

Kaveh Kavousi

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.

65
papers

544
citations

14
h-index

19
g-index

92
ext. papers

789
ext. citations

4.8
avg, IF

4.51
L-index

#	Paper	IF	Citations
65	Drug-target interaction prediction from PSSM based evolutionary information. <i>Journal of Pharmacological and Toxicological Methods</i> , 2016 , 78, 42-51	1.7	45
64	A novel thermostable cellulase cocktail enhances lignocellulosic bioconversion and biorefining in a broad range of pH. <i>International Journal of Biological Macromolecules</i> , 2020 , 154, 349-360	7.9	30
63	Identification and characterization of a novel thermostable xylanase from camel rumen metagenome. <i>International Journal of Biological Macromolecules</i> , 2019 , 126, 1295-1302	7.9	30
62	A protein fold classifier formed by fusing different modes of pseudo amino acid composition via PSSM. <i>Computational Biology and Chemistry</i> , 2011 , 35, 1-9	3.6	28
61	Mining of camel rumen metagenome to identify novel alkali-thermostable xylanase capable of enhancing the recalcitrant lignocellulosic biomass conversion. <i>Bioresource Technology</i> , 2019 , 281, 343-350 ¹¹	7.5	26
60	A novel high performance in-silico screened metagenome-derived alkali-thermostable endo- β -1,4-glucanase for lignocellulosic biomass hydrolysis in the harsh conditions. <i>BMC Biotechnology</i> , 2020 , 20, 56	3.5	23
59	Information theory in systems biology. Part I: Gene regulatory and metabolic networks. <i>Seminars in Cell and Developmental Biology</i> , 2016 , 51, 3-13	7.5	22
58	A Novel High Glucose-Tolerant β -Glucosidase: Targeted Computational Approach for Metagenomic Screening. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020 , 8, 813	5.8	21
57	A computational method for prediction of xylanase enzymes activity in strains of <i>Bacillus subtilis</i> based on pseudo amino acid composition features. <i>PLoS ONE</i> , 2018 , 13, e0205796	3.7	18
56	A combined Parzen-wavelet approach for detection of vuggy zones in fractured carbonate reservoirs using petrophysical logs. <i>Journal of Petroleum Science and Engineering</i> , 2014 , 119, 1-7	4.4	17
55	A novel metagenome-derived thermostable and poultry feed compatible α -amylase with enhanced biodegradation properties. <i>International Journal of Biological Macromolecules</i> , 2020 , 164, 2124-2133	7.9	16
54	IAMPE: NMR-Assisted Computational Prediction of Antimicrobial Peptides. <i>Journal of Chemical Information and Modeling</i> , 2020 , 60, 4691-4701	6.1	16
53	miR-548x and miR-4698 controlled cell proliferation by affecting the PI3K/AKT signaling pathway in Glioblastoma cell lines. <i>Scientific Reports</i> , 2020 , 10, 1558	4.9	15
52	Evidence theoretic protein fold classification based on the concept of hyperfold. <i>Mathematical Biosciences</i> , 2012 , 240, 148-60	3.9	15
51	The Stabilizing Mechanism of Immobilized Metagenomic Xylanases on Bio-Based Hydrogels to Improve Utilization Performance: Computational and Functional Perspectives. <i>Bioconjugate Chemistry</i> , 2020 , 31, 2158-2171	6.3	13
50	BIPEP: Sequence-based Prediction of Biofilm Inhibitory Peptides Using a Combination of NMR and Physicochemical Descriptors. <i>ACS Omega</i> , 2020 , 5, 7290-7297	3.9	12
49	Effect of compatible and noncompatible osmolytes on the enzymatic activity and thermal stability of bovine liver catalase. <i>Journal of Biomolecular Structure and Dynamics</i> , 2013 , 31, 1440-54	3.6	12

48	Efficient removal of various textile dyes from wastewater by novel thermo-halotolerant laccase. <i>Bioresource Technology</i> , 2021 , 337, 125468	11	12
47	Identification and Characterization of Novel miRNAs in <i>Chlamydomonas reinhardtii</i> by Computational Methods. <i>MicroRNA (Shariqah, United Arab Emirates)</i> , 2016 , 5, 66-77	2.9	11
46	Effects of zinc binding on the structure and thermal stability of camel alpha-lactalbumin. <i>Journal of Thermal Analysis and Calorimetry</i> , 2015 , 120, 481-488	4.1	9
45	Biochemical characterization of hemoglobins from Caspian Sea sturgeons (<i>Acipenser persicus</i> and <i>Acipenser stellatus</i>). <i>Cell Biochemistry and Biophysics</i> , 2012 , 62, 73-81	3.2	8
44	A Network Model for Vehicular Ad Hoc Networks: An Introduction to Obligatory Attachment Rule. <i>IEEE Transactions on Network Science and Engineering</i> , 2016 , 3, 82-94	4.9	8
43	A generalized machine-learning aided method for targeted identification of industrial enzymes from metagenome: A xylanase temperature dependence case study. <i>Biotechnology and Bioengineering</i> , 2021 , 118, 759-769	4.9	8
42	Upgrading the enzymatic hydrolysis of lignocellulosic biomass by immobilization of metagenome-derived novel halotolerant cellulase on the carboxymethyl cellulose-based hydrogel. <i>Cellulose</i> , 2021 , 28, 3485-3503	5.5	8
41	Genome-wide prediction and prioritization of human aging genes by data fusion: a machine learning approach. <i>BMC Genomics</i> , 2019 , 20, 832	4.5	7
40	Computational Identification of MicroRNAs and Their Transcript Target(s) in Field Mustard (L.). <i>Iranian Journal of Biotechnology</i> , 2017 , 15, 22-32	1	7
39	MCIC: Automated Identification of Cellulases From Metagenomic Data and Characterization Based on Temperature and pH Dependence. <i>Frontiers in Microbiology</i> , 2020 , 11, 567863	5.7	7
38	Link between short tandem repeats and translation initiation site selection. <i>Human Genomics</i> , 2018 , 12, 47	6.8	7
37	In Silico Identification of Conserved MiRNAs from <i>Physcomitrella patens</i> ESTs and their Target Characterization. <i>Current Bioinformatics</i> , 2018 , 14, 33-42	4.7	6
36	In-silico discovery of bifunctional enzymes with enhanced lignocellulose hydrolysis from microbiota big data. <i>International Journal of Biological Macromolecules</i> , 2021 , 177, 211-220	7.9	6
35	The Quest for Missing Proteins in Rice. <i>Molecular Plant</i> , 2019 , 12, 4-6	14.4	6
34	The role of MicroRNAs in defense against viral phytopathogens. <i>Physiological and Molecular Plant Pathology</i> , 2019 , 107, 8-13	2.6	5
33	FoPA: identifying perturbed signaling pathways in clinical conditions using formal methods. <i>BMC Bioinformatics</i> , 2019 , 20, 92	3.6	5
32	Co-abundance analysis reveals hidden players associated with high methane yield phenotype in sheep rumen microbiome. <i>Scientific Reports</i> , 2020 , 10, 4995	4.9	5
31	Architecture design of an intelligent information fusion agent for information retrieval from dynamic environments 2007 ,		5

30	The importance of CDC27 in cancer: molecular pathology and clinical aspects. <i>Cancer Cell International</i> , 2021 , 21, 160	6.4	5
29	EARN: an ensemble machine learning algorithm to predict driver genes in metastatic breast cancer. <i>BMC Medical Genomics</i> , 2021 , 14, 122	3.7	5
28	Denaturation and intermediates study of two sturgeon hemoglobins by n-dodecyl trimethylammonium bromide. <i>International Journal of Biological Macromolecules</i> , 2013 , 53, 107-13	7.9	4
27	An integrative Bayesian network approach to highlight key drivers in systemic lupus erythematosus. <i>Arthritis Research and Therapy</i> , 2020 , 22, 156	5.7	3
26	Beyond Taxonomic Analysis of Microbiomes: A Functional Approach for Revisiting Microbiome Changes in Colorectal Cancer. <i>Frontiers in Microbiology</i> , 2019 , 10, 3117	5.7	3
25	CpACpP: Cell-Penetrating Anticancer Peptide Prediction Using a Novel Bioinformatics Framework. <i>ACS Omega</i> , 2021 , 6, 19846-19859	3.9	3
24	Application of a time delay neural network for predicting positive and negative links in social networks. <i>Turkish Journal of Electrical Engineering and Computer Sciences</i> , 2016 , 24, 2825-2837	0.9	3
23	Synergistic Effect of Metagenome-Derived Starch-Degrading Enzymes on Quality of Functional Bread with Antioxidant Activity. <i>Starch/Staerke</i> , 2100098	2.3	3
22	Biogeography, distribution and conservation status of maples (Acer L.) in Iran. <i>Trees - Structure and Function</i> , 2017 , 31, 1583-1598	2.6	2
21	Micromorphological studies of leaf epidermal features in populations of maples (Acer L.) from Iran. <i>Phytotaxa</i> , 2017 , 299, 36	0.7	2
20	A computational learning paradigm to targeted discovery of biocatalysts from metagenomic data: a case study of lipase identification.. <i>Biotechnology and Bioengineering</i> , 2022 ,	4.9	2
19	Unraveling the molecular heterogeneity in type 2 diabetes: a potential subtype discovery followed by metabolic modeling. <i>BMC Medical Genomics</i> , 2020 , 13, 119	3.7	2
18	Distinct microbial community along the chronic oil pollution continuum of the Persian Gulf converge with oil spill accidents. <i>Scientific Reports</i> , 2021 , 11, 11316	4.9	2
17	CAMAMED: a pipeline for composition-aware mapping-based analysis of metagenomic data. <i>NAR Genomics and Bioinformatics</i> , 2021 , 3, lqaa107	3.7	2
16	Application of free and immobilized novel bifunctional biocatalyst in biotransformation of recalcitrant lignocellulosic biomass. <i>Chemosphere</i> , 2021 , 285, 131412	8.4	2
15	The novel homologue of the human β glucosidase inhibited by the non-germinated and germinated quinoa protein hydrolysates after in vitro gastrointestinal digestion.. <i>Journal of Food Biochemistry</i> , 2021 , e14030	3.3	2
14	Time-frequency approach in the cluster assignment of amino acids based on their NMR profiles. <i>Journal of the Iranian Chemical Society</i> , 2017 , 14, 2221-2228	2	1
13	Simultaneous hydrolysis of various protein-rich industrial wastes by a naturally evolved protease from tannery wastewater microbiota.. <i>Science of the Total Environment</i> , 2022 , 815, 152796	10.2	1

12	The species and heme pocket properties of sturgeon hemoglobins upon interaction with N-dodecyl trimethylammonium bromide. <i>Protein and Peptide Letters</i> , 2014 , 21, 171-8	1.9	1
11	The Role of MicroRNAs in Defense against Viral Phytopathogens. <i>Current Bioinformatics</i> , 2019 , 14,	4.7	1
10	BNrich: A Bayesian network approach to the pathway enrichment analysis		1
9	A generalized machine-learning aided method for targeted identification of industrial enzymes from metagenome: a xylanase temperature dependence case study		1
8	Agonist/antagonist compounds mechanism of action on estrogen receptor-positive breast cancer: A system-level investigation assisted by meta-analysis. <i>Informatics in Medicine Unlocked</i> , 2022 , 31, 100985-3	5.3	1
7	In vitro bioprocessing of corn as poultry feed additive by the influence of carbohydrate hydrolyzing metagenome derived enzyme cocktail.. <i>Scientific Reports</i> , 2022 , 12, 405	4.9	0
6	RNA Sequencing of CD4 T Cells in Relapsing-Remitting Multiple Sclerosis Patients at Relapse: Deciphering the Involvement of Novel genes and Pathways. <i>Journal of Molecular Neuroscience</i> , 2021 , 71, 2628-2645	3.3	0
5	A Pathway Analysis Approach Using Petri Net. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2021 , 25, 874-880	7.2	0
4	Highly Efficient Computationally Derived Novel Metagenome α -Amylase With Robust Stability Under Extreme Denaturing Conditions. <i>Frontiers in Microbiology</i> , 2021 , 12, 713125	5.7	0
3	Automated Plant Species Identification Using Leaf Shape-Based Classification Techniques: A Case Study on Iranian Maples. <i>Iranian Journal of Science and Technology - Transactions of Electrical Engineering</i> , 2021 , 45, 1051-1061	1.9	0
2	Enzymatically triggered delignification through a novel stable laccase: A mixed in-silico /in-vitro exploration of a complex environmental microbiota.. <i>International Journal of Biological Macromolecules</i> , 2022 , 211, 328-341	7.9	0
1	From indication to decision: A hierarchical approach to model the chemotactic behavior of Escherichia coli. <i>Journal of Theoretical Biology</i> , 2020 , 495, 110253	2.3	