Peter Uetz

List of Publications by Year
in descending order

119 papers	13,855 citations	47006 47 h-index	21540 114 g-index
138 all docs	138 docs citations	138 times ranked	15401 citing authors

#	Article	IF	Citations
1	A comprehensive analysis of protein–protein interactions in Saccharomyces cerevisiae. Nature, 2000, 403, 623-627.	27.8	4,490
2	A network of protein–protein interactions in yeast. Nature Biotechnology, 2000, 18, 1257-1261.	17.5	1,281
3	The Magnitude of Global Marine Species Diversity. Current Biology, 2012, 22, 2189-2202.	3.9	797
4	Conserved patterns of protein interaction in multiple species. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 1974-1979.	7.1	714
5	Protein interaction data curation: the International Molecular Exchange (IMEx) consortium. Nature Methods, 2012, 9, 345-350.	19.0	500
6	Herpesviral Protein Networks and Their Interaction with the Human Proteome. Science, 2006, 311, 239-242.	12.6	399
7	The global distribution of tetrapods reveals a need for targeted reptile conservation. Nature Ecology and Evolution, 2017, 1, 1677-1682.	7.8	378
8	The minimum information required for reporting a molecular interaction experiment (MIMIx). Nature Biotechnology, 2007, 25, 894-898.	17.5	274
9	The Burmese python genome reveals the molecular basis for extreme adaptation in snakes. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 20645-20650.	7.1	260
10	The binary protein-protein interaction landscape of Escherichia coli. Nature Biotechnology, 2014, 32, 285-290.	17.5	218
11	Towards an understanding of complex protein networks. Trends in Cell Biology, 2001, 11, 102-106.	7.9	164
12	Evolutionarily Conserved Herpesviral Protein Interaction Networks. PLoS Pathogens, 2009, 5, e1000570.	4.7	162
13	Global Taxonomic Diversity of Living Reptiles. PLoS ONE, 2013, 8, e59741.	2.5	129
14	Systematic and large-scale two-hybrid screens. Current Opinion in Microbiology, 2000, 3, 303-308.	5.1	125
15	MPIDB: the microbial protein interaction database. Bioinformatics, 2008, 24, 1743-1744.	4.1	118
16	Are lizards feeling the heat? A tale of ecology and evolution under two temperatures. Global Ecology and Biogeography, 2013, 22, 834-845.	5.8	116
17	Improving the yeast two-hybrid system with permutated fusions proteins: the Varicella Zoster Virus interactome. Proteome Science, 2010, 8, 8.	1.7	114
18	Protein Domains of Unknown Function Are Essential in Bacteria. MBio, 2014, 5, e00744-13.	4.1	112

#	Article	IF	Citations
19	A decadal view of biodiversity informatics: challenges and priorities. BMC Ecology, 2013, 13, 16.	3.0	110
20	Global landscape of cell envelope protein complexes in Escherichia coli. Nature Biotechnology, 2018, 36, 103-112.	17.5	110
21	The protein network of bacterial motility. Molecular Systems Biology, 2007, 3, 128.	7.2	103
22	Exhaustive benchmarking of the yeast two-hybrid system. Nature Methods, 2010, 7, 667-668.	19.0	103
23	[1] High-throughput screening for protein-protein interactions using two-hybrid assay. Methods in Enzymology, 2000, 328, 3-14.	1.0	100
24	Marine Reptiles. PLoS ONE, 2011, 6, e27373.	2.5	96
25	The Binary Protein Interactome of Treponema pallidum â€" The Syphilis Spirochete. PLoS ONE, 2008, 3, e2292.	2.5	92
26	RsfA (YbeB) Proteins Are Conserved Ribosomal Silencing Factors. PLoS Genetics, 2012, 8, e1002815.	3.5	88
27	What do we learn from high-throughput protein interaction data?. Expert Review of Proteomics, 2004, 1, 111-121.	3.0	86
28	Transcriptional activators in yeast. Nucleic Acids Research, 2006, 34, 955-967.	14.5	84
29	Two-hybrid arrays. Current Opinion in Chemical Biology, 2002, 6, 57-62.	6.1	83
30	The E. coli Effector Protein NleF Is a Caspase Inhibitor. PLoS ONE, 2013, 8, e58937.	2.5	83
31	Improving yeast two-hybrid screening systems. Briefings in Functional Genomics & Proteomics, 2008, 6, 302-312.	3.8	80
32	Late bloomers and baby boomers: ecological drivers of longevity in squamates and the tuatara. Global Ecology and Biogeography, 2015, 24, 396-405.	5.8	78
33	From protein networks to biological systems. FEBS Letters, 2005, 579, 1821-1827.	2.8	75
34	The elusive yeast interactome. Genome Biology, 2006, 7, 223.	9.6	73
35	Two-hybrid analysis of the<i>Saccharomyces cerevisiae</i>26S proteasome. Physiological Genomics, 2001, 7, 27-34.	2.3	67
36	Extinct, obscure or imaginary: The lizard species with the smallest ranges. Diversity and Distributions, 2018, 24, 262-273.	4.1	66

#	Article	IF	Citations
37	The protein interaction map of bacteriophage lambda. BMC Microbiology, 2011, 11, 213.	3.3	65
38	Bacteriophage Protein–Protein Interactions. Advances in Virus Research, 2012, 83, 219-298.	2.1	61
39	Sequencing the genome of the Burmese python (Python molurus bivittatus) as a model for studying extreme adaptations in snakes. Genome Biology, 2011, 12, 406.	9.6	58
40	Ubiquitin-like Protein Hub1 Is Required for Pre-mRNA Splicing and Localization of an Essential Splicing Factor in Fission Yeast. Current Biology, 2004, 14, 2283-2288.	3.9	56
41	The Yeast G Protein Î± Subunit Gpa1 Transmits a Signal through an RNA Binding Effector Protein Scp160. Molecular Cell, 2003, 12, 517-524.	9.7	55
42	Benchmarking yeast two‐hybrid systems using the interactions of bacterial motility proteins. Proteomics, 2009, 9, 5296-5302.	2.2	55
43	A Second-generation Protein–Protein Interaction Network of Helicobacter pylori. Molecular and Cellular Proteomics, 2014, 13, 1318-1329.	3.8	55
44	Toward More Transparent and Reproducible Omics Studies Through a Common Metadata Checklist and Data Publications. OMICS A Journal of Integrative Biology, 2014, 18, 10-14.	2.0	54
45	The Phox Homology (PX) Domain Protein Interaction Network in Yeast. Molecular and Cellular Proteomics, 2004, 3, 1053-1064.	3.8	53
46	The original descriptions of reptiles. Zootaxa, 2010, 2334, 59.	0.5	53
47	The Escherichia coli K-12 ORFeome: a resource for comparative molecular microbiology. BMC Genomics, 2010, 11, 470.	2.8	50
48	Genome Annotation and Intraviral Interactome for the <i>Streptococcus pneumoniae</i> Virulent Phage Dp-1. Journal of Bacteriology, 2011, 193, 551-562.	2.2	50
49	Functional elucidation of antibacterial phage ORFans targeting<i>P</i><i>seudomonas aeruginosa</i>. Cellular Microbiology, 2014, 16, 1822-1835.	2.1	47
50	The phosphocarrier protein HPr of the bacterial phosphotransferase system globally regulates energy metabolism by directly interacting with multiple enzymes in Escherichia coli. Journal of Biological Chemistry, 2017, 292, 14250-14257.	3.4	42
51	Regulation of Stress Response Signaling by the N-terminal Dishevelled/EGL-10/Pleckstrin Domain of Sst2, a Regulator of G Protein Signaling in Saccharomyces cerevisiae. Journal of Biological Chemistry, 2002, 277, 22156-22167.	3.4	40
52	The FF domains of yeast U1 snRNP protein Prp40 mediate interactions with Luc7 and Snu71. BMC Biochemistry, 2008, 9, 29.	4.4	40
53	The Yeast Two-Hybrid System: A Tool for Mapping Protein–Protein Interactions. Cold Spring Harbor Protocols, 2015, 2015, pdb.top083345.	0.3	40
54	A global catalog of primary reptile type specimens. Zootaxa, 2019, 4695, zootaxa.4695.5.2.	0.5	38

#	Article	IF	Citations
55	The geography of snake reproductive mode: a global analysis of the evolution of snake viviparity. Global Ecology and Biogeography, 2015, 24, 1433-1442.	5.8	36
56	A Comparison of Two-Hybrid Approaches for Detecting Protein–Protein Interactions. Methods in Enzymology, 2017, 586, 333-358.	1.0	36
57	Novel Conserved Assembly Factor of the Bacterial Flagellum. Journal of Bacteriology, 2006, 188, 7700-7706.	2.2	35
58	The EHEC-host interactome reveals novel targets for the translocated intimin receptor. Scientific Reports, 2014, 4, 7531.	3.3	35
59	Protein-protein interactions of human viruses. Seminars in Cell and Developmental Biology, 2020, 99, 31-39.	5.0	34
60	Organisation of the murine 5-HT3receptor gene and assignment tohuman chromosome 11. FEBS Letters, 1994, 339, 302-306.	2.8	33
61	Molecular Interaction between Limb Deformity Proteins (Formins) and Src Family Kinases. Journal of Biological Chemistry, 1996, 271, 33525-33530.	3.4	32
62	Global approaches to study protein–protein interactions among viruses and hosts. Future Microbiology, 2010, 5, 289-301.	2.0	32
63	From ORFeomes to Protein Interaction Maps in Viruses. Genome Research, 2004, 14, 2029-2033.	5.5	31
64	An ontology for microbial phenotypes. BMC Microbiology, 2014, 14, 294.	3.3	31
65	The original descriptions of reptiles and their subspecies. Zootaxa, 2018, 4375, 257-264.	0.5	31
66	The Protein Interaction Network of Bacteriophage Lambda with Its Host, Escherichia coli. Journal of Virology, 2013, 87, 12745-12755.	3.4	30
67	The Spindle Pole Body Assembly Component Mps3p/Nep98p Functions in Sister Chromatid Cohesion. Journal of Biological Chemistry, 2004, 279, 49542-49550.	3.4	29
68	A comparison and optimization of yeast two-hybrid systems. Methods, 2012, 58, 317-324.	3.8	28
69	TheEscherichia coliprotein YjjG is a house-cleaning nucleotidasein vivo. FEMS Microbiology Letters, 2007, 270, 49-57.	1.8	27
70	Protein interaction maps on the fly. Nature Biotechnology, 2004, 22, 43-44.	17.5	26
71	Conservation status of the world's skinks (Scincidae): Taxonomic and geographic patterns in extinction risk. Biological Conservation, 2021, 257, 109101.	4.1	26
72	Studying protein complexes by the yeast two-hybrid system. Methods, 2012, 58, 392-399.	3.8	24

#	Article	IF	Citations
73	Protein-protein Interaction Networks of E. coli and S. cerevisiae are similar. Scientific Reports, 2014, 4, 7187.	3.3	24
74	Analysis of Protein–Protein Interactions Using High-Throughput Yeast Two-Hybrid Screens. Methods in Molecular Biology, 2011, 781, 1-29.	0.9	22
75	The global biogeography of lizard functional groups. Journal of Biogeography, 2019, 46, 2147-2158.	3.0	21
76	Bam35 Tectivirus Intraviral Interaction Map Unveils New Function and Localization of Phage ORFan Proteins. Journal of Virology, 2017, 91, .	3.4	20
77	Bacterial protein meta-interactomes predict cross-species interactions and protein function. BMC Bioinformatics, 2017, 18, 171.	2.6	19
78	The Nitrogen Regulatory PII Protein (GlnB) and N-Acetylglucosamine 6-Phosphate Epimerase (NanE) Allosterically Activate Glucosamine 6-Phosphate Deaminase (NagB) in Escherichia coli. Journal of Bacteriology, 2018, 200, .	2.2	19
79	Analysis of Protein–Protein Interactions Using Array-Based Yeast Two-Hybrid Screens. Methods in Molecular Biology, 2009, 548, 223-245.	0.9	18
80	The Hepatitis E virus intraviral interactome. Scientific Reports, 2015, 5, 13872.	3.3	18
81	Stable isotope labeling by amino acids in cell culture based proteomics reveals differences in protein abundances between spiral and coccoid forms of the gastric pathogen Helicobacter pylori. Journal of Proteomics, 2015, 126, 34-45.	2.4	17
82	Mapping Protein–Protein Interactions Using Yeast Two-Hybrid Assays. Cold Spring Harbor Protocols, 2015, 2015, pdb.prot086157.	0.3	17
83	The Protein Interactome of Mycobacteriophage Giles Predicts Functions for Unknown Proteins. Journal of Bacteriology, 2015, 197, 2508-2516.	2.2	16
84	Protein Complexes in Bacteria. PLoS Computational Biology, 2015, 11, e1004107.	3.2	16
85	MPI-LIT: a literature-curated dataset of microbial binary protein--protein interactions. Bioinformatics, 2008, 24, 2622-2627.	4.1	15
86	The Proteome and Interactome of Streptococcus pneumoniae Phage Cp-1. Journal of Bacteriology, 2011, 193, 3135-3138.	2.2	15
87	Virus-host protein-protein interactions of mycobacteriophage Giles. Scientific Reports, 2017, 7, 16514.	3.3	15
88	Gecko diversity: a history of global discovery. Israel Journal of Ecology and Evolution, 2020, 66, 117-125.	0.6	14
89	The interactome of human EGF/ErbB receptors. Molecular Systems Biology, 2006, 2, 2006.0006.	7.2	13
90	The uridylyltransferase GlnD and tRNA modification GTPase MnmE allosterically control Escherichia coli folylpoly-γ-glutamate synthase FolC. Journal of Biological Chemistry, 2018, 293, 15725-15732.	3.4	11

#	Article	IF	Citations
91	The interactome of Streptococcus pneumoniae and its bacteriophages show highly specific patterns of interactions among bacteria and their phages. Scientific Reports, 2016, 6, 24597.	3.3	10
92	Citizen science and online data: Opportunities and challenges for snake ecology and action against snakebite. Toxicon: X, 2021, 9-10, 100071.	2.9	10
93	High‐Throughput Screening for Protein‐Protein Interactions Using Yeast Two‐Hybrid Arrays. Current Protocols in Protein Science, 2001, 24, Unit 19.6.	2.8	9
94	ZapG (YhcB/DUF1043), a novel cell division protein in gamma-proteobacteria linking the Z-ring to septal peptidoglycan synthesis. Journal of Biological Chemistry, 2021, 296, 100700.	3.4	9
95	Local Action with Global Impact: Highly Similar Infection Patterns of Human Viruses and Bacteriophages. MSystems, 2016, 1, .	3.8	8
96	Proteome Data Improves Protein Function Prediction in the Interactome of Helicobacter pylori. Molecular and Cellular Proteomics, 2018, 17, 961-973.	3.8	8
97	The disconnect between DNA and species names: lessons from reptile species in the NCBI taxonomy database. Zootaxa, 2019, 4706, zootaxa.4706.3.1.	0.5	8
98	Semi-supervised Learning of Text Classification on Bacterial Protein-Protein Interaction Documents. , 2009, , .		7
99	Species disconnected from DNA sequences. Nature, 2017, 545, 412-412.	27.8	7
100	Vectors for Expression of Protein-A-Tagged Proteins in Vertebrate Cells. Analytical Biochemistry, 1996, 237, 161-163.	2.4	5
101	7 Array-Based Yeast Two-Hybrid Screening for Protein–Protein Interactions. Methods in Microbiology, 2007, 36, 139-701.	0.8	5
102	Analyzing Protein Interaction Networks. , 0, , 1121-1177.		5
103	Toward More Transparent and Reproducible Omics Studies Through a Common Metadata Checklist and Data Publications. Big Data, 2013, 1, 196-201.	3.4	5
104	The Reptile Database: Curating the biodiversity literature without funding. Biodiversity Information Science and Standards, 0, 5, .	0.0	5
105	Matrix-Based Yeast Two-Hybrid Screen Strategies and Comparison of Systems. Methods in Molecular Biology, 2012, 812, 1-20.	0.9	5
106	Ubiquitin-like Protein Hub1 Is Required for pre-mRNA Splicing and Localization of an Essential Splicing Factor in Fission Yeast. Current Biology, 2006, 16, 2488.	3.9	3
107	Experimental Methods for Protein Interaction Identification and Characterization. Computational Biology, 2008, , 1-32.	0.2	3
108	Making the Right Choice: Critical Parameters of the Y2H Systems. Methods in Molecular Biology, 2018, 1794, 17-28.	0.9	3

#	Article	IF	Citations
109	`<p><strong>`An inventory of online reptile images`</strong></p>`. Zootaxa, 2020, 4896, 251-264.	0.5	3
110	The Protein Interactome of Glycolysis in Escherichia coli. Proteomes, 2021, 9, 16.	3.5	3
111	Array-Based Yeast Two-Hybrid Screens: A Practical Guide. Methods in Molecular Biology, 2012, 812, 21-38.	0.9	3
112	The yeast interactome. , 2005, , .		1
113	Comparison of classification methods on protein-protein interaction document classification. , 2008, , .		1
114	Editorial for â€œThe Yeast two-hybrid systemâ€• Methods, 2012, 58, 315-316.	3.8	1
115	Docking features for predicting binding loss due to protein mutation. , 2014, , .		1
116	Predicting nsSNPs that Disrupt Protein-Protein Interactions Using Docking. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 1082-1093.	3.0	1
117	Yeast Two-Hybrid Screens: Improvement of Array-Based Screening Results by N- and C-terminally Tagged Fusion Proteins. Methods in Molecular Biology, 2012, 815, 277-288.	0.9	1
118	Experimental methods for protein interaction identification. , 0, , 53-82.		0
119	ComputergestÃ¼tzte Auswertung von Protein-Interaktions-Screens. Informatik Aktuell, 2004, , 361-365.	0.6	0