David Ochoa

List of Publications by Year
in descending order

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	High-throughput functional characterization of protein phosphorylation sites in yeast. Nature Biotechnology, 2022, 40, 382-390.	17.5	24
2	Open Targets Genetics: systematic identification of trait-associated genes using large-scale genetics and functional genomics. Nucleic Acids Research, 2021, 49, D1311-D1320.	14.5	295
3	Open Targets Platform: supporting systematic drug–target identification and prioritisation. Nucleic Acids Research, 2021, 49, D1302-D1310.	14.5	265
4	Copy number aberrations drive kinase rewiring, leading to genetic vulnerabilities in cancer. Cell Reports, 2021, 35, 109155.	6.4	10
5	The PROTACtable genome. Nature Reviews Drug Discovery, 2021, 20, 789-797.	46.4	112
6	A proteome-wide genetic investigation identifies several SARS-CoV-2-exploited host targets of clinical relevance. ELife, 2021, 10, .	6.0	23
7	An open approach to systematically prioritize causal variants and genes at all published human GWAS trait-associated loci. Nature Genetics, 2021, 53, 1527-1533.	21.4	208
8	The functional landscape of the human phosphoproteome. Nature Biotechnology, 2020, 38, 365-373.	17.5	273
9	Capturing variation impact on molecular interactions in the IMEx Consortium mutations data set. Nature Communications, 2019, 10, 10.	12.8	193
10	Multi-omics Characterization of Interaction-mediated Control of Human Protein Abundance levels. Molecular and Cellular Proteomics, 2019, 18, S114-S125.	3.8	16
11	Conserved phosphorylation hotspots in eukaryotic protein domain families. Nature Communications, 2019, 10, 1977.	12.8	39
12	Evolution, dynamics and dysregulation of kinase signalling. Current Opinion in Structural Biology, 2018, 48, 133-140.	5.7	14
13	Benchmarking substrate-based kinase activity inference using phosphoproteomic data. Bioinformatics, 2017, 33, 1845-1851.	4.1	64
14	Systematic Analysis of Transcriptional and Post-transcriptional Regulation of Metabolism in Yeast. PLoS Computational Biology, 2017, 13, e1005297.	3.2	51
15	An atlas of human kinase regulation. Molecular Systems Biology, 2016, 12, 888.	7.2	98
16	Epigenomic Co-localization and Co-evolution Reveal a Key Role for 5hmC as a Communication Hub in the Chromatin Network of ESCs. Cell Reports, 2016, 14, 1246-1257.	6.4	38
17	Detection of significant protein coevolution. Bioinformatics, 2015, 31, 2166-2173.	4.1	32
18	Kinase–two–hybrid: towards the conditional interactome. Molecular Systems Biology, 2015, 11, 798.	7.2	1

#	ARTICLE	IF	CITATIONS
19	Practical aspects of protein co-evolution. Frontiers in Cell and Developmental Biology, 2014, 2, 14.	3.7	28
20	Incorporating information on predicted solvent accessibility to the co-evolution-based study of protein interactions. Molecular BioSystems, 2013, 9, 70-76.	2.9	8
21	Selection of organisms for the co-evolution-based study of protein interactions. BMC Bioinformatics, 2011, 12, 363.	2.6	13
22	Studying the co-evolution of protein families with the Mirrortree web server. Bioinformatics, 2010, 26, 1370-1371.	4.1	82