

Harpreet Kaur Saini

List of Publications by Year in descending order

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Version: 2024-02-01

45
papers

7,173
citations

185998
28
h-index

253896
43
g-index

45
all docs

45
docs citations

45
times ranked

12971
citing authors

#	ARTICLE	IF	CITATIONS
1	The role of SQSTM1 (p62) in mitochondrial function and clearance in human cortical neurons. <i>Stem Cell Reports</i> , 2021, 16, 1276-1289.	2.3	17
2	Antagonism of inhibitors of apoptosis proteins reveals a novel, immune response-based therapeutic approach for T-cell lymphoma. <i>Blood Advances</i> , 2021, 5, 4003-4016.	2.5	4
3	Combining the IAP Antagonist Tolinapant with a DNA Hypomethylating Agent Enhances Immunogenic Cell Death in Preclinical Models of T-Cell Lymphoma. <i>Blood</i> , 2021, 138, 3986-3986.	0.6	0
4	Dual-Mechanism ERK1/2 Inhibitors Exploit a Distinct Binding Mode to Block Phosphorylation and Nuclear Accumulation of ERK1/2. <i>Molecular Cancer Therapeutics</i> , 2020, 19, 525-539.	1.9	14
5	Visualization and analysis of RNA-Seq assembly graphs. <i>Nucleic Acids Research</i> , 2019, 47, 7262-7275.	6.5	4
6	COSMIC-3D provides structural perspectives on cancer genetics for drug discovery. <i>Nature Genetics</i> , 2018, 50, 1200-1202.	9.4	31
7	Fragment-Based Discovery of a Potent, Orally Bioavailable Inhibitor That Modulates the Phosphorylation and Catalytic Activity of ERK1/2. <i>Journal of Medicinal Chemistry</i> , 2018, 61, 4978-4992.	2.9	42
8	Transposon-driven transcription is a conserved feature of vertebrate spermatogenesis and transcript evolution. <i>EMBO Reports</i> , 2017, 18, 1231-1247.	2.0	34
9	Extracellular vesicles are independent metabolic units with asparaginase activity. <i>Nature Chemical Biology</i> , 2017, 13, 951-955.	3.9	107
10	Emergence of resistance to tyrosine kinase inhibitors in non-small-cell lung cancer can be delayed by an upfront combination with the HSP90 inhibitor onalespib. <i>British Journal of Cancer</i> , 2016, 115, 1069-1077.	2.9	26
11	Detection of secondary binding sites in proteins using fragment screening. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 15910-15915.	3.3	91
12	Turn: A novel Turn mimic in globular proteins stabilized by main chain to side chain C α -H α -O interaction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 203-214.	1.5	7
13	Solid Tumors of Childhood Display Specific Serum microRNA Profiles. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 350-360.	1.1	74
14	Integrated analysis of microRNA and mRNA expression and association with HIF binding reveals the complexity of microRNA expression regulation under hypoxia. <i>Molecular Cancer</i> , 2014, 13, 28.	7.9	135
15	Extracellular Vesicles from Neural Stem Cells Transfer IFN- γ via Ifngr1 to Activate Stat1 Signaling in Target Cells. <i>Molecular Cell</i> , 2014, 56, 193-204.	4.5	258
16	Multiple Epigenetic Mechanisms and the piRNA Pathway Enforce LINE1 Silencing during Adult Spermatogenesis. <i>Molecular Cell</i> , 2013, 50, 601-608.	4.5	170
17	Depletion of HPV16 early genes induces autophagy and senescence in a cervical carcinogenesis model, regardless of viral physical state. <i>Journal of Pathology</i> , 2013, 231, 354-366.	2.1	40
18	LIN28 Expression in Malignant Germ Cell Tumors Downregulates let-7 and Increases Oncogene Levels. <i>Cancer Research</i> , 2013, 73, 4872-4884.	0.4	61

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19	Messenger RNA and microRNA profiling during early mouse EB formation. <i>Gene Expression Patterns</i> , 2011, 11, 334-344.	0.3	17
20	Functional evidence that <i>Drosha</i> overexpression in cervical squamous cell carcinoma affects cell phenotype and microRNA profiles. <i>Journal of Pathology</i> , 2011, 224, 496-507.	2.1	71
21	MiR-221 Influences Effector Functions and Actin Cytoskeleton in Mast Cells. <i>PLoS ONE</i> , 2011, 6, e26133.	1.1	81
22	Malignant Germ Cell Tumors Display Common MicroRNA Profiles Resulting in Global Changes in Expression of Messenger RNA Targets. <i>Cancer Research</i> , 2010, 70, 2911-2923.	0.4	243
23	iMotifs: an integrated sequence motif visualization and analysis environment. <i>Bioinformatics</i> , 2010, 26, 843-844.	1.8	11
24	The two most common histological subtypes of malignant germ cell tumour are distinguished by global microRNA profiles, associated with differential transcription factor expression. <i>Molecular Cancer</i> , 2010, 9, 290.	7.9	60
25	Abstract 3424: Malignant germ cell tumors display common microRNA profiles resulting in global changes in expression of mRNA targets. , 2010, , .		0
26	Computational Prediction of Protein-Protein Interactions. <i>Molecular Biotechnology</i> , 2008, 38, 1-17.	1.3	201
27	Annotation of mammalian primary microRNAs. <i>BMC Genomics</i> , 2008, 9, 564.	1.2	121
28	Genomic analysis of human microRNA transcripts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 17719-17724.	3.3	466
29	PEPstr: A de novo Method for Tertiary Structure Prediction of Small Bioactive Peptides. <i>Protein and Peptide Letters</i> , 2007, 14, 626-631.	0.4	179
30	FRalanyzer: a tool for functional analysis of fold-recognition sequence-structure alignments. <i>Nucleic Acids Research</i> , 2007, 35, W499-W502.	6.5	3
31	miRBase: tools for microRNA genomics. <i>Nucleic Acids Research</i> , 2007, 36, D154-D158.	6.5	3,854
32	Structural and functional insights into Mimivirus ORFans. <i>BMC Genomics</i> , 2007, 8, 115.	1.2	22
33	Real value prediction of solvent accessibility in proteins using multiple sequence alignment and secondary structure. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 61, 318-324.	1.5	87
34	Meta-DP: domain prediction meta-server. <i>Bioinformatics</i> , 2005, 21, 2917-2920.	1.8	47
35	A putative novel alpha/beta hydrolase ORFan family in <i>Bacillus</i> . <i>FEBS Letters</i> , 2005, 579, 3175-3182.	1.3	12
36	A neural network method for prediction of β -turn types in proteins using evolutionary information. <i>Bioinformatics</i> , 2004, 20, 2751-2758.	1.8	97

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37	Prediction of transmembrane regions of $\hat{\Gamma}^2$ -barrel proteins using ANN- and SVM-based methods. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 56, 11-18.	1.5	98
38	Prediction of $\hat{\Gamma}^{\pm}$ -turns in proteins using PSI-BLAST profiles and secondary structure information. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 55, 83-90.	1.5	52
39	Role of evolutionary information in prediction of aromatic-backbone NH interactions in proteins. <i>FEBS Letters</i> , 2004, 564, 47-57.	1.3	9
40	Prediction of beta-turns in proteins from multiple alignment using neural network. <i>Protein Science</i> , 2003, 12, 627-634.	3.1	129
41	A neural-network based method for prediction of $\hat{\Gamma}^3$ -turns in proteins from multiple sequence alignment. <i>Protein Science</i> , 2003, 12, 923-929.	3.1	71
42	BTEVAL: A Server for Evaluation of $\hat{\Gamma}^2$ -Turn Prediction Methods. <i>Journal of Bioinformatics and Computational Biology</i> , 2003, 01, 495-504.	0.3	4
43	Locating probable genes using Fourier transform approach. <i>Bioinformatics</i> , 2002, 18, 196-197.	1.8	54
44	An evaluation of $\hat{\Gamma}$ -turn prediction methods. <i>Bioinformatics</i> , 2002, 18, 1508-1514.	1.8	46
45	BetaTPred: prediction of $\hat{\Gamma}$ -TURNS in a protein using statistical algorithms. <i>Bioinformatics</i> , 2002, 18, 498-499.	1.8	23