

David Ochoa

List of Publications by Year in descending order

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Version: 2024-02-01

22
papers

1,932
citations

567281

15
h-index

642732

23
g-index

35
all docs

35
docs citations

35
times ranked

3617
citing authors

#	ARTICLE	IF	CITATIONS
1	Open Targets Genetics: systematic identification of trait-associated genes using large-scale genetics and functional genomics. <i>Nucleic Acids Research</i> , 2021, 49, D1311-D1320.	14.5	295
2	The functional landscape of the human phosphoproteome. <i>Nature Biotechnology</i> , 2020, 38, 365-373.	17.5	273
3	Open Targets Platform: supporting systematic drug-target identification and prioritisation. <i>Nucleic Acids Research</i> , 2021, 49, D1302-D1310.	14.5	265
4	An open approach to systematically prioritize causal variants and genes at all published human GWAS trait-associated loci. <i>Nature Genetics</i> , 2021, 53, 1527-1533.	21.4	208
5	Capturing variation impact on molecular interactions in the IMEx Consortium mutations data set. <i>Nature Communications</i> , 2019, 10, 10.	12.8	193
6	The PROTACtable genome. <i>Nature Reviews Drug Discovery</i> , 2021, 20, 789-797.	46.4	112
7	An atlas of human kinase regulation. <i>Molecular Systems Biology</i> , 2016, 12, 888.	7.2	98
8	Studying the co-evolution of protein families with the Mirrortree web server. <i>Bioinformatics</i> , 2010, 26, 1370-1371.	4.1	82
9	Benchmarking substrate-based kinase activity inference using phosphoproteomic data. <i>Bioinformatics</i> , 2017, 33, 1845-1851.	4.1	64
10	Systematic Analysis of Transcriptional and Post-transcriptional Regulation of Metabolism in Yeast. <i>PLoS Computational Biology</i> , 2017, 13, e1005297.	3.2	51
11	Conserved phosphorylation hotspots in eukaryotic protein domain families. <i>Nature Communications</i> , 2019, 10, 1977.	12.8	39
12	Epigenomic Co-localization and Co-evolution Reveal a Key Role for 5hmC as a Communication Hub in the Chromatin Network of ESCs. <i>Cell Reports</i> , 2016, 14, 1246-1257.	6.4	38
13	Detection of significant protein coevolution. <i>Bioinformatics</i> , 2015, 31, 2166-2173.	4.1	32
14	Practical aspects of protein co-evolution. <i>Frontiers in Cell and Developmental Biology</i> , 2014, 2, 14.	3.7	28
15	High-throughput functional characterization of protein phosphorylation sites in yeast. <i>Nature Biotechnology</i> , 2022, 40, 382-390.	17.5	24
16	A proteome-wide genetic investigation identifies several SARS-CoV-2-exploited host targets of clinical relevance. <i>eLife</i> , 2021, 10, .	6.0	23
17	Multi-omics Characterization of Interaction-mediated Control of Human Protein Abundance levels. <i>Molecular and Cellular Proteomics</i> , 2019, 18, S114-S125.	3.8	16
18	Evolution, dynamics and dysregulation of kinase signalling. <i>Current Opinion in Structural Biology</i> , 2018, 48, 133-140.	5.7	14

#	ARTICLE	IF	CITATIONS
19	Selection of organisms for the co-evolution-based study of protein interactions. BMC Bioinformatics, 2011, 12, 363.	2.6	13
20	Copy number aberrations drive kinase rewiring, leading to genetic vulnerabilities in cancer. Cell Reports, 2021, 35, 109155.	6.4	10
21	Incorporating information on predicted solvent accessibility to the co-evolution-based study of protein interactions. Molecular BioSystems, 2013, 9, 70-76.	2.9	8
22	Kinaseâ€twoâ€hybrid: towards the conditional interactome. Molecular Systems Biology, 2015, 11, 798.	7.2	1