

# Manish Kumar

## List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

50  
papers

1,774  
citations

17  
h-index

42  
g-index

57  
ext. papers

2,203  
ext. citations

4.4  
avg, IF

5.2  
L-index

#	Paper	IF	Citations
50	MALDI-TOF mass spectrometry: an emerging technology for microbial identification and diagnosis. <i>Frontiers in Microbiology</i> , <b>2015</b> , 6, 791	5.7	659
49	Prediction of RNA binding sites in a protein using SVM and PSSM profile. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2008</b> , 71, 189-94	4.2	212
48	Identification of DNA-binding proteins using support vector machines and evolutionary profiles. <i>BMC Bioinformatics</i> , <b>2007</b> , 8, 463	3.6	174
47	Prediction of $\beta$ -lactamase and its class by Chou's pseudo-amino acid composition and support vector machine. <i>Journal of Theoretical Biology</i> , <b>2015</b> , 365, 96-103	2.3	124
46	SVM based prediction of RNA-binding proteins using binding residues and evolutionary information. <i>Journal of Molecular Recognition</i> , <b>2011</b> , 24, 303-13	2.6	88
45	Prediction of mitochondrial proteins using support vector machine and hidden Markov model. <i>Journal of Biological Chemistry</i> , <b>2006</b> , 281, 5357-63	5.4	80
44	PalmPred: an SVM based palmitoylation prediction method using sequence profile information. <i>PLoS ONE</i> , <b>2014</b> , 9, e89246	3.7	45
43	BlaPred: Predicting and classifying $\beta$ -lactamase using a 3-tier prediction system via Chou's general PseAAC. <i>Journal of Theoretical Biology</i> , <b>2018</b> , 457, 29-36	2.3	36
42	Prediction of nuclear proteins using SVM and HMM models. <i>BMC Bioinformatics</i> , <b>2009</b> , 10, 22	3.6	30
41	CBMAR: a comprehensive $\beta$ -lactamase molecular annotation resource. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2014</b> , 2014, bau111	5	25
40	Low complexity and disordered regions of proteins have different structural and amino acid preferences. <i>Molecular BioSystems</i> , <b>2015</b> , 11, 585-94		23
39	Evaluation of Bile Salt Hydrolases, Cholesterol-Lowering Capabilities, and Probiotic Potential of Isolated From Rhizosphere. <i>Frontiers in Microbiology</i> , <b>2019</b> , 10, 1567	5.7	22
38	MALDI-TOF MS in clinical parasitology: applications, constraints and prospects. <i>Parasitology</i> , <b>2016</b> , 143, 1491-500	2.7	21
37	LPS-annotate: complete annotation of compositionally biased regions in the protein knowledgebase. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2011</b> , 2011, baq031	5	19
36	In-silico design of a multivalent epitope-based vaccine against <i>Candida auris</i> . <i>Microbial Pathogenesis</i> , <b>2021</b> , 155, 104879	3.8	19
35	Proteome-wide prediction and annotation of mitochondrial and sub-mitochondrial proteins by incorporating domain information. <i>Mitochondrion</i> , <b>2018</b> , 42, 11-22	4.9	18
34	Protein sub-nuclear localization prediction using SVM and Pfam domain information. <i>PLoS ONE</i> , <b>2014</b> , 9, e98345	3.7	18

33	Proteome profiling of carbapenem-resistant <i>K. pneumoniae</i> clinical isolate (NDM-4): Exploring the mechanism of resistance and potential drug targets. <i>Journal of Proteomics</i> , <b>2019</b> , 200, 102-110	3.9	15
32	Prediction of endoplasmic reticulum resident proteins using fragmented amino acid composition and support vector machine. <i>PeerJ</i> , <b>2017</b> , 5, e3561	3.1	15
31	Molecular analysis of $\beta$ -lactamase genes to understand their differential expression in strains of <i>Yersinia enterocolitica</i> biotype 1A. <i>Scientific Reports</i> , <b>2014</b> , 4, 5270	4.9	13
30	mRNALoc: a novel machine-learning based in-silico tool to predict mRNA subcellular localization. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, W239-W243	20.1	13
29	Prediction of zinc binding sites in proteins using sequence derived information. <i>Journal of Biomolecular Structure and Dynamics</i> , <b>2018</b> , 36, 4413-4423	3.6	13
28	Support vector machine based prediction of glutathione S-transferase proteins. <i>Protein and Peptide Letters</i> , <b>2007</b> , 14, 575-80	1.9	12
27	NRfamPred: a proteome-scale two level method for prediction of nuclear receptor proteins and their sub-families. <i>Scientific Reports</i> , <b>2014</b> , 4, 6810	4.9	9
26	PredHSP: Sequence Based Proteome-Wide Heat Shock Protein Prediction and Classification Tool to Unlock the Stress Biology. <i>PLoS ONE</i> , <b>2016</b> , 11, e0155872	3.7	9
25	Down-Regulation of Flagellar, Fimbriae, and Pili Proteins in Carbapenem-Resistant (NDM-4) Clinical Isolates: A Novel Linkage to Drug Resistance. <i>Frontiers in Microbiology</i> , <b>2019</b> , 10, 2865	5.7	9
24	CrAgDb--a database of annotated chaperone repertoire in archaeal genomes. <i>FEMS Microbiology Letters</i> , <b>2016</b> , 363,	2.9	7
23	miPepBase: A Database of Experimentally Verified Peptides Involved in Molecular Mimicry. <i>Frontiers in Microbiology</i> , <b>2017</b> , 8, 2053	5.7	7
22	Identification of family specific fingerprints in $\beta$ -lactamase families. <i>Scientific World Journal, The</i> , <b>2014</b> , 2014, 980572	2.2	6
21	BacEffluxPred: A two-tier system to predict and categorize bacterial efflux mediated antibiotic resistance proteins. <i>Scientific Reports</i> , <b>2020</b> , 10, 9287	4.9	5
20	Rhizospheric <i>Lactobacillus plantarum</i> ( <i>Lactiplantibacillus plantarum</i> ) strains exhibit bile salt hydrolysis, hypocholesterolemic and probiotic capabilities in vitro. <i>Scientific Reports</i> , <b>2021</b> , 11, 15288	4.9	4
19	Comparative functional analysis of proteins containing low-complexity predicted amyloid regions. <i>PeerJ</i> , <b>2018</b> , 6, e5823	3.1	3
18	Using molecular-mimicry-inducing pathways of pathogens as novel drug targets. <i>Drug Discovery Today</i> , <b>2019</b> , 24, 1943-1952	8.8	3
17	High Prevalence of Drug Resistance and Class 1 Integrons in Isolated From River Yamuna, India: A Serious Public Health Risk. <i>Frontiers in Microbiology</i> , <b>2021</b> , 12, 621564	5.7	3
16	Antimicrobial resistance and its relationship with biofilm production and virulence-related factors in biotype 1A. <i>Heliyon</i> , <b>2019</b> , 5, e01777	3.6	2

15	Molecular Characteristics of "BlaB-Like" Chromosomal Inducible Cephalosporinase of Biotype 1A Strains. <i>Microbial Drug Resistance</i> , <b>2019</b> , 25, 824-829	2.9	2
14	Prediction of Rare Palmitoylation Events in Proteins. <i>Journal of Computational Biology</i> , <b>2018</b> , 25, 997-1008	3.7	2
13	Structural Variabilities in $\beta$ Lactamase (blaA) of Different Biovars of <i>Yersinia enterocolitica</i> : Implications for $\beta$ Lactam Antibiotic and $\beta$ Lactamase Inhibitor Susceptibilities. <i>PLoS ONE</i> , <b>2014</b> , 10, e0123564	3.7	2
12	Molecular analysis of ampR and ampD to understand variability in inducible expression of "BlaB-like" cephalosporinase in <i>Yersinia enterocolitica</i> biotype 1A. <i>Gene</i> , <b>2019</b> , 704, 25-30	3.8	1
11	ampD homologs in biotypes of <i>Yersinia enterocolitica</i> : Implications in regulation of chromosomal AmpC-type cephalosporinases. <i>Infection, Genetics and Evolution</i> , <b>2019</b> , 69, 211-215	4.5	1
10	Exploring the genetic determinants underlying the differential production of an inducible chromosomal cephalosporinase - BlaB in <i>Yersinia enterocolitica</i> biotypes 1A, 1B, 2 and 4. <i>Scientific Reports</i> , <b>2020</b> , 10, 10167	4.9	1
9	Comparative in-silico proteomic analysis discerns potential granuloma proteins of <i>Yersinia pseudotuberculosis</i> . <i>Scientific Reports</i> , <b>2020</b> , 10, 3036	4.9	1
8	Exploring the genetic mechanisms underlying amoxicillin-clavulanate resistance in waterborne <i>Escherichia coli</i> . <i>Infection, Genetics and Evolution</i> , <b>2021</b> , 90, 104767	4.5	1
7	Identifying residues that determine palmitoylation using association rule mining. <i>Bioinformatics</i> , <b>2019</b> , 35, 2887-2890	7.2	1
6	Biophysical and Biochemical Characterization of Nascent Polypeptide-Associated Complex of and Elucidation of Its Interacting Partners. <i>Frontiers in Microbiology</i> , <b>2020</b> , 11, 915	5.7	0
5	Efficacy of signal peptide predictors in identifying signal peptides in the experimental secretome of <i>Picrophilus torridus</i> , a thermoacidophilic archaeon. <i>PLoS ONE</i> , <b>2021</b> , 16, e0255826	3.7	0
4	Investigating the disordered regions (MoRFs, SLiMs and LCRs) and functions of mimicry proteins/peptides in silico.. <i>PLoS ONE</i> , <b>2022</b> , 17, e0265657	3.7	0
3	Comparative Proteomics of Commensal and Pathogenic Strains of. <i>Protein and Peptide Letters</i> , <b>2020</b> , 27, 1171-1177	1.9	
2	Identification of Binding Partners of CsaA - An Archaeal Chaperonic Protein of <i>Picrophilus torridus</i> . <i>Protein and Peptide Letters</i> , <b>2021</b> , 28, 675-679	1.9	
1	Public health implications of plasmid-mediated quinolone and aminoglycoside resistance genes in inhabiting a major anthropogenic river of India.. <i>Epidemiology and Infection</i> , <b>2022</b> , 1-21	4.3	