

Gorka Lasso Cabrera

List of Publications by Year in descending order

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Version: 2024-02-01

28
papers

1,660
citations

471509

17
h-index

552781

26
g-index

47
all docs

47
docs citations

47
times ranked

3869
citing authors

#	ARTICLE	IF	CITATIONS
1	Longitudinally monitored immune biomarkers predict the timing of COVID-19 outcomes. PLoS Computational Biology, 2022, 18, e1009778.	3.2	10
2	Genotype-specific features reduce the susceptibility of South American yellow fever virus strains to vaccine-induced antibodies. Cell Host and Microbe, 2022, 30, 248-259.e6.	11.0	11
3	Efficacy and Safety of COVID-19 Convalescent Plasma in Hospitalized Patients. JAMA Internal Medicine, 2022, 182, 115.	5.1	63
4	Computational strategies to combat COVID-19: useful tools to accelerate SARS-CoV-2 and coronavirus research. Briefings in Bioinformatics, 2021, 22, 642-663.	6.5	110
5	A Sweep of Earth's Virome Reveals Host-Guided Viral Protein Structural Mimicry and Points to Determinants of Human Disease. Cell Systems, 2021, 12, 82-91.e3.	6.2	24
6	The evolutionary history of ACE2 usage within the coronavirus subgenus <i>Sarbecovirus</i> . Virus Evolution, 2021, 7, veab007.	4.9	54
7	Single-Dilution COVID-19 Antibody Test with Qualitative and Quantitative Readouts. MSphere, 2021, 6, .	2.9	11
8	A Combination of Receptor-Binding Domain and N-Terminal Domain Neutralizing Antibodies Limits the Generation of SARS-CoV-2 Spike Neutralization-Escape Mutants. MBio, 2021, 12, e0247321.	4.1	35
9	A Virion-Based Assay for Glycoprotein Thermostability Reveals Key Determinants of Filovirus Entry and Its Inhibition. Journal of Virology, 2020, 94, .	3.4	7
10	A Replication-Competent Vesicular Stomatitis Virus for Studies of SARS-CoV-2 Spike-Mediated Cell Entry and Its Inhibition. Cell Host and Microbe, 2020, 28, 486-496.e6.	11.0	178
11	A Structure-Informed Atlas of Human-Virus Interactions. Cell, 2019, 178, 1526-1541.e16.	28.9	108
12	The discovery of Bombali virus adds further support for bats as hosts of ebolaviruses. Nature Microbiology, 2018, 3, 1084-1089.	13.3	283
13	Substrate translocation involves specific lysine residues of the central channel of the conjugative coupling protein TrwB. Molecular Genetics and Genomics, 2017, 292, 1037-1049.	2.1	6
14	Acetylation-regulated interaction between p53 and SET reveals a widespread regulatory mode. Nature, 2016, 538, 118-122.	27.8	160
15	Structural basis of adhesive binding by desmocollins and desmogleins. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 7160-7165.	7.1	137
16	A High-Throughput Strategy for Dissecting Mammalian Genetic Interactions. PLoS ONE, 2016, 11, e0167617.	2.5	4
17	Template-based prediction of protein function. Current Opinion in Structural Biology, 2015, 32, 33-38.	5.7	39
18	The near-atomic cryoEM structure of a flexible filamentous plant virus shows homology of its coat protein with nucleoproteins of animal viruses. ELife, 2015, 4, e11795.	6.0	61

#	ARTICLE	IF	CITATIONS
19	Functional Conformations for Pyruvate Carboxylase during Catalysis Explored by Cryoelectron Microscopy. <i>Structure</i> , 2014, 22, 911-922.	3.3	23
20	Electron microscopy studies on the quaternary structure of p53 reveal different binding modes for p53 tetramers in complex with DNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 557-562.	7.1	65
21	The Cryo-EM Structure of a Complete 30S Translation Initiation Complex from <i>Escherichia coli</i> . <i>PLoS Biology</i> , 2011, 9, e1001095.	5.6	102
22	Cryo-EM Analysis Reveals New Insights into the Mechanism of Action of Pyruvate Carboxylase. <i>Structure</i> , 2010, 18, 1300-1310.	3.3	27
23	Computational Methods for Analysis of Two-Dimensional Gels. <i>Methods in Molecular Biology</i> , 2010, 593, 231-262.	0.9	0
24	A Symmetrical Tetramer for <i>S. aureus</i> Pyruvate Carboxylase in Complex with Coenzyme A. <i>Structure</i> , 2009, 17, 823-832.	3.3	55
25	ContDist: a tool for the analysis of quantitative gene and promoter properties. <i>BMC Bioinformatics</i> , 2009, 10, 7.	2.6	8
26	A combinatorial pattern discovery approach for the prediction of membrane dipping (re-entrant) loops. <i>Bioinformatics</i> , 2006, 22, e290-e297.	4.1	27
27	A Structure Informed Atlas of Pan-Viral Interactions Reveals Features of Human Infection. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
28	Editorial: Influence of Protein-Protein Interactions (PPIs) on the Outcome of Viral Infections. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	1