

Pedro Beltrao

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3700206/publications.pdf>

Version: 2024-02-01

73
papers

11,916
citations

94269

37
h-index

88477

70
g-index

115
all docs

115
docs citations

115
times ranked

21822
citing authors

#	ARTICLE	IF	CITATIONS
1	High-throughput functional characterization of protein phosphorylation sites in yeast. <i>Nature Biotechnology</i> , 2022, 40, 382-390.	9.4	24
2	Evolution of enhanced innate immune evasion by SARS-CoV-2. <i>Nature</i> , 2022, 602, 487-495.	13.7	237
3	Global post-translational modification profiling of HIV-1-infected cells reveals mechanisms of host cellular pathway remodeling. <i>Cell Reports</i> , 2022, 39, 110690.	2.9	12
4	A high dimensional map of phosphorylation-dependent signaling in budding yeast. <i>FASEB Journal</i> , 2022, 36, .	0.2	0
5	Sequence and Structure-Based Analysis of Specificity Determinants in Eukaryotic Protein Kinases. <i>Cell Reports</i> , 2021, 34, 108602.	2.9	22
6	SARS-CoV-2 infection remodels the host protein thermal stability landscape. <i>Molecular Systems Biology</i> , 2021, 17, e10188.	3.2	17
7	Genome-wide meta-analysis, fine-mapping and integrative prioritization implicate new Alzheimer's disease risk genes. <i>Nature Genetics</i> , 2021, 53, 392-402.	9.4	258
8	Actionable druggable genome-wide Mendelian randomization identifies repurposing opportunities for COVID-19. <i>Nature Medicine</i> , 2021, 27, 668-676.	15.2	120
9	Copy number aberrations drive kinase rewiring, leading to genetic vulnerabilities in cancer. <i>Cell Reports</i> , 2021, 35, 109155.	2.9	10
10	Exploring amino acid functions in a deep mutational landscape. <i>Molecular Systems Biology</i> , 2021, 17, e10305.	3.2	31
11	Individual COVID-19 disease trajectories revealed by plasma proteomics. <i>EMBO Molecular Medicine</i> , 2021, 13, e14532.	3.3	10
12	Causal integration of multi-omics data with prior knowledge to generate mechanistic hypotheses. <i>Molecular Systems Biology</i> , 2021, 17, e9730.	3.2	78
13	The functional landscape of the human phosphoproteome. <i>Nature Biotechnology</i> , 2020, 38, 365-373.	9.4	273
14	Comparative host-coronavirus protein interaction networks reveal pan-viral disease mechanisms. <i>Science</i> , 2020, 370, .	6.0	508
15	Unraveling tumor immune heterogeneity in advanced ovarian cancer uncovers immunogenic effect of chemotherapy. <i>Nature Genetics</i> , 2020, 52, 582-593.	9.4	136
16	Prediction of Signed Protein Kinase Regulatory Circuits. <i>Cell Systems</i> , 2020, 10, 384-396.e9.	2.9	23
17	Spatiotemporal proteomics uncovers cathepsin-dependent macrophage cell death during Salmonella infection. <i>Nature Microbiology</i> , 2020, 5, 1119-1133.	5.9	30
18	The Global Phosphorylation Landscape of SARS-CoV-2 Infection. <i>Cell</i> , 2020, 182, 685-712.e19.	13.5	825

#	ARTICLE	IF	CITATIONS
19	A SARS-CoV-2 protein interaction map reveals targets for drug repurposing. <i>Nature</i> , 2020, 583, 459-468.	13.7	3,542
20	Major role of iron uptake systems in the intrinsic extra-intestinal virulence of the genus <i>Escherichia</i> revealed by a genome-wide association study. <i>PLoS Genetics</i> , 2020, 16, e1009065.	1.5	56
21	Title is missing!. , 2020, 16, e1009065.		0
22	Title is missing!. , 2020, 16, e1009065.		0
23	Title is missing!. , 2020, 16, e1009065.		0
24	Title is missing!. , 2020, 16, e1009065.		0
25	Selective deployment of transcription factor paralogs with submaximal strength facilitates gene regulation in the immune system. <i>Nature Immunology</i> , 2019, 20, 1372-1380.	7.0	17
26	Capturing variation impact on molecular interactions in the IMEx Consortium mutations data set. <i>Nature Communications</i> , 2019, 10, 10.	5.8	193
27	iProteinDB: An Integrative Database of <i>Drosophila</i> Post-translational Modifications. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1-11.	0.8	24
28	Evolution of protein kinase substrate recognition at the active site. <i>PLoS Biology</i> , 2019, 17, e3000341.	2.6	52
29	Multi-omics Characterization of Interaction-mediated Control of Human Protein Abundance levels. <i>Molecular and Cellular Proteomics</i> , 2019, 18, S114-S125.	2.5	16
30	Conserved phosphorylation hotspots in eukaryotic protein domain families. <i>Nature Communications</i> , 2019, 10, 1977.	5.8	39
31	The impact of the genetic background on gene deletion phenotypes in <i>Saccharomyces cerevisiae</i> . <i>Molecular Systems Biology</i> , 2019, 15, e8831.	3.2	44
32	Evolution, dynamics and dysregulation of kinase signalling. <i>Current Opinion in Structural Biology</i> , 2018, 48, 133-140.	2.6	14
33	A resource of variant effect predictions of single nucleotide variants in model organisms. <i>Molecular Systems Biology</i> , 2018, 14, e8430.	3.2	84
34	Reconstructing phosphorylation signalling networks from quantitative phosphoproteomic data. <i>Essays in Biochemistry</i> , 2018, 62, 525-534.	2.1	43
35	Identifications of Putative PKA Substrates with Quantitative Phosphoproteomics and Primary-Sequence-Based Scoring. <i>Journal of Proteome Research</i> , 2017, 16, 1825-1830.	1.8	26
36	Widespread Post-transcriptional Attenuation of Genomic Copy-Number Variation in Cancer. <i>Cell Systems</i> , 2017, 5, 386-398.e4.	2.9	102

#	ARTICLE	IF	CITATIONS
37	Genomic Determinants of Protein Abundance Variation in Colorectal Cancer Cells. <i>Cell Reports</i> , 2017, 20, 2201-2214.	2.9	95
38	Sub-minute Phosphoregulation of Cell Cycle Systems during Plasmodium Gamete Formation. <i>Cell Reports</i> , 2017, 21, 2017-2029.	2.9	59
39	Benchmarking substrate-based kinase activity inference using phosphoproteomic data. <i>Bioinformatics</i> , 2017, 33, 1845-1851.	1.8	64
40	Systematic Analysis of Transcriptional and Post-transcriptional Regulation of Metabolism in Yeast. <i>PLoS Computational Biology</i> , 2017, 13, e1005297.	1.5	51
41	Phenotype inference in an Escherichia coli strain panel. <i>ELife</i> , 2017, 6, .	2.8	38
42	An atlas of human kinase regulation. <i>Molecular Systems Biology</i> , 2016, 12, 888.	3.2	98
43	Evolution of protein phosphorylation across 18 fungal species. <i>Science</i> , 2016, 354, 229-232.	6.0	93
44	Uncovering Phosphorylation-Based Specificities through Functional Interaction Networks. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 236-245.	2.5	68
45	Towards the computational design of protein post-translational regulation. <i>Bioorganic and Medicinal Chemistry</i> , 2015, 23, 2877-2882.	1.4	24
46	Differential genetic interactions of yeast stress response <sc>MAPK</sc> pathways. <i>Molecular Systems Biology</i> , 2015, 11, 800.	3.2	47
47	Kinase- ϵ -hybrid: towards the conditional interactome. <i>Molecular Systems Biology</i> , 2015, 11, 798.	3.2	1
48	Prediction of Functionally Important Phospho-Regulatory Events in Xenopus laevis Oocytes. <i>PLoS Computational Biology</i> , 2015, 11, e1004362.	1.5	14
49	Phosphoproteomic Analysis Reveals Regulatory Mechanisms at the Kidney Filtration Barrier. <i>Journal of the American Society of Nephrology: JASN</i> , 2014, 25, 1509-1522.	3.0	40
50	Global analysis of phosphorylation and ubiquitylation cross-talk in protein degradation. <i>Nature Methods</i> , 2013, 10, 676-682.	9.0	520
51	Evolution and functional cross-talk of protein post-translational modifications. <i>Molecular Systems Biology</i> , 2013, 9, 714.	3.2	294
52	Hierarchical Modularity and the Evolution of Genetic Interactomes across Species. <i>Molecular Cell</i> , 2012, 46, 691-704.	4.5	185
53	Systematic Functional Prioritization of Protein Posttranslational Modifications. <i>Cell</i> , 2012, 150, 413-425.	13.5	375
54	Comparative Interaction Networks: Bridging Genotype to Phenotype. <i>Advances in Experimental Medicine and Biology</i> , 2012, 751, 139-156.	0.8	9

#	ARTICLE	IF	CITATIONS
55	Phenotypic Landscape of a Bacterial Cell. <i>Cell</i> , 2011, 144, 143-156.	13.5	623
56	Site-specific acetylation mark on an essential chromatin-remodeling complex promotes resistance to replication stress. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 10620-10625.	3.3	20
57	A human B-cell interactome identifies MYB and FOXM1 as master regulators of proliferation in germinal centers. <i>Molecular Systems Biology</i> , 2010, 6, 377.	3.2	336
58	Cross-species chemogenomic profiling reveals evolutionarily conserved drug mode of action. <i>Molecular Systems Biology</i> , 2010, 6, 451.	3.2	143
59	Quantitative Genetic Interactions Reveal Biological Modularity. <i>Cell</i> , 2010, 141, 739-745.	13.5	140
60	Evolution of Phosphoregulation: Comparison of Phosphorylation Patterns across Yeast Species. <i>PLoS Biology</i> , 2009, 7, e1000134.	2.6	170
61	Microblogging the ISMB: A New Approach to Conference Reporting. <i>PLoS Computational Biology</i> , 2009, 5, e1000263.	1.5	14
62	ADAN: a database for prediction of protein-protein interaction of modular domains mediated by linear motifs. <i>Bioinformatics</i> , 2009, 25, 2418-2424.	1.8	36
63	Structure-Based Prediction of the <i>Saccharomyces cerevisiae</i> SH3-Ligand Interactions. <i>Journal of Molecular Biology</i> , 2009, 388, 902-916.	2.0	33
64	Evolvability and hierarchy in rewired bacterial gene networks. <i>Nature</i> , 2008, 452, 840-845.	13.7	285
65	Analyzing Protein Interaction Networks Using Structural Information. <i>Annual Review of Biochemistry</i> , 2008, 77, 415-441.	5.0	85
66	Genome-Wide Prediction of SH2 Domain Targets Using Structural Information and the FoldX Algorithm. <i>PLoS Computational Biology</i> , 2008, 4, e1000052.	1.5	39
67	Specificity and Evolvability in Eukaryotic Protein Interaction Networks. <i>PLoS Computational Biology</i> , 2007, 3, e25.	1.5	111
68	A Genome-wide Ras-Effector Interaction Network. <i>Journal of Molecular Biology</i> , 2007, 370, 1020-1032.	2.0	34
69	Structures in systems biology. <i>Current Opinion in Structural Biology</i> , 2007, 17, 378-384.	2.6	67
70	Comparative Genomics and Disorder Prediction Identify Biologically Relevant SH3 Protein Interactions. <i>PLoS Computational Biology</i> , 2005, 1, e26.	1.5	40
71	Comparative genomics and disorder prediction identify biologically relevant SH3 protein interactions. <i>PLoS Computational Biology</i> , 2005, preprint, e26.	1.5	0
72	SmartCell, a framework to simulate cellular processes that combines stochastic approximation with diffusion and localisation: analysis of simple networks. <i>IET Systems Biology</i> , 2004, 1, 129-138.	2.0	127

#	ARTICLE	IF	CITATIONS
73	Comparative Evolutionary Genomics Unveils the Molecular Mechanism of Reassignment of the CTG Codon in <i>Candida</i> spp.. <i>Genome Research</i> , 2003, 13, 544-557.	2.4	111