Harpreet Kaur Saini

List of Publications by Year
in descending order

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	miRBase: tools for microRNA genomics. Nucleic Acids Research, 2007, 36, D154-D158.	6.5	3,854
2	Genomic analysis of human microRNA transcripts. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 17719-17724.	3.3	466
3	Extracellular Vesicles from Neural Stem Cells Transfer IFN-Î³ via Ifngr1 to Activate Stat1 Signaling in Target Cells. Molecular Cell, 2014, 56, 193-204.	4.5	258
4	Malignant Germ Cell Tumors Display Common MicroRNA Profiles Resulting in Global Changes in Expression of Messenger RNA Targets. Cancer Research, 2010, 70, 2911-2923.	0.4	243
5	Computational Prediction of Proteinâ€"Protein Interactions. Molecular Biotechnology, 2008, 38, 1-17.	1.3	201
6	PEPstr: A de novo Method for Tertiary Structure Prediction of Small Bioactive Peptides. Protein and Peptide Letters, 2007, 14, 626-631.	0.4	179
7	Multiple Epigenetic Mechanisms and the piRNA Pathway Enforce LINE1 Silencing during Adult Spermatogenesis. Molecular Cell, 2013, 50, 601-608.	4.5	170
8	Integrated analysis of microRNA and mRNA expression and association with HIF binding reveals the complexity of microRNA expression regulation under hypoxia. Molecular Cancer, 2014, 13, 28.	7.9	135
9	Prediction of beta-turns in proteins from multiple alignment using neural network. Protein Science, 2003, 12, 627-634.	3.1	129
10	Annotation of mammalian primary microRNAs. BMC Genomics, 2008, 9, 564.	1.2	121
11	Extracellular vesicles are independent metabolic units with asparaginase activity. Nature Chemical Biology, 2017, 13, 951-955.	3.9	107
12	Prediction of transmembrane regions of Î²-barrel proteins using ANN- and SVM-based methods. Proteins: Structure, Function and Bioinformatics, 2004, 56, 11-18.	1.5	98
13	A neural network method for prediction of Â-turn types in proteins using evolutionary information. Bioinformatics, 2004, 20, 2751-2758.	1.8	97
14	Detection of secondary binding sites in proteins using fragment screening. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 15910-15915.	3.3	91
15	Real value prediction of solvent accessibility in proteins using multiple sequence alignment and secondary structure. Proteins: Structure, Function and Bioinformatics, 2005, 61, 318-324.	1.5	87
16	MiR-221 Influences Effector Functions and Actin Cytoskeleton in Mast Cells. PLoS ONE, 2011, 6, e26133.	1.1	81
17	Solid Tumors of Childhood Display Specific Serum microRNA Profiles. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 350-360.	1.1	74
18	A neural-network based method for prediction of Î³-turns in proteins from multiple sequence alignment. Protein Science, 2003, 12, 923-929.	3.1	71

#	Article	IF	Citations
19	Functional evidence that *Drosha* overexpression in cervical squamous cell carcinoma affects cell phenotype and microRNA profiles. Journal of Pathology, 2011, 224, 496-507.	2.1	71
20	*LIN28* Expression in Malignant Germ Cell Tumors Downregulates *let-7* and Increases Oncogene Levels. Cancer Research, 2013, 73, 4872-4884.	0.4	61
21	The two most common histological subtypes of malignant germ cell tumour are distinguished by global microRNA profiles, associated with differential transcription factor expression. Molecular Cancer, 2010, 9, 290.	7.9	60
22	Locating probable genes using Fourier transform approach. Bioinformatics, 2002, 18, 196-197.	1.8	54
23	Prediction of Î±-turns in proteins using PSI-BLAST profiles and secondary structure information. Proteins: Structure, Function and Bioinformatics, 2004, 55, 83-90.	1.5	52
24	Meta-DP: domain prediction meta-server. Bioinformatics, 2005, 21, 2917-2920.	1.8	47
25	An evaluation of Â-turn prediction methods. Bioinformatics, 2002, 18, 1508-1514.	1.8	46
26	Fragment-Based Discovery of a Potent, Orally Bioavailable Inhibitor That Modulates the Phosphorylation and Catalytic Activity of ERK1/2. Journal of Medicinal Chemistry, 2018, 61, 4978-4992.	2.9	42
27	Depletion of HPV16 early genes induces autophagy and senescence in a cervical carcinogenesis model, regardless of viral physical state. Journal of Pathology, 2013, 231, 354-366.	2.1	40
28	Transposonâ€driven transcription is a conserved feature of vertebrate spermatogenesis and transcript evolution. EMBO Reports, 2017, 18, 1231-1247.	2.0	34
29	COSMIC-3D provides structural perspectives on cancer genetics for drug discovery. Nature Genetics, 2018, 50, 1200-1202.	9.4	31
30	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. British Journal of Cancer, 2016, 115, 1069-1077.	2.9	26
31	BetaTPred: prediction of Â-TURNS in a protein using statistical algorithms. Bioinformatics, 2002, 18, 498-499.	1.8	23
32	Structural and functional insights into Mimivirus ORFans. BMC Genomics, 2007, 8, 115.	1.2	22
33	Messenger RNA and microRNA profiling during early mouse EB formation. Gene Expression Patterns, 2011, 11, 334-344.	0.3	17
34	The role of SQSTM1 (p62) in mitochondrial function and clearance in human cortical neurons. Stem Cell Reports, 2021, 16, 1276-1289.	2.3	17
35	Dual-Mechanism ERK1/2 Inhibitors Exploit a Distinct Binding Mode to Block Phosphorylation and Nuclear Accumulation of ERK1/2. Molecular Cancer Therapeutics, 2020, 19, 525-539.	1.9	14
36	A putative novel alpha/beta hydrolase ORFan family inBacillus. FEBS Letters, 2005, 579, 3175-3182.	1.3	12

#	Article	IF	Citations
37	iMotifs: an integrated sequence motif visualization and analysis environment. Bioinformatics, 2010, 26, 843-844.	1.8	11
38	Role of evolutionary information in prediction of aromatic-backbone NH interactions in proteins. FEBS Letters, 2004, 564, 47-57.	1.3	9
39	Ï‰â€Turn: A novel Î²â€turn mimic in globular proteins stabilized by mainâ€chain to sideâ€chain CÏ£¿HÂ·Â·Â·O interaction. Proteins: Structure, Function and Bioinformatics, 2015, 83, 203-214.	1.5	7
40	BTEVAL: A Server for Evaluation of Î²-Turn Prediction Methods. Journal of Bioinformatics and Computational Biology, 2003, 01, 495-504.	0.3	4
41	Visualization and analysis of RNA-Seq assembly graphs. Nucleic Acids Research, 2019, 47, 7262-7275.	6.5	4
42	Antagonism of inhibitors of apoptosis proteins reveals a novel, immune response-based therapeutic approach for T-cell lymphoma. Blood Advances, 2021, 5, 4003-4016.	2.5	4
43	FRalanyzer: a tool for functional analysis of fold-recognition sequence-structure alignments. Nucleic Acids Research, 2007, 35, W499-W502.	6.5	3
44	Abstract 3424: Malignant germ cell tumors display common microRNA profiles resulting in global changes in expression of mRNA targets. , 2010, , .		0
45	Combining the IAP Antagonist Tolinapant with a DNA Hypomethylating Agent Enhances Immunogenic Cell Death in Preclinical Models of T-Cell Lymphoma. Blood, 2021, 138, 3986-3986.	0.6	0