

Peter Uetz

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/571663/publications.pdf>

Version: 2024-02-01

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	The Protein Interactome of Glycolysis in Escherichia coli. <i>Proteomes</i> , 2021, 9, 16.	3.5	3
2	Conservation status of the world's skinks (Scincidae): Taxonomic and geographic patterns in extinction risk. <i>Biological Conservation</i> , 2021, 257, 109101.	4.1	26
3	Citizen science and online data: Opportunities and challenges for snake ecology and action against snakebite. <i>Toxicon: X</i> , 2021, 9-10, 100071.	2.9	10
4	ZapG (YhcB/DUF1043), a novel cell division protein in gamma-proteobacteria linking the Z-ring to septal peptidoglycan synthesis. <i>Journal of Biological Chemistry</i> , 2021, 296, 100700.	3.4	9
5	Protein-protein interactions of human viruses. <i>Seminars in Cell and Developmental Biology</i> , 2020, 99, 31-39.	5.0	34
6	<p><p>An inventory of online reptile images</p>. <i>Zootaxa</i>, 2020, 4896, 251-264.</p>	0.5	3
7	Gecko diversity: a history of global discovery. <i>Israel Journal of Ecology and Evolution</i> , 2020, 66, 117-125.	0.6	14
8	The global biogeography of lizard functional groups. <i>Journal of Biogeography</i> , 2019, 46, 2147-2158.	3.0	21
9	A global catalog of primary reptile type specimens. <i>Zootaxa</i> , 2019, 4695, zootaxa.4695.5.2.	0.5	38
10	The disconnect between DNA and species names: lessons from reptile species in the NCBI taxonomy database. <i>Zootaxa</i> , 2019, 4706, zootaxa.4706.3.1.	0.5	8
11	Proteome Data Improves Protein Function Prediction in the Interactome of <i>Helicobacter pylori</i> . <i>Molecular and Cellular Proteomics</i> , 2018, 17, 961-973.	3.8	8
12	Extinct, obscure or imaginary: The lizard species with the smallest ranges. <i>Diversity and Distributions</i> , 2018, 24, 262-273.	4.1	66
13	The Nitrogen Regulatory PII Protein (GlnB) and <i>N</i> -Acetylglucosamine 6-Phosphate Epimerase (NanE) Allosterically Activate Glucosamine 6-Phosphate Deaminase (NagB) in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2018, 200, .	2.2	19
14	The original descriptions of reptiles and their subspecies. <i>Zootaxa</i> , 2018, 4375, 257-264.	0.5	31
15	Making the Right Choice: Critical Parameters of the Y2H Systems. <i>Methods in Molecular Biology</i> , 2018, 1794, 17-28.	0.9	3
16	The uridylyltransferase GlnD and tRNA modification GTPase MnmE allosterically control <i>Escherichia coli</i> folylpoly- β -glutamate synthase FolC. <i>Journal of Biological Chemistry</i> , 2018, 293, 15725-15732.	3.4	11
17	Global landscape of cell envelope protein complexes in <i>Escherichia coli</i> . <i>Nature Biotechnology</i> , 2018, 36, 103-112.	17.5	110
18	Predicting nsSNPs that Disrupt Protein-Protein Interactions Using Docking. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017, 14, 1082-1093.	3.0	1

#	ARTICLE	IF	CITATIONS
19	A Comparison of Two-Hybrid Approaches for Detecting Protein-Protein Interactions. <i>Methods in Enzymology</i> , 2017, 586, 333-358.	1.0	36
20	The phosphocarrier protein HPr of the bacterial phosphotransferase system globally regulates energy metabolism by directly interacting with multiple enzymes in <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 2017, 292, 14250-14257.	3.4	42
21	Species disconnected from DNA sequences. <i>Nature</i> , 2017, 545, 412-412.	27.8	7
22	Bacterial protein meta-interactomes predict cross-species interactions and protein function. <i>BMC Bioinformatics</i> , 2017, 18, 171.	2.6	19
23	The global distribution of tetrapods reveals a need for targeted reptile conservation. <i>Nature Ecology and Evolution</i> , 2017, 1, 1677-1682.	7.8	378
24	Bam35 Tectivirus Intraviral Interaction Map Unveils New Function and Localization of Phage ORFan Proteins. <i>Journal of Virology</i> , 2017, 91, .	3.4	20
25	Virus-host protein-protein interactions of mycobacteriophage Giles. <i>Scientific Reports</i> , 2017, 7, 16514.	3.3	15
26	Local Action with Global Impact: Highly Similar Infection Patterns of Human Viruses and Bacteriophages. <i>MSystems</i> , 2016, 1, .	3.8	8
27	The interactome of <i>Streptococcus pneumoniae</i> and its bacteriophages show highly specific patterns of interactions among bacteria and their phages. <i>Scientific Reports</i> , 2016, 6, 24597.	3.3	10
28	The Hepatitis E virus intraviral interactome. <i>Scientific Reports</i> , 2015, 5, 13872.	3.3	18
29	The Protein Interactome of Mycobacteriophage Giles Predicts Functions for Unknown Proteins. <i>Journal of Bacteriology</i> , 2015, 197, 2508-2516.	2.2	16
30	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 <i>Helicobacter pylori</i> . <i>Journal of Proteomics</i> , 2015, 126, 34-45.	2.4	17
31	Protein Complexes in Bacteria. <i>PLoS Computational Biology</i> , 2015, 11, e1004107.	3.2	16
32	Mapping Protein-Protein Interactions Using Yeast Two-Hybrid Assays. <i>Cold Spring Harbor Protocols</i> , 2015, 2015, pdb.prot086157.	0.3	17
33	The Yeast Two-Hybrid System: A Tool for Mapping Protein-Protein Interactions. <i>Cold Spring Harbor Protocols</i> , 2015, 2015, pdb.top083345.	0.3	40
34	The geography of snake reproductive mode: a global analysis of the evolution of snake viviparity. <i>Global Ecology and Biogeography</i> , 2015, 24, 1433-1442.	5.8	36
35	Late bloomers and baby boomers: ecological drivers of longevity in squamates and the tuatara. <i>Global Ecology and Biogeography</i> , 2015, 24, 396-405.	5.8	78
36	An ontology for microbial phenotypes. <i>BMC Microbiology</i> , 2014, 14, 294.	3.3	31

#	ARTICLE	IF	CITATIONS
37	Docking features for predicting binding loss due to protein mutation. , 2014, , .		1
38	A Second-generation Proteinâ€“Protein Interaction Network of Helicobacter pylori. Molecular and Cellular Proteomics, 2014, 13, 1318-1329.	3.8	55
39	Functional elucidation of antibacterial phage ORFans targeting <i>Pseudomonas aeruginosa</i> . Cellular Microbiology, 2014, 16, 1822-1835.	2.1	47
40	Protein Domains of Unknown Function Are Essential in Bacteria. MBio, 2014, 5, e00744-13.	4.1	112
41	The binary protein-protein interaction landscape of Escherichia coli. Nature Biotechnology, 2014, 32, 285-290.	17.5	218
42	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
43	The EHEC-host interactome reveals novel targets for the translocated intimin receptor. Scientific Reports, 2014, 4, 7531.	3.3	35
44	Protein-protein Interaction Networks of E. coli and S. cerevisiae are similar. Scientific Reports, 2014, 4, 7187.	3.3	24
45	A decadal view of biodiversity informatics: challenges and priorities. BMC Ecology, 2013, 13, 16.	3.0	110
46	The Protein Interaction Network of Bacteriophage Lambda with Its Host, Escherichia coli. Journal of Virology, 2013, 87, 12745-12755.	3.4	30
47	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
48	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
49	Toward More Transparent and Reproducible Omics Studies Through a Common Metadata Checklist and Data Publications. Big Data, 2013, 1, 196-201.	3.4	5
50	The E. coli Effector Protein NleF Is a Caspase Inhibitor. PLoS ONE, 2013, 8, e58937.	2.5	83
51	Global Taxonomic Diversity of Living Reptiles. PLoS ONE, 2013, 8, e59741.	2.5	129
52	RsfA (YbeB) Proteins Are Conserved Ribosomal Silencing Factors. PLoS Genetics, 2012, 8, e1002815.	3.5	88
53	Protein interaction data curation: the International Molecular Exchange (IMEx) consortium. Nature Methods, 2012, 9, 345-350.	19.0	500
54	Studying protein complexes by the yeast two-hybrid system. Methods, 2012, 58, 392-399.	3.8	24

#	ARTICLE	IF	CITATIONS
55	The Magnitude of Global Marine Species Diversity. <i>Current Biology</i> , 2012, 22, 2189-2202.	3.9	797
56	Editorial for "The Yeast two-hybrid system". <i>Methods</i> , 2012, 58, 315-316.	3.8	1
57	Bacteriophage Protein-Protein Interactions. <i>Advances in Virus Research</i> , 2012, 83, 219-298.	2.1	61
58	A comparison and optimization of yeast two-hybrid systems. <i>Methods</i> , 2012, 58, 317-324.	3.8	28
59	Yeast Two-Hybrid Screens: Improvement of Array-Based Screening Results by N- and C-terminally Tagged Fusion Proteins. <i>Methods in Molecular Biology</i> , 2012, 815, 277-288.	0.9	1
60	Matrix-Based Yeast Two-Hybrid Screen Strategies and Comparison of Systems. <i>Methods in Molecular Biology</i> , 2012, 812, 1-20.	0.9	5
61	Array-Based Yeast Two-Hybrid Screens: A Practical Guide. <i>Methods in Molecular Biology</i> , 2012, 812, 21-38.	0.9	3
62	Analysis of Protein-Protein Interactions Using High-Throughput Yeast Two-Hybrid Screens. <i>Methods in Molecular Biology</i> , 2011, 781, 1-29.	0.9	22
63	Sequencing the genome of the Burmese python (<i>Python molurus bivittatus</i>) as a model for studying extreme adaptations in snakes. <i>Genome Biology</i> , 2011, 12, 406.	9.6	58
64	Marine Reptiles. <i>PLoS ONE</i> , 2011, 6, e27373.	2.5	96
65	The protein interaction map of bacteriophage lambda. <i>BMC Microbiology</i> , 2011, 11, 213.	3.3	65
66	The Proteome and Interactome of <i>Streptococcus pneumoniae</i> Phage Cp-1. <i>Journal of Bacteriology</i> , 2011, 193, 3135-3138.	2.2	15
67	Genome Annotation and Intraviral Interactome for the <i>Streptococcus pneumoniae</i> Virulent Phage Dp-1. <i>Journal of Bacteriology</i> , 2011, 193, 551-562.	2.2	50
68	Improving the yeast two-hybrid system with permutated fusions proteins: the Varicella Zoster Virus interactome. <i>Proteome Science</i> , 2010, 8, 8.	1.7	114
69	Exhaustive benchmarking of the yeast two-hybrid system. <i>Nature Methods</i> , 2010, 7, 667-668.	19.0	103
70	The original descriptions of reptiles. <i>Zootaxa</i> , 2010, 2334, 59.	0.5	53
71	Global approaches to study protein-protein interactions among viruses and hosts. <i>Future Microbiology</i> , 2010, 5, 289-301.	2.0	32
72	The <i>Escherichia coli</i> K-12 ORFeome: a resource for comparative molecular microbiology. <i>BMC Genomics</i> , 2010, 11, 470.	2.8	50

#	ARTICLE	IF	CITATIONS
73	Analysis of Protein-Protein Interactions Using Array-Based Yeast Two-Hybrid Screens. <i>Methods in Molecular Biology</i> , 2009, 548, 223-245.	0.9	18
74	Evolutionarily Conserved Herpesviral Protein Interaction Networks. <i>PLoS Pathogens</i> , 2009, 5, e1000570.	4.7	162
75	Benchmarking yeast two-hybrid systems using the interactions of bacterial motility proteins. <i>Proteomics</i> , 2009, 9, 5296-5302.	2.2	55
76	Semi-supervised Learning of Text Classification on Bacterial Protein-Protein Interaction Documents. , 2009, , .		7
77	The FF domains of yeast U1 snRNP protein Prp40 mediate interactions with Luc7 and Snu71. <i>BMC Biochemistry</i> , 2008, 9, 29.	4.4	40
78	Experimental Methods for Protein Interaction Identification and Characterization. <i>Computational Biology</i> , 2008, , 1-32.	0.2	3
79	MPI-LIT: a literature-curated dataset of microbial binary protein-protein interactions. <i>Bioinformatics</i> , 2008, 24, 2622-2627.	4.1	15
80	Improving yeast two-hybrid screening systems. <i>Briefings in Functional Genomics & Proteomics</i> , 2008, 6, 302-312.	3.8	80
81	MPIDB: the microbial protein interaction database. <i>Bioinformatics</i> , 2008, 24, 1743-1744.	4.1	118
82	Comparison of classification methods on protein-protein interaction document classification. , 2008, , .		1
83	The Binary Protein Interactome of <i>Treponema pallidum</i> - The Syphilis Spirochete. <i>PLoS ONE</i> , 2008, 3, e2292.	2.5	92
84	The protein network of bacterial motility. <i>Molecular Systems Biology</i> , 2007, 3, 128.	7.2	103
85	7 Array-Based Yeast Two-Hybrid Screening for Protein-Protein Interactions. <i>Methods in Microbiology</i> , 2007, 36, 139-701.	0.8	5
86	The minimum information required for reporting a molecular interaction experiment (MIMIx). <i>Nature Biotechnology</i> , 2007, 25, 894-898.	17.5	274
87	The <i>Escherichia coli</i> protein YjjG is a house-cleaning nucleotidase <i>in vivo</i> . <i>FEMS Microbiology Letters</i> , 2007, 270, 49-57.	1.8	27
88	The elusive yeast interactome. <i>Genome Biology</i> , 2006, 7, 223.	9.6	73
89	The interactome of human EGF/ErbB receptors. <i>Molecular Systems Biology</i> , 2006, 2, 2006.0006.	7.2	13
90	Transcriptional activators in yeast. <i>Nucleic Acids Research</i> , 2006, 34, 955-967.	14.5	84

#	ARTICLE	IF	CITATIONS
91	Herpesviral Protein Networks and Their Interaction with the Human Proteome. <i>Science</i> , 2006, 311, 239-242.	12.6	399
92	Ubiquitin-like Protein Hub1 Is Required for pre-mRNA Splicing and Localization of an Essential Splicing Factor in Fission Yeast. <i>Current Biology</i> , 2006, 16, 2488.	3.9	3
93	Novel Conserved Assembly Factor of the Bacterial Flagellum. <i>Journal of Bacteriology</i> , 2006, 188, 7700-7706.	2.2	35
94	The yeast interactome. , 2005, , .		1
95	Conserved patterns of protein interaction in multiple species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 1974-1979.	7.1	714
96	From protein networks to biological systems. <i>FEBS Letters</i> , 2005, 579, 1821-1827.	2.8	75
97	The Phox Homology (PX) Domain Protein Interaction Network in Yeast. <i>Molecular and Cellular Proteomics</i> , 2004, 3, 1053-1064.	3.8	53
98	From ORFeomes to Protein Interaction Maps in Viruses. <i>Genome Research</i> , 2004, 14, 2029-2033.	5.5	31
99	The Spindle Pole Body Assembly Component Mps3p/Nep98p Functions in Sister Chromatid Cohesion. <i>Journal of Biological Chemistry</i> , 2004, 279, 49542-49550.	3.4	29
100	Protein interaction maps on the fly. <i>Nature Biotechnology</i> , 2004, 22, 43-44.	17.5	26
101	Ubiquitin-like Protein Hub1 Is Required for Pre-mRNA Splicing and Localization of an Essential Splicing Factor in Fission Yeast. <i>Current Biology</i> , 2004, 14, 2283-2288.	3.9	56
102	What do we learn from high-throughput protein interaction data?. <i>Expert Review of Proteomics</i> , 2004, 1, 111-121.	3.0	86
103	Computergestützte Auswertung von Protein-Interaktions-Screens. <i>Informatik Aktuell</i> , 2004, , 361-365.	0.6	0
104	The Yeast G Protein β Subunit Gpa1 Transmits a Signal through an RNA Binding Effector Protein Scp160. <i>Molecular Cell</i> , 2003, 12, 517-524.	9.7	55
105	Regulation of Stress Response Signaling by the N-terminal Dishevelled/EGL-10/Pleckstrin Domain of Sst2, a Regulator of G Protein Signaling in <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2002, 277, 22156-22167.	3.4	40
106	Two-hybrid arrays. <i>Current Opinion in Chemical Biology</i> , 2002, 6, 57-62.	6.1	83
107	High-throughput Screening for Protein-Protein Interactions Using Yeast Two-hybrid Arrays. <i>Current Protocols in Protein Science</i> , 2001, 24, Unit 19.6.	2.8	9
108	Two-hybrid analysis of the <i>Saccharomyces cerevisiae</i> 26S proteasome. <i>Physiological Genomics</i> , 2001, 7, 27-34.	2.3	67

#	ARTICLE	IF	CITATIONS
109	Towards an understanding of complex protein networks. Trends in Cell Biology, 2001, 11, 102-106.	7.9	164
110	A network of protein-protein interactions in yeast. Nature Biotechnology, 2000, 18, 1257-1261.	17.5	1,281
111	A comprehensive analysis of protein-protein interactions in Saccharomyces cerevisiae. Nature, 2000, 403, 623-627.	27.8	4,490
112	Systematic and large-scale two-hybrid screens. Current Opinion in Microbiology, 2000, 3, 303-308.	5.1	125
113	[1] High-throughput screening for protein-protein interactions using two-hybrid assay. Methods in Enzymology, 2000, 328, 3-14.	1.0	100
114	Vectors for Expression of Protein-A-Tagged Proteins in Vertebrate Cells. Analytical Biochemistry, 1996, 237, 161-163.	2.4	5
115	Molecular Interaction between Limb Deformity Proteins (Formins) and Src Family Kinases. Journal of Biological Chemistry, 1996, 271, 33525-33530.	3.4	32
116	Organisation of the murine 5-HT3receptor gene and assignment to human chromosome 11. FEBS Letters, 1994, 339, 302-306.	2.8	33
117	Analyzing Protein Interaction Networks. , 0, , 1121-1177.		5
118	Experimental methods for protein interaction identification. , 0, , 53-82.		0
119	The Reptile Database: Curating the biodiversity literature without funding. Biodiversity Information Science and Standards, 0, 5, .	0.0	5