

Pedro Beltrao

List of Publications by Year in descending order

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Version: 2024-02-01

73
papers

11,916
citations

94433

37
h-index

88630

70
g-index

115
all docs

115
docs citations

115
times ranked

21822
citing authors

#	ARTICLE	IF	CITATIONS
1	A SARS-CoV-2 protein interaction map reveals targets for drug repurposing. Nature, 2020, 583, 459-468.	27.8	3,542
2	The Global Phosphorylation Landscape of SARS-CoV-2 Infection. Cell, 2020, 182, 685-712.e19.	28.9	825
3	Phenotypic Landscape of a Bacterial Cell. Cell, 2011, 144, 143-156.	28.9	623
4	Global analysis of phosphorylation and ubiquitylation cross-talk in protein degradation. Nature Methods, 2013, 10, 676-682.	19.0	520
5	Comparative host-coronavirus protein interaction networks reveal pan-viral disease mechanisms. Science, 2020, 370, .	12.6	508
6	Systematic Functional Prioritization of Protein Posttranslational Modifications. Cell, 2012, 150, 413-425.	28.9	375
7	A human B-cell interactome identifies MYB and FOXM1 as master regulators of proliferation in germinal centers. Molecular Systems Biology, 2010, 6, 377.	7.2	336
8	Evolution and functional cross-talk of protein post-translational modifications. Molecular Systems Biology, 2013, 9, 714.	7.2	294
9	Evolvability and hierarchy in rewired bacterial gene networks. Nature, 2008, 452, 840-845.	27.8	285
10	The functional landscape of the human phosphoproteome. Nature Biotechnology, 2020, 38, 365-373.	17.5	273
11	Genome-wide meta-analysis, fine-mapping and integrative prioritization implicate new Alzheimer's disease risk genes. Nature Genetics, 2021, 53, 392-402.	21.4	258
12	Evolution of enhanced innate immune evasion by SARS-CoV-2. Nature, 2022, 602, 487-495.	27.8	237
13	Capturing variation impact on molecular interactions in the IMEx Consortium mutations data set. Nature Communications, 2019, 10, 10.	12.8	193
14	Hierarchical Modularity and the Evolution of Genetic Interactomes across Species. Molecular Cell, 2012, 46, 691-704.	9.7	185
15	Evolution of Phosphoregulation: Comparison of Phosphorylation Patterns across Yeast Species. PLoS Biology, 2009, 7, e1000134.	5.6	170
16	Cross-species chemogenomic profiling reveals evolutionarily conserved drug mode of action. Molecular Systems Biology, 2010, 6, 451.	7.2	143
17	Quantitative Genetic Interactions Reveal Biological Modularity. Cell, 2010, 141, 739-745.	28.9	140
18	Unraveling tumor-immune heterogeneity in advanced ovarian cancer uncovers immunogenic effect of chemotherapy. Nature Genetics, 2020, 52, 582-593.	21.4	136

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19	SmartCell, a framework to simulate cellular processes that combines stochastic approximation with diffusion and localisation: analysis of simple networks. IET Systems Biology, 2004, 1, 129-138.	2.0	127
20	Actionable druggable genome-wide Mendelian randomization identifies repurposing opportunities for COVID-19. Nature Medicine, 2021, 27, 668-676.	30.7	120
21	Comparative Evolutionary Genomics Unveils the Molecular Mechanism of Reassignment of the CTG Codon in Candida spp.. Genome Research, 2003, 13, 544-557.	5.5	111
22	Specificity and Evolvability in Eukaryotic Protein Interaction Networks. PLoS Computational Biology, 2007, 3, e25.	3.2	111
23	Widespread Post-transcriptional Attenuation of Genomic Copy-Number Variation in Cancer. Cell Systems, 2017, 5, 386-398.e4.	6.2	102
24	An atlas of human kinase regulation. Molecular Systems Biology, 2016, 12, 888.	7.2	98
25	Genomic Determinants of Protein Abundance Variation in Colorectal Cancer Cells. Cell Reports, 2017, 20, 2201-2214.	6.4	95
26	Evolution of protein phosphorylation across 18 fungal species. Science, 2016, 354, 229-232.	12.6	93
27	Analyzing Protein Interaction Networks Using Structural Information. Annual Review of Biochemistry, 2008, 77, 415-441.	11.1	85
28	A resource of variant effect predictions of single nucleotide variants in model organisms. Molecular Systems Biology, 2018, 14, e8430.	7.2	84
29	Causal integration of multi-omics data with prior knowledge to generate mechanistic hypotheses. Molecular Systems Biology, 2021, 17, e9730.	7.2	78
30	Uncovering Phosphorylation-Based Specificities through Functional Interaction Networks. Molecular and Cellular Proteomics, 2016, 15, 236-245.	3.8	68
31	Structures in systems biology. Current Opinion in Structural Biology, 2007, 17, 378-384.	5.7	67
32	Benchmarking substrate-based kinase activity inference using phosphoproteomic data. Bioinformatics, 2017, 33, 1845-1851.	4.1	64
33	Sub-minute Phosphoregulation of Cell Cycle Systems during Plasmodium Gamete Formation. Cell Reports, 2017, 21, 2017-2029.	6.4	59
34	Major role of iron uptake systems in the intrinsic extra-intestinal virulence of the genus Escherichia revealed by a genome-wide association study. PLoS Genetics, 2020, 16, e1009065.	3.5	56
35	Evolution of protein kinase substrate recognition at the active site. PLoS Biology, 2019, 17, e3000341.	5.6	52
36	Systematic Analysis of Transcriptional and Post-transcriptional Regulation of Metabolism in Yeast. PLoS Computational Biology, 2017, 13, e1005297.	3.2	51

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37	Differential genetic interactions of yeast stress response <scp>MAPK</scp> pathways. Molecular Systems Biology, 2015, 11, 800.	7.2	47
38	The impact of the genetic background on gene deletion phenotypes in <i>Saccharomyces cerevisiae</i>. Molecular Systems Biology, 2019, 15, e8831.	7.2	44
39	Reconstructing phosphorylation signalling networks from quantitative phosphoproteomic data. Essays in Biochemistry, 2018, 62, 525-534.	4.7	43
40	Comparative Genomics and Disorder Prediction Identify Biologically Relevant SH3 Protein Interactions. PLoS Computational Biology, 2005, 1, e26.	3.2	40
41	Phosphoproteomic Analysis Reveals Regulatory Mechanisms at the Kidney Filtration Barrier. Journal of the American Society of Nephrology: JASN, 2014, 25, 1509-1522.	6.1	40
42	Genome-Wide Prediction of SH2 Domain Targets Using Structural Information and the FoldX Algorithm. PLoS Computational Biology, 2008, 4, e1000052.	3.2	39
43	Conserved phosphorylation hotspots in eukaryotic protein domain families. Nature Communications, 2019, 10, 1977.	12.8	39
44	Phenotype inference in an Escherichia coli strain panel. ELife, 2017, 6, .	6.0	38
45	ADAN: a database for prediction of proteinâ€“protein interaction of modular domains mediated by linear motifs. Bioinformatics, 2009, 25, 2418-2424.	4.1	36
46	A Genome-wide Ras-Effector Interaction Network. Journal of Molecular Biology, 2007, 370, 1020-1032.	4.2	34
47	Structure-Based Prediction of the Saccharomyces cerevisiae SH3â€“Ligand Interactions. Journal of Molecular Biology, 2009, 388, 902-916.	4.2	33
48	Exploring amino acid functions in a deep mutational landscape. Molecular Systems Biology, 2021, 17, e10305.	7.2	31
49	Spatiotemporal proteomics uncovers cathepsin-dependent macrophage cell death during Salmonella infection. Nature Microbiology, 2020, 5, 1119-1133.	13.3	30
50	Identifications of Putative PKA Substrates with Quantitative Phosphoproteomics and Primary-Sequence-Based Scoring. Journal of Proteome Research, 2017, 16, 1825-1830.	3.7	26
51	Towards the computational design of protein post-translational regulation. Bioorganic and Medicinal Chemistry, 2015, 23, 2877-2882.	3.0	24
52	iProteinDB: An Integrative Database of <i>Drosophila</i> Post-translational Modifications. G3: Genes, Genomes, Genetics, 2019, 9, 1-11.	1.8	24
53	High-throughput functional characterization of protein phosphorylation sites in yeast. Nature Biotechnology, 2022, 40, 382-390.	17.5	24
54	Prediction of Signed Protein Kinase Regulatory Circuits. Cell Systems, 2020, 10, 384-396.e9.	6.2	23

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55	Sequence and Structure-Based Analysis of Specificity Determinants in Eukaryotic Protein Kinases. Cell Reports, 2021, 34, 108602.	6.4	22
56	Site-specific acetylation mark on an essential chromatin-remodeling complex promotes resistance to replication stress. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 10620-10625.	7.1	20
57	Selective deployment of transcription factor paralogs with submaximal strength facilitates gene regulation in the immune system. Nature Immunology, 2019, 20, 1372-1380.	14.5	17
58	SARS-CoV-2 infection remodels the host protein thermal stability landscape. Molecular Systems Biology, 2021, 17, e10188.	7.2	17
59	Multi-omics Characterization of Interaction-mediated Control of Human Protein Abundance levels. Molecular and Cellular Proteomics, 2019, 18, S114-S125.	3.8	16
60	Microblogging the ISMB: A New Approach to Conference Reporting. PLoS Computational Biology, 2009, 5, e1000263.	3.2	14
61	Evolution, dynamics and dysregulation of kinase signalling. Current Opinion in Structural Biology, 2018, 48, 133-140.	5.7	14
62	Prediction of Functionally Important Phospho-Regulatory Events in Xenopus laevis Oocytes. PLoS Computational Biology, 2015, 11, e1004362.	3.2	14
63	Global post-translational modification profiling of HIV-1-infected cells reveals mechanisms of host cellular pathway remodeling. Cell Reports, 2022, 39, 110690.	6.4	12
64	Copy number aberrations drive kinase rewiring, leading to genetic vulnerabilities in cancer. Cell Reports, 2021, 35, 109155.	6.4	10
65	Individual COVID-19 disease trajectories revealed by plasma proteomics. EMBO Molecular Medicine, 2021, 13, e14532.	6.9	10
66	Comparative Interaction Networks: Bridging Genotype to Phenotype. Advances in Experimental Medicine and Biology, 2012, 751, 139-156.	1.6	9
67	Kinase- ϵ -hybrid: towards the conditional interactome. Molecular Systems Biology, 2015, 11, 798.	7.2	1
68	Comparative genomics and disorder prediction identify biologically relevant SH3 protein interactions. PLoS Computational Biology, 2005, preprint, e26.	3.2	0
69	Title is missing!. , 2020, 16, e1009065.		0
70	Title is missing!. , 2020, 16, e1009065.		0
71	Title is missing!. , 2020, 16, e1009065.		0
72	Title is missing!. , 2020, 16, e1009065.		0

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73	A high dimensional map of phosphorylationâ€dependent signaling in budding yeast. FASEB Journal, 2022, 36, .	0.5	0