

Susan Idicula-Thomas

List of Publications by Year in descending order

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Version: 2024-02-01

39
papers

1,908
citations

516710

16
h-index

315739

38
g-index

40
all docs

40
docs citations

40
times ranked

2797
citing authors

#	ARTICLE	IF	CITATIONS
1	Mapping of FSHR agonists and antagonists binding sites to identify potential peptidomimetic modulators. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2022, 1864, 183842.	2.6	3
2	FSHR antagonists can trigger a PCOS-like state. <i>Systems Biology in Reproductive Medicine</i> , 2022, 68, 129-137.	2.1	4
3	Multimorbidity landscape of schizophrenia: Insights from meta-analysis of genome wide association studies. <i>Schizophrenia Research</i> , 2022, 243, 214-216.	2.0	1
4	GeDiPNet: Online resource of curated gene-disease associations for polypharmacological targets discovery. <i>Genes and Diseases</i> , 2022, , .	3.4	1
5	A 5-mer peptide derived from hinge region of hFSHR can function as positive allosteric modulator in vivo. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2021, 1863, 183492.	2.6	4
6	Enrichment analyses of diseases and pathways associated with precocious puberty using PrecocityDB. <i>Scientific Reports</i> , 2021, 11, 4203.	3.3	4
7	Exploring the druggable proteome of <i>Candida</i> species through comprehensive computational analysis. <i>Genomics</i> , 2021, 113, 728-739.	2.9	8
8	A Recombinant Fragment of Human Surfactant Protein D Binds Spike Protein and Inhibits Infectivity and Replication of SARS-CoV-2 in Clinical Samples. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2021, 65, 41-53.	2.9	29
9	Central residues of FSH ¹⁻² (89-97) peptide are not critical for FSHR binding: Implications for peptidomimetic design. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2021, 44, 128132.	2.2	2
10	Comparison of machine learning algorithms applied to symptoms to determine infectious causes of death in children: national survey of 18,000 verbal autopsies in the Million Death Study in India. <i>BMC Public Health</i> , 2021, 21, 1787.	2.9	2
11	Collection of antimicrobial peptides database and its derivatives: Applications and beyond. <i>Protein Science</i> , 2020, 29, 36-42.	7.6	82
12	PCOSKBR2: a database of genes, diseases, pathways, and networks associated with polycystic ovary syndrome. <i>Scientific Reports</i> , 2020, 10, 14738.	3.3	16
13	A QSAR modeling approach for predicting myeloid antimicrobial peptides with high sequence similarity. <i>Chemical Biology and Drug Design</i> , 2020, 96, 1408-1417.	3.2	2
14	A steady-state modeling approach for simulation of antimicrobial peptide-cell membrane interaction. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2020, 1862, 183242.	2.6	9
15	Identification and in vivo validation of a 9-mer peptide derived from FSH ¹⁻² with FSHR antagonist activity. <i>Peptides</i> , 2020, 132, 170367.	2.4	10
16	Meta-analysis of gene expression profiles of lean and obese PCOS to identify differentially regulated pathways and risk of comorbidities. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 1735-1745.	4.1	10
17	Effect of diversity in gp41 membrane proximal external region of primary HIV-1 Indian subtype C sequences on interaction with broadly neutralizing antibodies 4E10 and 10E8. <i>Virus Research</i> , 2019, 273, 197763.	2.2	6
18	Discovery of small molecule binders of human FSHR(TMD) with novel structural scaffolds by integrating structural bioinformatics and machine learning algorithms. <i>Journal of Molecular Graphics and Modelling</i> , 2019, 89, 156-166.	2.4	5

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19	Designing Antibacterial Peptides with Enhanced Killing Kinetics. <i>Frontiers in Microbiology</i> , 2018, 9, 325.	3.5	29
20	Evaluation of 4-thiazolidinone derivatives as potential reverse transcriptase inhibitors against HIV-1 drug resistant strains. <i>Bioorganic Chemistry</i> , 2017, 71, 211-218.	4.1	34
21	Protein-Protein Interaction between Surfactant Protein D and DC-SIGN via C-Type Lectin Domain Can Suppress HIV-1 Transfer. <i>Frontiers in Immunology</i> , 2017, 8, 834.	4.8	23
22	Leveraging family-specific signatures for AMP discovery and high-throughput annotation. <i>Scientific Reports</i> , 2016, 6, 24684.	3.3	16
23	CAMP_{R3}: a database on sequences, structures and signatures of antimicrobial peptides: Table 1.. <i>Nucleic Acids Research</i> , 2016, 44, D1094-D1097.	14.5	521
24	PCOSKB: A KnowledgeBase on genes, diseases, ontology terms and biochemical pathways associated with Polycystic Ovary Syndrome. <i>Nucleic Acids Research</i> , 2016, 44, D1032-D1035.	14.5	46
25	CAMP: Collection of sequences and structures of antimicrobial peptides. <i>Nucleic Acids Research</i> , 2014, 42, D1154-D1158.	14.5	219
26	HPV16 E6 variants: Frequency, association with HPV types and in silico analysis of the identified novel variants. <i>Journal of Medical Virology</i> , 2014, 86, 968-974.	5.0	6
27	Cervical cancer in Indian women reveals contrasting association among common sub-family of HLA class I alleles. <i>Immunogenetics</i> , 2014, 66, 683-691.	2.4	11
28	A Chemical Proteomics Approach to Profiling the ATP-binding Proteome of Mycobacterium tuberculosis. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 1644-1660.	3.8	41
29	In Silico Study on Binding Specificity of Gonadotropins and Their Receptors: Design of a Novel and Selective Peptidomimetic for Human Follicle Stimulating Hormone Receptor. <i>PLoS ONE</i> , 2013, 8, e64475.	2.5	5
30	ClassAMP: A Prediction Tool for Classification of Antimicrobial Peptides. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 1535-1538.	3.0	108
31	Identification of Novel Mutations in HEXA Gene in Children Affected with Tay Sachs Disease from India. <i>PLoS ONE</i> , 2012, 7, e39122.	2.5	37
32	Imatinib resistance due to a novel tri-nucleotide insertion in the SH2/C lobe interface of BCR/ABL kinase domain between position K357 and N358. <i>Leukemia Research</i> , 2012, 36, e110-e112.	0.8	4
33	Novel homozygous mutations in Desert Hedgehog gene in patients with 46,XY complete gonadal dysgenesis and prediction of its structural and functional implications by computational methods. <i>European Journal of Medical Genetics</i> , 2011, 54, e529-e534.	1.3	49
34	CAMP: a useful resource for research on antimicrobial peptides. <i>Nucleic Acids Research</i> , 2010, 38, D774-D780.	14.5	352
35	Phenotypic and genotypic characterization of Factor VII deficiency patients from Western India. <i>Clinica Chimica Acta</i> , 2009, 409, 106-111.	1.1	22
36	Hereditary basis of protein C deficiency (PCD) in thrombosis patients: first report from India. <i>Thrombosis and Haemostasis</i> , 2009, 101, 785-7.	3.4	0

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37	Correlation between the structural stability and aggregation propensity of proteins. <i>In Silico Biology</i> , 2007, 7, 225-37.	0.9	14
38	Understanding the relationship between the primary structure of proteins and their amyloidogenic propensity: clues from inclusion body formation. <i>Protein Engineering, Design and Selection</i> , 2005, 18, 175-180.	2.1	24
39	Understanding the relationship between the primary structure of proteins and its propensity to be soluble on overexpression in <i>Escherichia coli</i> . <i>Protein Science</i> , 2005, 14, 582-592.	7.6	147