-665.	6.0	367
28	Cancer Proliferation Gene Discovery Through Functional Genomics. <i>Science</i> , 2008, 319, 620-624.	6.0	365
29	Comprehensive serological profiling of human populations using a synthetic human virome. <i>Science</i> , 2015, 348, aaa0698.	6.0	364
30	Origins of lymphatic and distant metastases in human colorectal cancer. <i>Science</i> , 2017, 357, 55-60.	6.0	358
31	A Role for the Deubiquitinating Enzyme USP28 in Control of the DNA-Damage Response. <i>Cell</i> , 2006, 126, 529-542.	13.5	296
32	Measles virus infection diminishes preexisting antibodies that offer protection from other pathogens. <i>Science</i> , 2019, 366, 599-606.	6.0	294
33	Quantitative Proteomic Atlas of Ubiquitination and Acetylation in the DNA Damage Response. <i>Molecular Cell</i> , 2015, 59, 867-881.	4.5	288
34	Autoantigen discovery with a synthetic human peptidome. <i>Nature Biotechnology</i> , 2011, 29, 535-541.	9.4	267
35	DNA damage and cell cycle regulation of ribonucleotide reductase. <i>BioEssays</i> , 1993, 15, 333-339.	1.2	222
36	FANCI phosphorylation functions as a molecular switch to turn on the Fanconi anemia pathway. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 1138-1146.	3.6	207

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37	The Eukaryotic Proteome Is Shaped by E3 Ubiquitin Ligases Targeting C-Terminal Degrons. <i>Cell</i> , 2018, 173, 1622-1635.e14.	13.5	198
38	Recurrent Hemizygous Deletions in Cancers May Optimize Proliferative Potential. <i>Science</i> , 2012, 337, 104-109.	6.0	172
39	Identification of SCF Ubiquitin Ligase Substrates by Global Protein Stability Profiling. <i>Science</i> , 2008, 322, 923-929.	6.0	170
40	How autophagy both activates and inhibits cellular senescence. <i>Autophagy</i> , 2016, 12, 898-899.	4.3	164
41	T-Scan: A Genome-wide Method for the Systematic Discovery of T Cell Epitopes. <i>Cell</i> , 2019, 178, 1016-1028.e13.	13.5	150
42	Profound Tissue Specificity in Proliferation Control Underlies Cancer Drivers and Aneuploidy Patterns. <i>Cell</i> , 2018, 173, 499-514.e23.	13.5	147
43	Design of 240,000 orthogonal 25mer DNA barcode probes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 2289-2294.	3.3	139
44	Genetic Screens Reveal FEN1 and APEX2 as BRCA2 Synthetic Lethal Targets. <i>Molecular Cell</i> , 2019, 73, 885-899.e6.	4.5	137
45	A Systematic Analysis of Factors Localized to Damaged Chromatin Reveals PARP-Dependent Recruitment of Transcription Factors. <i>Cell Reports</i> , 2015, 11, 1486-1500.	2.9	134
46	A glycine-specific N-degron pathway mediates the quality control of protein N-myristoylation. <i>Science</i> , 2019, 365, .	6.0	131
47	Tissue-specificity in cancer: The rule, not the exception. <i>Science</i> , 2019, 363, 1150-1151.	6.0	127
48	Nudt21 Controls Cell Fate by Connecting Alternative Polyadenylation to Chromatin Signaling. <i>Cell</i> , 2018, 172, 106-120.e21.	13.5	123
49	C-Terminal End-Directed Protein Elimination by CRL2 Ubiquitin Ligases. <i>Molecular Cell</i> , 2018, 70, 602-613.e3.	4.5	123
50	p53 sends nucleotides to repair DNA. <i>Nature</i> , 2000, 404, 24-25.	13.7	112
51	The primary mechanism of cytotoxicity of the chemotherapeutic agent CX-5461 is topoisomerase II poisoning. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 4053-4060.	3.3	112
52	Amphotericin B Increases Influenza A Virus Infection by Preventing IFITM3-Mediated Restriction. <i>Cell Reports</i> , 2013, 5, 895-908.	2.9	108
53	RFWD3-Dependent Ubiquitination of RPA Regulates Repair at Stalled Replication Forks. <i>Molecular Cell</i> , 2015, 60, 280-293.	4.5	103
54	Treacher Collins syndrome TCOF1 protein cooperates with NBS1 in the DNA damage response. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 18631-18636.	3.3	92

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55	The adaptive immune system is a major driver of selection for tumor suppressor gene inactivation. <i>Science</i> , 2021, 373, 1327-1335.	6.0	83
56	Systematic autoantigen analysis identifies a distinct subtype of scleroderma with coincident cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E7526-E7534.	3.3	75
57	Structural basis for antibody inhibition of flavivirus NS1-triggered endothelial dysfunction. <i>Science</i> , 2021, 371, 194-200.	6.0	74
58	A Role for Mitochondrial Translation in Promotion of Viability in K-Ras Mutant Cells. <i>Cell Reports</i> , 2017, 20, 427-438.	2.9	73
59	MAPK Pathway Suppression Unmasks Latent DNA Repair Defects and Confers a Chemical Synthetic Vulnerability in <i>BRAF</i> -, <i>NRAS</i> -, and <i>NF1</i> -Mutant Melanomas. <i>Cancer Discovery</i> , 2019, 9, 526-545.	7.7	73
60	Human <i>CPR</i> (Cell Cycle Progression Restoration) Genes Impart a Far Phenotype on Yeast Cells. <i>Genetics</i> , 1997, 147, 1063-1076.	1.2	72
61	Stopped for repairs. <i>BioEssays</i> , 1995, 17, 545-548.	1.2	70
62	Aneuploidy in Cancer: Seq-ing Answers to Old Questions. <i>Annual Review of Cancer Biology</i> , 2017, 1, 335-354.	2.3	65
63	Sources of Error in Mammalian Genetic Screens. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2781-2790.	0.8	64
64	Brief Report: Anti-RNPC Antibodies As a Marker of Cancer-Associated Scleroderma. <i>Arthritis and Rheumatology</i> , 2017, 69, 1306-1312.	2.9	61
65	A genetic interaction analysis identifies cancer drivers that modify EGFR dependency. <i>Genes and Development</i> , 2017, 31, 184-196.	2.7	58
66	Antibody responses to endemic coronaviruses modulate COVID-19 convalescent plasma functionality. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	58
67	Integrated proteogenetic analysis reveals the landscape of a mitochondrial-autophagosome synapse during PARK2-dependent mitophagy. <i>Science Advances</i> , 2019, 5, eaay4624.	4.7	55
68	Mechanism of DNA interstrand cross-link processing by repair nuclease FAN1. <i>Science</i> , 2014, 346, 1127-1130.	6.0	53
69	Protein interaction discovery using parallel analysis of translated ORFs (PLATO). <i>Nature Biotechnology</i> , 2013, 31, 331-334.	9.4	52
70	Profiling DNA damage-induced phosphorylation in budding yeast reveals diverse signaling networks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E3667-75.	3.3	52
71	Genetic modifiers of the BRD4-NUT dependency of NUT midline carcinoma uncovers a synergism between BETs and CDK4/6is. <i>Genes and Development</i> , 2018, 32, 1188-1200.	2.7	52
72	A Serial shRNA Screen for Roadblocks to Reprogramming Identifies the Protein Modifier SUMO2. <i>Stem Cell Reports</i> , 2016, 6, 704-716.	2.3	50

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73	A Druggable Genome Screen Identifies Modifiers of α -Synuclein Levels via a Tiered Cross-Species Validation Approach. <i>Journal of Neuroscience</i> , 2018, 38, 9286-9301.	1.7	49
74	Comprehensive Identification of Host Modulators of HIV-1 Replication using Multiple Orthologous RNAi Reagents. <i>Cell Reports</i> , 2014, 9, 752-766.	2.9	48
75	Mitotic treasures in the nucleolus. <i>Nature</i> , 1999, 398, 757-758.	13.7	43
76	FACT Proteins, SUPT16H and SSRP1, Are Transcriptional Suppressors of HIV-1 and HTLV-1 That Facilitate Viral Latency. <i>Journal of Biological Chemistry</i> , 2015, 290, 27297-27310.	1.6	43
77	CARM1 Inhibition Enables Immunotherapy of Resistant Tumors by Dual Action on Tumor Cells and T Cells. <i>Cancer Discovery</i> , 2021, 11, 2050-2071.	7.7	43
78	An adjuvant strategy enabled by modulation of the physical properties of microbial ligands expands antigen immunogenicity. <i>Cell</i> , 2022, 185, 614-629.e21.	13.5	40
79	Functional kinomics establishes a critical node of volume-sensitive cation-Cl ⁻ cotransporter regulation in the mammalian brain. <i>Scientific Reports</i> , 2016, 6, 35986.	1.6	38
80	Cloning of the complete coding region for human protein phosphatase inhibitor 2 using the two hybrid system and expression of inhibitor 2 in <i>E. coli</i> . <i>FEBS Letters</i> , 1994, 340, 93-98.	1.3	36
81	Systematic characterization of mutations altering protein degradation in human cancers. <i>Molecular Cell</i> , 2021, 81, 1292-1308.e11.	4.5	36
82	A family of vectors that facilitate transposon and insertional mutagenesis of cloned genes in yeast. <i>Yeast</i> , 1994, 10, 1267-1272.	0.8	35
83	<i>Chlamydia trachomatis</i> -Induced Alterations in the Host Cell Proteome Are Required for Intracellular Growth. <i>Cell Host and Microbe</i> , 2014, 15, 113-124.	5.1	35
84	A Deregulated HOX Gene Axis Confers an Epigenetic Vulnerability in KRAS-Mutant Lung Cancers. <i>Cancer Cell</i> , 2020, 37, 705-719.e6.	7.7	35
85	Identification of FUBP1 as a Long Tail Cancer Driver and Widespread Regulator of Tumor Suppressor and Oncogene Alternative Splicing. <i>Cell Reports</i> , 2019, 28, 3435-3449.e5.	2.9	32
86	Coordinate regulation of the senescent state by selective autophagy. <i>Developmental Cell</i> , 2021, 56, 1512-1525.e7.	3.1	29
87	Conducting the mitotic symphony. <i>Nature</i> , 2000, 406, 354-356.	13.7	28
88	Genetic interrogation of replicative senescence uncovers a dual role for USP28 in coordinating the p53 and GATA4 branches of the senescence program. <i>Genes and Development</i> , 2017, 31, 1933-1938.	2.7	28
89	Natural selection contributed to immunological differences between hunter-gatherers and agriculturalists. <i>Nature Ecology and Evolution</i> , 2019, 3, 1253-1264.	3.4	28
90	Ontogeny of Recognition Specificity and Functionality for the Broadly Neutralizing Anti-HIV Antibody 4E10. <i>PLoS Pathogens</i> , 2014, 10, e1004403.	2.1	27

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91	NatB Domain-Containing CRA-1 Antagonizes Hydrolase ACER-1 Linking Acetyl-CoA Metabolism to the Initiation of Recombination during <i>C. elegans</i> Meiosis. <i>PLoS Genetics</i> , 2015, 11, e1005029.	1.5	27
92	Comprehensive Profiling of HIV Antibody Evolution. <i>Cell Reports</i> , 2019, 27, 1422-1433.e4.	2.9	27
93	ORF10â€Cullin-2â€ZYG11B complex is not required for SARS-CoV-2 infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	26
94	High-resolution epitope mapping by AllerScan reveals relationships between IgE and IgG repertoires during peanut oral immunotherapy. <i>Cell Reports Medicine</i> , 2021, 2, 100410.	3.3	25
95	Empirical identification and validation of tumor-targeting T cell receptors from circulation using autologous pancreatic tumor organoids. , 2021, 9, e003213.		25
96	RNAi-based functional selection identifies novel cell migration determinants dependent on PI3K and AKT pathways. <i>Nature Communications</i> , 2014, 5, 5217.	5.8	24
97	A gain-of-function senescence bypass screen identifies the homeobox transcription factor DLX2 as a regulator of ATMâ€p53 signaling. <i>Genes and Development</i> , 2016, 30, 293-306.	2.7	24
98	PAT1 , an evolutionarily conserved acetyltransferase homologue, is required for multiple steps in the cell cycle. <i>Genes To Cells</i> , 1996, 1, 923-942.	0.5	21
99	Troponin T is capable of binding dystrophin via a leucine zipper. <i>FEBS Letters</i> , 1994, 354, 183-186.	1.3	18
100	The Protexin complex counters resection on stalled forks to promote homologous recombination and crosslink repair. <i>Molecular Cell</i> , 2021, 81, 4440-4456.e7.	4.5	17
101	Gain-of-function genetic screening identifies the antiviral function of TMEM120A via STING activation. <i>Nature Communications</i> , 2022, 13, 105.	5.8	17
102	Temporal virus serological profiling of kidney graft recipients using VirScan. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 10899-10904.	3.3	16
103	Discovery of protein interactions using parallel analysis of translated ORFs (PLATO). <i>Nature Protocols</i> , 2014, 9, 90-103.	5.5	15
104	Interspecies analysis of MYC targets identifies tRNA synthetases as mediators of growth and survival in MYC-overexpressing cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 14614-14619.	3.3	14
105	Identification of S-phase DNA damage-response targets in fission yeast reveals conservation of damage-response networks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E3676-E3685.	3.3	13
106	CRISPR-based peptide library display and programmable microarray self-assembly for rapid quantitative protein binding assays. <i>Molecular Cell</i> , 2021, 81, 3650-3658.e5.	4.5	13
107	The DNA Damage Responseâ€Self-awareness for DNA. <i>JAMA - Journal of the American Medical Association</i> , 2015, 314, 1111.	3.8	12
108	Genetic analysis of cancer drivers reveals cohesin and CTCF as suppressors of PD-L1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	12

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109	Functional genomics reveals that tumors with activating phosphoinositide 3-kinase mutations are dependent on accelerated protein turnover. <i>Genes and Development</i> , 2016, 30, 2684-2695.	2.7	11
110	Robust dengue virus infection in bat cells and limited innate immune responses coupled with positive serology from bats in IndoMalaya and Australasia. <i>Cellular and Molecular Life Sciences</i> , 2020, 77, 1607-1622.	2.4	11
111	Integrated loss- and gain-of-function screens define a core network governing human embryonic stem cell behavior. <i>Genes and Development</i> , 2021, 35, 1527-1547.	2.7	11
112	Aneuploidy Police Detect Chromosomal Imbalance Triggering Immune Crackdown!. <i>Trends in Genetics</i> , 2017, 33, 662-664.	2.9	9
113	Comprehensive viromewide antibody responses by systematic epitope scanning after hematopoietic cell transplantation. <i>Blood</i> , 2019, 134, 503-514.	0.6	9
114	High-Throughput Screening of Kawasaki Disease Sera for Antiviral Antibodies. <i>Journal of Infectious Diseases</i> , 2020, 222, 1853-1857.	1.9	9
115	A GATA4-regulated secretory program suppresses tumors through recruitment of cytotoxic CD8 T cells. <i>Nature Communications</i> , 2022, 13, 256.	5.8	8
116	VirScan: High-throughput Profiling of Antiviral Antibody Epitopes. <i>Bio-protocol</i> , 2022, 12, .	0.2	7
117	Diversified Application of Barcoded PLATO (PLATO-BC) Platform for Identification of Protein Interactions. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 319-331.	3.0	5
118	V-CARMA: A tool for the detection and modification of antigen-specific T cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2116277119.	3.3	5
119	Taking the brakes off telomerase. <i>ELife</i> , 2015, 4, .	2.8	3
120	When noise makes music: HIV reactivation with transcriptional noise enhancers. <i>Genome Medicine</i> , 2014, 6, 55.	3.6	1
121	The uncharacterized SANT and BTB domain-containing protein SANBR inhibits class switch recombination. <i>Journal of Biological Chemistry</i> , 2021, 296, 100625.	1.6	1
122	Reply. <i>Arthritis and Rheumatology</i> , 2017, 69, 1915-1916.	2.9	0
123	Sequencer Hacking Unlocks Quantitative Protein Studies. <i>Molecular Cell</i> , 2019, 73, 863-865.	4.5	0
124	Checkpoint signaling and protein degradation. <i>FASEB Journal</i> , 2007, 21, A154.	0.2	0