

Jack Greenblatt

List of Publications by Year in descending order

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66
papers

12,562
citations

71102

41
h-index

110387

64
g-index

67
all docs

67
docs citations

67
times ranked

13910
citing authors

#	ARTICLE	IF	CITATIONS
1	Epstein-Barr Virus BGLF2 commandeers RISC to interfere with cellular miRNA function. <i>PLoS Pathogens</i> , 2022, 18, e1010235.	4.7	6
2	Characterization of a cancer-associated Epstein-Barr virus EBNA1 variant reveals a novel interaction with PLOD1 and PLOD3. <i>Virology</i> , 2021, 562, 103-109.	2.4	7
3	Identification of ARKL1 as a Negative Regulator of Epstein-Barr Virus Reactivation. <i>Journal of Virology</i> , 2019, 93, .	3.4	4
4	The Med31 Conserved Component of the Divergent Mediator Complex in <i>Tetrahymena thermophila</i> Participates in Developmental Regulation. <i>Current Biology</i> , 2019, 29, 2371-2379.e6.	3.9	13
5	The Epstein-Barr Virus BMRF1 Protein Activates Transcription and Inhibits the DNA Damage Response by Binding NuRD. <i>Journal of Virology</i> , 2019, 93, .	3.4	16
6	USP7 Regulates Cytokinesis through FBXO38 and KIF20B. <i>Scientific Reports</i> , 2019, 9, 2724.	3.3	25
7	Direct interaction between the PRDM3 and PRDM16 tumor suppressors and the NuRD chromatin remodeling complex. <i>Nucleic Acids Research</i> , 2019, 47, 1225-1238.	14.5	32
8	Epstein-Barr virus BORF2 inhibits cellular APOBEC3B to preserve viral genome integrity. <i>Nature Microbiology</i> , 2019, 4, 78-88.	13.3	95
9	Identification and Characterization of USP7 Targets in Cancer Cells. <i>Scientific Reports</i> , 2018, 8, 15833.	3.3	43
10	A Screen for Epstein-Barr Virus Proteins That Inhibit the DNA Damage Response Reveals a Novel Histone Binding Protein. <i>Journal of Virology</i> , 2018, 92, .	3.4	30
11	Proteome-wide dataset supporting the study of ancient metazoan macromolecular complexes. <i>Data in Brief</i> , 2016, 6, 715-721.	1.0	5
12	C2H2 zinc finger proteins greatly expand the human regulatory lexicon. <i>Nature Biotechnology</i> , 2015, 33, 555-562.	17.5	271
13	Extracting high confidence protein interactions from affinity purification data: At the crossroads. <i>Journal of Proteomics</i> , 2015, 118, 63-80.	2.4	30
14	Panorama of ancient metazoan macromolecular complexes. <i>Nature</i> , 2015, 525, 339-344.	27.8	478
15	Quantitative Genome-Wide Genetic Interaction Screens Reveal Global Epistatic Relationships of Protein Complexes in <i>Escherichia coli</i> . <i>PLoS Genetics</i> , 2014, 10, e1004120.	3.5	96
16	Human-Chromatin-Related Protein Interactions Identify a Demethylase Complex Required for Chromosome Segregation. <i>Cell Reports</i> , 2014, 8, 297-310.	6.4	72
17	Networks of Histone Demethylases and Their Relevance to the Regulation of Chromatin Structure and Dynamics. , 2014, , 1-32.		0
18	Histone Methyltransferase Complexes in Transcription, Development, and Cancer. , 2014, , 33-47.		0

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19	Mapping Bacterial Functional Networks and Pathways in <i>Escherichia coli</i> using Synthetic Genetic Arrays. <i>Journal of Visualized Experiments</i> , 2012, , .	0.3	9
20	Identification of Protein Complexes in <i>Escherichia coli</i> using Sequential Peptide Affinity Purification in Combination with Tandem Mass Spectrometry. <i>Journal of Visualized Experiments</i> , 2012, , .	0.3	2
21	Array-Based Synthetic Genetic Screens to Map Bacterial Pathways and Functional Networks in <i>Escherichia coli</i> . <i>Methods in Molecular Biology</i> , 2011, 765, 125-153.	0.9	7
22	A dual function of the CRISPR-Cas system in bacterial antiviral immunity and DNA repair. <i>Molecular Microbiology</i> , 2011, 79, 484-502.	2.5	241
23	A Lentiviral Functional Proteomics Approach Identifies Chromatin Remodeling Complexes Important for the Induction of Pluripotency. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 811-823.	3.8	83
24	Epistatic relationships reveal the functional organization of yeast transcription factors. <i>Molecular Systems Biology</i> , 2010, 6, 420.	7.2	50
25	Conserved Network of Proteins Essential for Bacterial Viability. <i>Journal of Bacteriology</i> , 2009, 191, 4732-4749.	2.2	71
26	Two-Color Cell Array Screen Reveals Interdependent Roles for Histone Chaperones and a Chromatin Boundary Regulator in Histone Gene Repression. <i>Molecular Cell</i> , 2009, 35, 340-351.	9.7	88
27	An atlas of chaperone-protein interactions in <i>Saccharomyces cerevisiae</i> : implications to protein folding pathways in the cell. <i>Molecular Systems Biology</i> , 2009, 5, 275.	7.2	202
28	Interacting proteins Rtt109 and Vps75 affect the efficiency of non-homologous end-joining in <i>Saccharomyces cerevisiae</i> . <i>Archives of Biochemistry and Biophysics</i> , 2008, 469, 157-164.	3.0	39
29	Local coherence in genetic interaction patterns reveals prevalent functional versatility. <i>Bioinformatics</i> , 2008, 24, 2376-2383.	4.1	26
30	Systematic Analysis of the Protein Interaction Network for the Human Transcription Machinery Reveals the Identity of the 7SK Capping Enzyme. <i>Molecular Cell</i> , 2007, 27, 262-274.	9.7	404
31	Investigating the in vivo activity of the DeaD protein using protein-protein interactions and the translational activity of structured chloramphenicol acetyltransferase mRNAs. <i>Journal of Cellular Biochemistry</i> , 2007, 100, 642-652.	2.6	19
32	Identifying functional modules in the physical interactome of <i>Saccharomyces cerevisiae</i> . <i>Proteomics</i> , 2007, 7, 944-960.	2.2	135
33	PIPE: a protein-protein interaction prediction engine based on the re-occurring short polypeptide sequences between known interacting protein pairs. <i>BMC Bioinformatics</i> , 2006, 7, 365.	2.6	157
34	Formation of a Distinctive Complex between the Inducible Bacterial Lysine Decarboxylase and a Novel AAA+ ATPase. <i>Journal of Biological Chemistry</i> , 2006, 281, 1532-1546.	3.4	54
35	Interaction network containing conserved and essential protein complexes in <i>Escherichia coli</i> . <i>Nature</i> , 2005, 433, 531-537.	27.8	1,093
36	Navigating the Chaperone Network: An Integrative Map of Physical and Genetic Interactions Mediated by the Hsp90 Chaperone. <i>Cell</i> , 2005, 120, 715-727.	28.9	729

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37	Global Mapping of the Yeast Genetic Interaction Network. <i>Science</i> , 2004, 303, 808-813.	12.6	1,908
38	The functional landscape of mouse gene expression. <i>Journal of Biology</i> , 2004, 3, 21.	2.7	259
39	Solution Structure of the Carboxyl-Terminal Domain of RAP74 and NMR Characterization of the FCP1-Binding Sites of RAP74 and Human TFIIB. <i>Biochemistry</i> , 2003, 42, 1460-1469.	2.5	19
40	Methylation of Histone H3 by Set2 in <i>Saccharomyces cerevisiae</i> Is Linked to Transcriptional Elongation by RNA Polymerase II. <i>Molecular and Cellular Biology</i> , 2003, 23, 4207-4218.	2.3	600
41	NMR structure of a complex containing the TFIIF subunit RAP74 and the RNA polymerase II carboxyl-terminal domain phosphatase FCP1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 5688-5693.	7.1	38
42	Organization and Function of APT, a Subcomplex of the Yeast Cleavage and Polyadenylation Factor Involved in the Formation of mRNA and Small Nucleolar RNA 3'-Ends. <i>Journal of Biological Chemistry</i> , 2003, 278, 33000-33010.	3.4	161
43	Regulation of transcription elongation by phosphorylation. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 2002, 1577, 261-275.	2.4	169
44	Opposing effects of Ctk1 kinase and Fcp1 phosphatase at Ser 2 of the RNA polymerase II C-terminal domain. <i>Genes and Development</i> , 2001, 15, 3319-3329.	5.9	356
45	The Acute Myeloid Leukemia-Associated Protein, Dek, Forms a Splicing-Dependent Interaction with Exon-Product Complexes. <i>Journal of Cell Biology</i> , 2000, 150, 309-320.	5.2	118
46	Topological Localization of the Carboxyl-Terminal Domain of RNA Polymerase II in the Initiation Complex. <i>Journal of Biological Chemistry</i> , 1999, 274, 19868-19873.	3.4	15
47	Activation of the Murine Dihydrofolate Reductase Promoter by E2F1. <i>Journal of Biological Chemistry</i> , 1999, 274, 15883-15891.	3.4	47
48	Functional importance of regions in Escherichia coli elongation factor NusA that interact with RNA polymerase, the bacteriophage lambda N protein and RNA. <i>Molecular Microbiology</i> , 1999, 34, 523-537.	2.5	50
49	NMR Structure of the Bacteriophage λ N Peptide/boxB RNA Complex: Recognition of a GNRA Fold by an Arginine-Rich Motif. <i>Cell</i> , 1998, 93, 289-299.	28.9	257
50	Interaction of Elongation Factors TFIIS and Elongin A with a Human RNA Polymerase II Holoenzyme Capable of Promoter-specific Initiation and Responsive to Transcriptional Activators. <i>Journal of Biological Chemistry</i> , 1997, 272, 24563-24571.	3.4	90
51	Methods for Measurement of Intermolecular NOEs by Multinuclear NMR Spectroscopy: Application to a Bacteriophage λ N-Peptide/boxBRNA Complex. <i>Journal of the American Chemical Society</i> , 1997, 119, 6711-6721.	13.7	583
52	RNA polymerase II holoenzyme and transcriptional regulation. <i>Current Opinion in Cell Biology</i> , 1997, 9, 310-319.	5.4	105
53	Modular organization of the E2F1 activation domain and its interaction with general transcription factors TBP and TFIIF. <i>Oncogene</i> , 1997, 15, 2643-2658.	5.9	52
54	The C-terminal domain of RNA polymerase II couples mRNA processing to transcription. <i>Nature</i> , 1997, 385, 357-361.	27.8	844

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55	Interaction between acidic transcriptional activation domains of herpes simplex virus activator protein VP16 and transcriptional initiation factor IID. <i>Methods in Enzymology</i> , 1996, 274, 120-133.	1.0	5
56	The upstream activator CTF/NF1 and RNA polymerase II share a common element involved in transcriptional activation. <i>Nucleic Acids Research</i> , 1994, 22, 1966-1973.	14.5	60
57	Altered promoter binding of the TATA box-binding factor induced by the transcriptional activation domain of VP16 and suppressed by TF11A. <i>Molecular Genetics and Genomics</i> , 1993, 241-241, 694-699.	2.4	13
58	Transcriptional antitermination. <i>Nature</i> , 1993, 364, 401-406.	27.8	253
59	The transactivator proteins VP16 and GAL4 bind replication factor A. <i>Cell</i> , 1993, 73, 1223-1232.	28.9	247
60	Riding high on the TATA box. <i>Nature</i> , 1992, 360, 16-17.	27.8	37
61	Roles of TFIID in transcriptional initiation by RNA polymerase II. <i>Cell</i> , 1991, 66, 1067-1070.	28.9	199
62	Reduced binding of TFIID to transcriptionally compromised mutants of VP16. <i>Nature</i> , 1991, 351, 588-590.	27.8	365
63	[3] Using protein affinity chromatography to probe structure of protein machines. <i>Methods in Enzymology</i> , 1991, 208, 24-45.	1.0	53
64	Direct and selective binding of an acidic transcriptional activation domain to the TATA-box factor TFIID. <i>Nature</i> , 1990, 345, 783-786.	27.8	681
65	Structure and associated DNA-helicase activity of a general transcription initiation factor that binds to RNA polymerase II. <i>Nature</i> , 1989, 341, 410-414.	27.8	205
66	Termination of transcription by nusA gene protein of Escherichia coli. <i>Nature</i> , 1981, 292, 215-220.	27.8	141