

# Harpreet Kaur Saini

## List of Publications by Citations

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44  
papers

6,002  
citations

26  
h-index

45  
g-index

45  
ext. papers

6,624  
ext. citations

9.7  
avg, IF

5.67  
L-index

#	Paper	IF	Citations
44	miRBase: tools for microRNA genomics. <i>Nucleic Acids Research</i> , <b>2008</b> , 36, D154-8	20.1	3326
43	Genomic analysis of human microRNA transcripts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2007</b> , 104, 17719-24	11.5	402
42	Malignant germ cell tumors display common microRNA profiles resulting in global changes in expression of messenger RNA targets. <i>Cancer Research</i> , <b>2010</b> , 70, 2911-23	10.1	201
41	Extracellular vesicles from neural stem cells transfer IFN- $\gamma$ via Ifngr1 to activate Stat1 signaling in target cells. <i>Molecular Cell</i> , <b>2014</b> , 56, 193-204	17.6	195
40	Computational prediction of protein-protein interactions. <i>Molecular Biotechnology</i> , <b>2008</b> , 38, 1-17	3	152
39	PEPstr: a de novo method for tertiary structure prediction of small bioactive peptides. <i>Protein and Peptide Letters</i> , <b>2007</b> , 14, 626-31	1.9	152
38	Multiple epigenetic mechanisms and the piRNA pathway enforce LINE1 silencing during adult spermatogenesis. <i>Molecular Cell</i> , <b>2013</b> , 50, 601-8	17.6	134
37	Prediction of beta-turns in proteins from multiple alignment using neural network. <i>Protein Science</i> , <b>2003</b> , 12, 627-34	6.3	117
36	Annotation of mammalian primary microRNAs. <i>BMC Genomics</i> , <b>2008</b> , 9, 564	4.5	110
35	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> , <b>2014</b> , 13, 28	42.1	104
34	Prediction of transmembrane regions of beta-barrel proteins using ANN- and SVM-based methods. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2004</b> , 56, 11-8	4.2	85
33	A neural network method for prediction of beta-turn types in proteins using evolutionary information. <i>Bioinformatics</i> , <b>2004</b> , 20, 2751-8	7.2	80
32	Real value prediction of solvent accessibility in proteins using multiple sequence alignment and secondary structure. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2005</b> , 61, 318-24	4.2	73
31	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> , <b>2015</b> , 112, 15910-5	11.5	71
30	Extracellular vesicles are independent metabolic units with asparaginase activity. <i>Nature Chemical Biology</i> , <b>2017</b> , 13, 951-955	11.7	70
29	MiR-221 influences effector functions and actin cytoskeleton in mast cells. <i>PLoS ONE</i> , <b>2011</b> , 6, e26133	3.7	69
28	Functional evidence that Drosha overexpression in cervical squamous cell carcinoma affects cell phenotype and microRNA profiles. <i>Journal of Pathology</i> , <b>2011</b> , 224, 496-507	9.4	61

27	A neural-network based method for prediction of gamma-turns in proteins from multiple sequence alignment. <i>Protein Science</i> , <b>2003</b> , 12, 923-9	6.3	61
26	Solid tumors of childhood display specific serum microRNA profiles. <i>Cancer Epidemiology Biomarkers and Prevention</i> , <b>2015</b> , 24, 350-60	4	50
25	LIN28 Expression in malignant germ cell tumors downregulates let-7 and increases oncogene levels. <i>Cancer Research</i> , <b>2013</b> , 73, 4872-84	10.1	50
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> , <b>2010</b> , 9, 290	42.1	48
23	Locating probable genes using Fourier transform approach. <i>Bioinformatics</i> , <b>2002</b> , 18, 196-7	7.2	45
22	Prediction of alpha-turns in proteins using PSI-BLAST profiles and secondary structure information. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2004</b> , 55, 83-90	4.2	44
21	Meta-DP: domain prediction meta-server. <i>Bioinformatics</i> , <b>2005</b> , 21, 2917-20	7.2	43
20	An evaluation of beta-turn prediction methods. <i>Bioinformatics</i> , <b>2002</b> , 18, 1508-14	7.2	41
19	Depletion of HPV16 early genes induces autophagy and senescence in a cervical carcinogenesis model, regardless of viral physical state. <i>Journal of Pathology</i> , <b>2013</b> , 231, 354-66	9.4	28
18	Transposon-driven transcription is a conserved feature of vertebrate spermatogenesis and transcript evolution. <i>EMBO Reports</i> , <b>2017</b> , 18, 1231-1247	6.5	26
17	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> , <b>2016</b> , 115, 1069-1077	8.7	23
16	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> , <b>2018</b> , 61, 4978-4992	8.3	22
15	BetaTPred: prediction of beta-TURNS in a protein using statistical algorithms. <i>Bioinformatics</i> , <b>2002</b> , 18, 498-9	7.2	21
14	COSMIC-3D provides structural perspectives on cancer genetics for drug discovery. <i>Nature Genetics</i> , <b>2018</b> , 50, 1200-1202	36.3	18
13	Messenger RNA and microRNA profiling during early mouse EB formation. <i>Gene Expression Patterns</i> , <b>2011</b> , 11, 334-44	1.5	16
12	Structural and functional insights into Mimivirus ORFans. <i>BMC Genomics</i> , <b>2007</b> , 8, 115	4.5	15
11	A putative novel alpha/beta hydrolase ORFan family in Bacillus. <i>FEBS Letters</i> , <b>2005</b> , 579, 3175-82	3.8	12
10	Role of evolutionary information in prediction of aromatic-backbone NH interactions in proteins. <i>FEBS Letters</i> , <b>2004</b> , 564, 47-57	3.8	8

9	iMotifs: an integrated sequence motif visualization and analysis environment. <i>Bioinformatics</i> , <b>2010</b> , 26, 843-4	7.2	7
8	ETurn: a novel Eturn mimic in globular proteins stabilized by main-chain to side-chain CβH <sub>1</sub> O interaction. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2015</b> , 83, 203-14	4.2	6
7	Dual-Mechanism ERK1/2 Inhibitors Exploit a Distinct Binding Mode to Block Phosphorylation and Nuclear Accumulation of ERK1/2. <i>Molecular Cancer Therapeutics</i> , <b>2020</b> , 19, 525-539	6.1	5
6	FRalalyzer: a tool for functional analysis of fold-recognition sequence-structure alignments. <i>Nucleic Acids Research</i> , <b>2007</b> , 35, W499-502	20.1	3
5	BTEVAL: a server for evaluation of beta-turn prediction methods. <i>Journal of Bioinformatics and Computational Biology</i> , <b>2003</b> , 1, 495-504	1	3
4	The role of SQSTM1 (p62) in mitochondrial function and clearance in human cortical neurons. <i>Stem Cell Reports</i> , <b>2021</b> , 16, 1276-1289	8	3
3	Visualization and analysis of RNA-Seq assembly graphs. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, 7262-7275	20.1	1
2	Antagonism of inhibitors of apoptosis proteins reveals a novel, immune response-based therapeutic approach for T-cell lymphoma. <i>Blood Advances</i> , <b>2021</b> , 5, 4003-4016	7.8	1
1	Combining the IAP Antagonist Tolinapant with a DNA Hypomethylating Agent Enhances Immunogenic Cell Death in Preclinical Models of T-Cell Lymphoma. <i>Blood</i> , <b>2021</b> , 138, 3986-3986	2.2	