

Sonu Kumar

List of Publications by Year in descending order

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Version: 2024-02-01

28
papers

850
citations

566801

15
h-index

525886

27
g-index

31
all docs

31
docs citations

31
times ranked

1631
citing authors

#	ARTICLE	IF	CITATIONS
1	A cross-neutralizing antibody between HIV-1 and influenza virus. PLoS Pathogens, 2021, 17, e1009407.	2.1	23
2	Single-component multilayered self-assembling nanoparticles presenting rationally designed glycoprotein trimers as Ebola virus vaccines. Nature Communications, 2021, 12, 2633.	5.8	25
3	Neutralizing Antibodies Induced by First-Generation gp41-Stabilized HIV-1 Envelope Trimers and Nanoparticles. MBio, 2021, 12, e0042921.	1.8	6
4	A V _H 1-69 antibody lineage from an infected Chinese donor potentially neutralizes HIV-1 by targeting the V3 glycan supersite. Science Advances, 2020, 6, .	4.7	19
5	Structure and immunogenicity of a stabilized HIV-1 envelope trimer based on a group-M consensus sequence. Nature Communications, 2019, 10, 2355.	5.8	116
6	Conformational Plasticity in the HIV-1 Fusion Peptide Facilitates Recognition by Broadly Neutralizing Antibodies. Cell Host and Microbe, 2019, 25, 873-883.e5.	5.1	42
7	Capturing the inherent structural dynamics of the HIV-1 envelope glycoprotein fusion peptide. Nature Communications, 2019, 10, 763.	5.8	30
8	Closing and Opening Holes in the Glycan Shield of HIV-1 Envelope Glycoprotein SOSIP Trimers Can Redirect the Neutralizing Antibody Response to the Newly Unmasked Epitopes. Journal of Virology, 2019, 93, .	1.5	66
9	Effect of phosphorylation and single nucleotide polymorphisms on caspase substrates processing. Apoptosis: an International Journal on Programmed Cell Death, 2018, 23, 194-200.	2.2	12
10	HIV-1 vaccine design through minimizing envelope metastability. Science Advances, 2018, 4, eaau6769.	4.7	75
11	Structure of a cleavage-independent HIV Env recapitulates the glycoprotein architecture of the native cleaved trimer. Nature Communications, 2018, 9, 1956.	5.8	50
12	The human naive B cell repertoire contains distinct subclasses for a germline-targeting HIV-1 vaccine immunogen. Science Translational Medicine, 2018, 10, .	5.8	113
13	Role of N-glycosylation in activation of proMMP-9. A molecular dynamics simulations study. PLoS ONE, 2018, 13, e0191157.	1.1	11
14	CaspNeuroD: a knowledgebase of predicted caspase cleavage sites in human proteins related to neurodegenerative diseases. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw142.	1.4	5
15	CleavPredict: A Platform for Reasoning about Matrix Metalloproteinases Proteolytic Events. PLoS ONE, 2015, 10, e0127877.	1.1	32
16	Letter to the Editor: Caspase cleavage sites in the human proteome: CaspDB, a database of predicted substrates. Apoptosis: an International Journal on Programmed Cell Death, 2015, 20, 421-421.	2.2	3
17	High-Throughput Multiplexed Peptide-Centric Profiling Illustrates Both Substrate Cleavage Redundancy and Specificity in the MMP Family. Chemistry and Biology, 2015, 22, 1122-1133.	6.2	26
18	Matrix Metalloproteinase (MMP) Proteolysis of the Extracellular Loop of Voltage-gated Sodium Channels and Potential Alterations in Pain Signaling. Journal of Biological Chemistry, 2015, 290, 22939-22944.	1.6	11

#	ARTICLE	IF	CITATIONS
19	Phosphorylation of multifunctional galectins by protein kinases CK1, CK2, and PKA. <i>Analytical Biochemistry</i> , 2014, 449, 109-117.	1.1	2
20	Caspase Cleavage Sites in the Human Proteome: CaspDB, a Database of Predicted Substrates. <i>PLoS ONE</i> , 2014, 9, e110539.	1.1	59
21	Understanding the Specificity of Human Galectin-8C Domain Interactions with Its Glycan Ligands Based on Molecular Dynamics Simulations. <i>PLoS ONE</i> , 2013, 8, e59761.	1.1	26
22	GlycoCD: a repository for carbohydrate-related CD antigens. <i>Bioinformatics</i> , 2012, 28, 2553-2555.	1.8	13
23	Protein Aggregation in Neurodegenerative Diseases: Insights from Computational Analyses. <i>Current Bioinformatics</i> , 2012, 7, 87-95.	0.7	6
24	The G protein-coupled receptors in the pufferfish <i>Takifugu rubripes</i> . <i>BMC Bioinformatics</i> , 2011, 12, S3.	1.2	37
25	Analysis and Prediction of DNA-Recognition by Zinc Finger Proteins. <i>Advances in Bioinformatics and Biomedical Engineering Book Series</i> , 2011, , 303-317.	0.2	0
26	ZiF-Predict: A Web Tool for Predicting DNA-Binding Specificity in C2H2 Zinc Finger Proteins. <i>Genomics, Proteomics and Bioinformatics</i> , 2010, 8, 122-126.	3.0	20
27	Controlling aggregation propensity in A53T mutant of alpha-synuclein causing Parkinson's disease. <i>Biochemical and Biophysical Research Communications</i> , 2009, 387, 305-309.	1.0	15
28	Analysis and Prediction of DNA-Recognition by Zinc Finger Proteins. , 0, , 330-344.		0