Manish Kumar

List of Publications by Year in Descending Order

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.
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	Public health implications of plasmid-mediated quinolone and aminoglycoside resistance genes in inhabiting a major anthropogenic river of India.. *Epidemiology and Infection*, **2022**, 1-21	4.3	
49	Investigating the disordered regions (MoRFs, SLiMs and LCRs) and functions of mimicry proteins/peptides in silico.. *PLoS ONE*, **2022**, 17, e0265657	3.7	0
48	Exploring the genetic mechanisms underlying amoxicillin-clavulanate resistance in waterborne Escherichia coli. *Infection, Genetics and Evolution*, **2021**, 90, 104767	4.5	1
47	In-silico design of a multivalent epitope-based vaccine against Candida auris. *Microbial Pathogenesis*, **2021**, 155, 104879	3.8	19
46	Identification of Binding Partners of CsaA - An Archaeal Chaperonic Protein of Picrophilus torridus. *Protein and Peptide Letters*, **2021**, 28, 675-679	1.9	
45	High Prevalence of Drug Resistance and Class 1 Integrons in Isolated From River Yamuna, India: A Serious Public Health Risk. *Frontiers in Microbiology*, **2021**, 12, 621564	5.7	3
44	Rhizospheric Lactobacillus plantarum (Lactiplantibacillus plantarum) strains exhibit bile salt hydrolysis, hypocholestrolemic and probiotic capabilities in vitro. *Scientific Reports*, **2021**, 11, 15288	4.9	4
43	Efficacy of signal peptide predictors in identifying signal peptides in the experimental secretome of Picrophilous torridus, a thermoacidophilic archaeon. *PLoS ONE*, **2021**, 16, e0255826	3.7	0
42	mRNALoc: a novel machine-learning based in-silico tool to predict mRNA subcellular localization. *Nucleic Acids Research*, **2020**, 48, W239-W243	20.1	13
41	Biophysical and Biochemical Characterization of Nascent Polypeptide-Associated Complex of and Elucidation of Its Interacting Partners. *Frontiers in Microbiology*, **2020**, 11, 915	5.7	0
40	Exploring the genetic determinants underlying the differential production of an inducible chromosomal cephalosporinase - BlaB in Yersinia enterocolitica biotypes 1A, 1B, 2 and 4. *Scientific Reports*, **2020**, 10, 10167	4.9	1
39	Comparative in-silico proteomic analysis discerns potential granuloma proteins of Yersinia pseudotuberculosis. *Scientific Reports*, **2020**, 10, 3036	4.9	1
38	Comparative Proteomics of Commensal and Pathogenic Strains of. *Protein and Peptide Letters*, **2020**, 27, 1171-1177	1.9	
37	BacEffluxPred: A two-tier system to predict and categorize bacterial efflux mediated antibiotic resistance proteins. *Scientific Reports*, **2020**, 10, 9287	4.9	5
36	Antimicrobial resistance and its relationship with biofilm production and virulence-related factors in biotype 1A. *Heliyon*, **2019**, 5, e01777	3.6	2
35	Molecular analysis of ampR and ampD to understand variability in inducible expression of "BlaB-like" cephalosporinase in Yersinia enterocolitica biotype 1A. *Gene*, **2019**, 704, 25-30	3.8	1
34	Molecular Characteristics of "BlaB-Like" Chromosomal Inducible Cephalosporinase of Biotype 1A Strains. *Microbial Drug Resistance*, **2019**, 25, 824-829	2.9	2

33	Proteome profiling of carbapenem-resistant K. pneumoniae clinical isolate (NDM-4): Exploring the mechanism of resistance and potential drug targets. *Journal of Proteomics*, **2019**, 200, 102-110	3.9	15
32	ampD homologs in biotypes of Yersinia enterocolitica: Implications in regulation of chromosomal AmpC-type cephalosporinases. *Infection, Genetics and Evolution*, **2019**, 69, 211-215	4.5	1
31	Evaluation of Bile Salt Hydrolases, Cholesterol-Lowering Capabilities, and Probiotic Potential of Isolated From Rhizosphere. *Frontiers in Microbiology*, **2019**, 10, 1567	5.7	22
30	Down-Regulation of Flagellar, Fimbriae, and Pili Proteins in Carbapenem-Resistant (NDM-4) Clinical Isolates: A Novel Linkage to Drug Resistance. *Frontiers in Microbiology*, **2019**, 10, 2865	5.7	9
29	Identifying residues that determine palmitoylation using association rule mining. *Bioinformatics*, **2019**, 35, 2887-2890	7.2	1
28	Using molecular-mimicry-inducing pathways of pathogens as novel drug targets. *Drug Discovery Today*, **2019**, 24, 1943-1952	8.8	3
27	Prediction of zinc binding sites in proteins using sequence derived information. *Journal of Biomolecular Structure and Dynamics*, **2018**, 36, 4413-4423	3.6	13
26	Proteome-wide prediction and annotation of mitochondrial and sub-mitochondrial proteins by incorporating domain information. *Mitochondrion*, **2018**, 42, 11-22	4.9	18
25	Prediction of Rare Palmitoylation Events in Proteins. *Journal of Computational Biology*, **2018**, 25, 997-1002	1.7	2
24	BlaPred: Predicting and classifying ꞵ-lactamase using a 3-tier prediction system via Chou's general PseAAC. *Journal of Theoretical Biology*, **2018**, 457, 29-36	2.3	36
23	Comparative functional analysis of proteins containing low-complexity predicted amyloid regions. *PeerJ*, **2018**, 6, e5823	3.1	3
22	miPepBase: A Database of Experimentally Verified Peptides Involved in Molecular Mimicry. *Frontiers in Microbiology*, **2017**, 8, 2053	5.7	7
21	Prediction of endoplasmic reticulum resident proteins using fragmented amino acid composition and support vector machine. *PeerJ*, **2017**, 5, e3561	3.1	15
20	CrAgDb--a database of annotated chaperone repertoire in archaeal genomes. *FEMS Microbiology Letters*, **2016**, 363,	2.9	7
19	PredHSP: Sequence Based Proteome-Wide Heat Shock Protein Prediction and Classification Tool to Unlock the Stress Biology. *PLoS ONE*, **2016**, 11, e0155872	3.7	9
18	MALDI-TOF MS in clinical parasitology: applications, constraints and prospects. *Parasitology*, **2016**, 143, 1491-500	2.7	21
17	Low complexity and disordered regions of proteins have different structural and amino acid preferences. *Molecular BioSystems*, **2015**, 11, 585-94		23
16	Prediction of ꞵ-lactamase and its class by Chou's pseudo-amino acid composition and support vector machine. *Journal of Theoretical Biology*, **2015**, 365, 96-103	2.3	124

15	MALDI-TOF mass spectrometry: an emerging technology for microbial identification and diagnosis. *Frontiers in Microbiology*, **2015**, 6, 791	5.7	659
14	Molecular analysis of β-lactamase genes to understand their differential expression in strains of Yersinia enterocolitica biotype 1A. *Scientific Reports*, **2014**, 4, 5270	4.9	13
13	NRfamPred: a proteome-scale two level method for prediction of nuclear receptor proteins and their sub-families. *Scientific Reports*, **2014**, 4, 6810	4.9	9
12	PalmPred: an SVM based palmitoylation prediction method using sequence profile information. *PLoS ONE*, **2014**, 9, e89246	3.7	45
11	Identification of family specific fingerprints in β-lactamase families. *Scientific World Journal, The*, **2014**, 2014, 980572	2.2	6
10	CBMAR: a comprehensive β-lactamase molecular annotation resource. *Database: the Journal of Biological Databases and Curation*, **2014**, 2014, bau111	5	25
9	Protein sub-nuclear localization prediction using SVM and Pfam domain information. *PLoS ONE*, **2014**, 9, e98345	3.7	18
8	Structural Variabilities in β-Lactamase (blaA) of Different Biovars of Yersinia enterocolitica: Implications for β-Lactam Antibiotic and β-Lactamase Inhibitor Susceptibilities. *PLoS ONE*, **2014**, 10, e0123564	3.7	2
7	LPS-annotate: complete annotation of compositionally biased regions in the protein knowledgebase. *Database: the Journal of Biological Databases and Curation*, **2011**, 2011, baq031	5	19
6	SVM based prediction of RNA-binding proteins using binding residues and evolutionary information. *Journal of Molecular Recognition*, **2011**, 24, 303-13	2.6	88
5	Prediction of nuclear proteins using SVM and HMM models. *BMC Bioinformatics*, **2009**, 10, 22	3.6	30
4	Prediction of RNA binding sites in a protein using SVM and PSSM profile. *Proteins: Structure, Function and Bioinformatics*, **2008**, 71, 189-94	4.2	212
3	Identification of DNA-binding proteins using support vector machines and evolutionary profiles. *BMC Bioinformatics*, **2007**, 8, 463	3.6	174
2	Support vector machine based prediction of glutathione S-transferase proteins. *Protein and Peptide Letters*, **2007**, 14, 575-80	1.9	12
1	Prediction of mitochondrial proteins using support vector machine and hidden Markov model. *Journal of Biological Chemistry*, **2006**, 281, 5357-63	5.4	80