

Mohd Shahir Shamsir

List of Publications by Year in Descending Order

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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.

95
papers

670
citations

14
h-index

21
g-index

115
ext. papers

835
ext. citations

2.7
avg, IF

4.21
L-index

#	Paper	IF	Citations
95	The complete mitochondrial genome data of the Common Rose butterfly, (Lepidoptera, Papilionoidea, Papilionidae) from Malaysia.. <i>Data in Brief</i> , 2022 , 40, 107740	1.2	3
94	Thermophiles and carbohydrate-active enzymes (CAZymes) in biofilm microbial consortia that decompose lignocellulosic plant litters at high temperatures.. <i>Scientific Reports</i> , 2022 , 12, 2850	4.9	0
93	Mitochondrial Barcodes of Three Malaysian Butterflies Originating from Taman Negara Endau Rompin Johor, Malaysia. <i>IOP Conference Series: Earth and Environmental Science</i> , 2021 , 736, 012053	0.3	
92	Temporal changes of bat diversity in the urban habitat island of Batu Caves, Malaysia. <i>IOP Conference Series: Earth and Environmental Science</i> , 2021 , 736, 012051	0.3	1
91	Mitochondrial Barcodes of Dragonflies and Damselflies Originated from Taman Negara Endau Rompin, Johor, Malaysia. <i>IOP Conference Series: Earth and Environmental Science</i> , 2021 , 736, 012032	0.3	
90	Genome sequence of an uncharted halophilic bacterium <i>Robertkochia marina</i> with deciphering its phosphate-solubilizing ability. <i>Brazilian Journal of Microbiology</i> , 2021 , 52, 251-256	2.2	2
89	Psychrophilic enzymes: structural adaptation, pharmaceutical and industrial applications. <i>Applied Microbiology and Biotechnology</i> , 2021 , 105, 899-907	5.7	9
88	The first mitochondrial genome data of an old world fruit bat, from Malaysia. <i>Mitochondrial DNA Part B: Resources</i> , 2021 , 6, 53-55	0.5	0
87	Development of a Haddon Matrix Framework for Higher Education Pandemic Preparedness: Scoping Review and Experiences of Malaysian Universities During the COVID-19 Pandemic. <i>Higher Education Policy</i> , 2021 , 1-40	1.5	2
86	Characterization of the mitogenomes of long-tailed giant rat, and a comparative analysis with other species. <i>Mitochondrial DNA Part B: Resources</i> , 2021 , 6, 502-504	0.5	1
85	In silico analysis prediction of HepTH1-5 as a potential therapeutic agent by targeting tumour suppressor protein networks.. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021 , 1-27	3.6	
84	Structural and functional characterisation of HepTH1-5 peptide as a potential hepcidin replacement. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021 , 1-24	3.6	1
83	Genome sequence data of sp. strain CR14 isolated from mangrove forest at Tanjung Piai National Park, Malaysia. <i>Data in Brief</i> , 2020 , 30, 105658	1.2	3
82	The first complete mitochondrial genome data of originating from Malaysia. <i>Data in Brief</i> , 2020 , 31, 105721	1.2	7
81	Draft genome sequence of <i>Parvularcula flava</i> strain NH6-79, revealing its role as a cellulolytic enzymes producer. <i>Archives of Microbiology</i> , 2020 , 202, 2591-2597	3	1
80	Characterisation of a catalytic triad and reaction selectivity in the dual mechanism of the catalyse hydride transfer in xylitol phosphate dehydrogenase. <i>Journal of Molecular Graphics and Modelling</i> , 2020 , 97, 107548	2.8	2
79	The first complete mitochondrial genome data of <i>Geoffroya roussette</i> , originating from Malaysia. <i>Mitochondrial DNA Part B: Resources</i> , 2020 , 5, 3262-3264	0.5	0

78	Molecular identification and phylogenetic analysis of a complete mitogenome from Peninsular Malaysia. <i>Mitochondrial DNA Part B: Resources</i> , 2020 , 5, 3004-3006	0.5	2
77	Characterizing a Halo-Tolerant GH10 Xylanase from Strain RA and Its CBM-Truncated Variant. <i>International Journal of Molecular Sciences</i> , 2019 , 20,	6.3	17
76	Heterologous expression, purification and biochemical characterization of a new endo-1,4-Xylanase from Rhodothermaceae bacterium RA. <i>Protein Expression and Purification</i> , 2019 , 164, 105464	2	9
75	Theoretical analyses on enantiospecificity of L-2-haloacid dehalogenase (DehL) from Rhizobium sp. RC1 towards 2-chloropropionic acid. <i>Journal of Molecular Graphics and Modelling</i> , 2019 , 92, 131-139	2.8	4
74	Model-guided Metabolic Gene Knockout of pflA in Escherichia coli Increases Succinic Acid Production from Glycerol Carbon Source. <i>Current Metabolomics</i> , 2019 , 6, 201-206	1	1
73	Evaluation of potential molecular interaction between quorum sensing receptor, LuxP and grouper fatty acids: in-silico screening and simulation. <i>PeerJ</i> , 2019 , 7, e6568	3.1	4
72	Molecular Modeling and Simulation of Transketolase from Orthosiphon stamineus. <i>Current Computer-Aided Drug Design</i> , 2019 , 15, 308-317	1.4	
71	Computer aided analysis of disease linked protein networks. <i>Bioinformatics</i> , 2019 , 15, 513-522	1.1	0
70	The two mutations of actin-myosin interface and their effect on the dynamics, structures, and functions of skeletal muscle actin. <i>Journal of Biomolecular Structure and Dynamics</i> , 2019 , 37, 372-382	3.6	1
69	Purification and characterization of a novel GH1 beta-glucosidase from Jeotgalibacillus malaysiensis. <i>International Journal of Biological Macromolecules</i> , 2018 , 115, 1094-1102	7.9	26
68	Assessing product adulteration of Eurycoma longifolia (Tongkat Ali) herbal medicinal product using DNA barcoding and HPLC analysis. <i>Pharmaceutical Biology</i> , 2018 , 56, 368-377	3.8	12
67	Temperature adaptation analysis of a psychrophilic mannanase through structural, functional and molecular dynamics simulation. <i>Molecular Simulation</i> , 2018 , 44, 1270-1277	2	1
66	Molecular dynamics simulations suggest changes in electrostatic interactions as a potential mechanism through which serine phosphorylation inhibits DNA polymerase β activity. <i>Journal of Molecular Graphics and Modelling</i> , 2018 , 84, 236-241	2.8	1
65	Comparison of Different DNA Extraction Methods from Leaves and Roots of Eurycoma longifolia Plant. <i>Advanced Science Letters</i> , 2018 , 24, 3641-3645	0.1	3
64	Molecular dynamics simulations suggest changes in electrostatic interactions as a potential mechanism through which serine phosphorylation inhibits DNA Polymerase β activity. <i>Journal of Molecular Graphics and Modelling</i> , 2018 , 79, 192	2.8	1
63	Complete genome sequence of bacterium RA with cellulolytic and xylanolytic activities. <i>3 Biotech</i> , 2018 , 8, 376	2.8	6
62	The role of alternative salt bridges in cold adaptation of a novel psychrophilic laminarinase. <i>Journal of Biomolecular Structure and Dynamics</i> , 2017 , 35, 1685-1692	3.6	10
61	Assessing Bat Roosts Using the LiDAR System at Wind Cave Nature Reserve in Sarawak, Malaysian Borneo. <i>Acta Chiropterologica</i> , 2017 , 19, 199	1	8

60	Deficiency in Sperm-Egg Protein Interaction as a Major Cause of Fertilization Failure. <i>Journal of Membrane Biology</i> , 2017 , 250, 133-144	2.3	2
59	Review: DNA Barcoding and Chromatography Fingerprints for the Authentication of Botanicals in Herbal Medicinal Products. <i>Evidence-based Complementary and Alternative Medicine</i> , 2017 , 2017, 1352948-3	3.3	19
58	An expanded mammal mitogenome dataset from Southeast Asia. <i>GigaScience</i> , 2017 , 6, 1-8	7.6	20
57	Deciphering the catalytic amino acid residues of L-2-haloacid dehalogenase (DehL) from <i>Rhizobium</i> sp. RC1: An in silico analysis. <i>Computational Biology and Chemistry</i> , 2017 , 70, 125-132	3.6	8
56	Multi-template homology-based structural model of L-2-haloacid dehalogenase (DehL) from <i>Rhizobium</i> sp. RC1. <i>Journal of Biomolecular Structure and Dynamics</i> , 2017 , 35, 3285-3296	3.6	12
55	Structural, functional and molecular dynamics analysis of the native and mutated actin to study its effect on congenital myopathy. <i>Journal of Biomolecular Structure and Dynamics</i> , 2017 , 35, 1608-1614	3.6	5
54	Global transcriptomic response of <i>Anoxybacillus</i> sp. SK 3-4 to aluminum exposure. <i>Journal of Basic Microbiology</i> , 2017 , 57, 151-161	2.7	5
53	Effects of Physiochemical Factors on Prokaryotic Biodiversity in Malaysian Circumneutral Hot Springs. <i>Frontiers in Microbiology</i> , 2017 , 8, 1252	5.7	34
52	Characterization of a glucose-tolerant α -glucosidase from <i>Anoxybacillus</i> sp. DT3-1. <i>Biotechnology for Biofuels</i> , 2016 , 9, 174	7.8	33
51	Model-guided metabolic gene knockout of <i>gnd</i> for enhanced succinate production in <i>Escherichia coli</i> from glucose and glycerol substrates. <i>Computational Biology and Chemistry</i> , 2016 , 61, 130-7	3.6	11
50	Model-assisted formate dehydrogenase-O (<i>fdoH</i>) gene knockout for enhanced succinate production in <i>Escherichia coli</i> from glucose and glycerol carbon sources. <i>Journal of Biomolecular Structure and Dynamics</i> , 2016 , 34, 2305-16	3.6	8
49	Model-aided <i>atpE</i> gene knockout strategy in <i>Escherichia coli</i> for enhanced succinic acid production from glycerol. <i>Journal of Biomolecular Structure and Dynamics</i> , 2016 , 34, 1705-16	3.6	12
48	Genome Analysis of a New Rhodothermaceae Strain Isolated from a Hot Spring. <i>Frontiers in Microbiology</i> , 2016 , 7, 1109	5.7	11
47	Systematic Analysis of Protein Interaction Network Associated with Azoospermia. <i>International Journal of Molecular Sciences</i> , 2016 , 17,	6.3	10
46	Crystal structure of <i>Anoxybacillus</i> α -amylase provides insights into maltose binding of a new glycosyl hydrolase subclass. <i>Scientific Reports</i> , 2016 , 6, 23126	4.9	27
45	Structural prediction of a novel laminarinase from the psychrophilic <i>Glaciozyma antarctica</i> PI12 and its temperature adaptation analysis. <i>Journal of Molecular Modeling</i> , 2015 , 21, 63	2	11
44	In silico deletion of <i>PtsG</i> gene in <i>Escherichia coli</i> genome-scale model predicts increased succinate production from glycerol. <i>Journal of Biomolecular Structure and Dynamics</i> , 2015 , 33, 2380-9	3.6	10
43	Prediction of recombinant protein overexpression in <i>Escherichia coli</i> using a machine learning based model (RPOLP). <i>Computers in Biology and Medicine</i> , 2015 , 66, 330-6	7	1

42	Identification of putative drug targets for human sperm-egg interaction defect using protein network approach. <i>BMC Systems Biology</i> , 2015 , 9, 37	3.5	4
41	Characterization of aluminum resistant <i>Anoxybacillus</i> sp. SK 3-4 isolated from a hot spring. <i>Journal of Basic Microbiology</i> , 2015 , 55, 514-9	2.7	5
40	Molecular Dynamics Simulations of the Temperature Induced Unfolding of Crambin Follow the Arrhenius Equation. <i>F1000Research</i> , 2015 , 4, 589	3.6	3
39	An S188V mutation alters substrate specificity of non-stereospecific haloalkanoic acid dehalogenase E (DehE). <i>PLoS ONE</i> , 2015 , 10, e0121687	3.7	11
38	An overview of pathway prediction tools for synthetic design of microbial chemical factories. <i>AIMS Bioengineering</i> , 2015 , 2, 1-14	3.4	4
37	Model-driven in Silico glpC Gene Knockout Predicts Increased Succinate Production from Glycerol in <i>Escherichia Coli</i> . <i>AIMS Bioengineering</i> , 2015 , 2, 40-48	3.4	4
36	Spatial occurrence of dengue fever and its relationship with land use in Selangor, Malaysia. <i>BMC Public Health</i> , 2014 , 14,	4.1	2
35	Weighted voting-based consensus clustering for chemical structure databases. <i>Journal of Computer-Aided Molecular Design</i> , 2014 , 28, 675-84	4.2	3
34	Structural and functional analysis of a novel psychrophilic Mannanase from <i>Glaciozyma antarctica</i> PI12. <i>Journal of Computer-Aided Molecular Design</i> , 2014 , 28, 685-98	4.2	24
33	An improved differential evolution algorithm for enhancing biochemical pathways simulation and production. <i>International Journal of Data Mining and Bioinformatics</i> , 2014 , 10, 424-39	0.5	
32	Development of a mobile application for amphibian species recognition. <i>IOP Conference Series: Earth and Environmental Science</i> , 2014 , 18, 012091	0.3	
31	Interactions of non-natural halogenated substrates with D-specific dehalogenase (DehD) mutants using studies. <i>Biotechnology and Biotechnological Equipment</i> , 2014 , 28, 949-957	1.6	3
30	Insights into the stereospecificity of the d-specific dehalogenase from sp. RC1 toward d- and l-2-chloropropionate. <i>Biotechnology and Biotechnological Equipment</i> , 2014 , 28, 608-615	1.6	9
29	Parameter Estimation by Using an Improved Bee Memory Differential Evolution Algorithm (IBMDE) to Simulate Biochemical Pathways. <i>Current Bioinformatics</i> , 2014 , 9, 65-75	4.7	3
28	USING AN IMPROVED BEE MEMORY DIFFERENTIAL EVOLUTION ALGORITHM FOR PARAMETER ESTIMATION TO SIMULATE BIOCHEMICAL PATHWAYS. <i>Journal of Biological Systems</i> , 2014 , 22, 101-121	1.6	1
27	Functional features and protein network of human sperm-egg interaction. <i>Systems Biology in Reproductive Medicine</i> , 2014 , 60, 329-37	2.9	12
26	MHealth application: Mobile thalassemia patient management application 2014 ,		2
25	A Review on Modelling Methods, Pathway Simulation Software and Recent Development on Differential Evolution Algorithms for Metabolic Pathways in Systems Biology. <i>Current Bioinformatics</i> , 2014 , 9, 509-521	4.7	5

24	Sequence and structural investigation of a novel psychrophilic α -amylase from <i>Glaciozyma antarctica</i> PI12 for cold-adaptation analysis. <i>Journal of Molecular Modeling</i> , 2013 , 19, 3369-83	2	26
23	Molecular Modelling and Functional Studies of the Non-Stereospecific α -Haloalkanoic Acid Dehalogenase (DehE) from <i>Rhizobium</i> SP. RC1 and its Association with 3-Chloropropionic Acid (α -Chlorinated Aliphatic Acid). <i>Biotechnology and Biotechnological Equipment</i> , 2013 , 27, 3725-3736	1.6	17
22	Improving Molecular Dynamics Simulation Performance on Low-Cost Systems. <i>Computing in Science and Engineering</i> , 2013 , 15, 64-70	1.5	
21	Development and Deployment of an Ethnobotanical and Phytochemical Knowledge Database of Malaysia. <i>Jurnal Teknologi (Sciences and Engineering)</i> , 2013 , 64,	1.2	1
20	Comparison of Computational Tools for Protein-Protein Interaction (PPI) Mapping and Analysis. <i>Jurnal Teknologi (Sciences and Engineering)</i> , 2013 , 63,	1.2	1
19	Estimating Kinetic Parameters for Essential Amino Acid Production in <i>Arabidopsis Thaliana</i> by Using Particle Swarm Optimization. <i>Jurnal Teknologi (Sciences and Engineering)</i> , 2013 , 64,	1.2	2
18	Construction and Analysis of the Cell Surface α Protein Network for Human Sperm-Egg Interaction. <i>ISRN Bioinformatics</i> , 2013 , 2013, 962760		6
17	Threonine Biosynthesis Pathway Simulation Using IBMDE with Parameter Estimation. <i>Lecture Notes in Computer Science</i> , 2013 , 191-200	0.9	
16	Using Particle Swarm Optimization for Estimating Kinetics Parameters on Essential Amino Acid Production of <i>Arabidopsis Thaliana</i> . <i>Studies in Computational Intelligence</i> , 2013 , 51-61	0.8	
15	Using Ant Colony Optimization (ACO) on Kinetic Modeling of the Acetoin Production in <i>Lactococcus Lactis</i> C7. <i>Studies in Computational Intelligence</i> , 2013 , 25-35	0.8	3
14	Structural prediction of a novel chitinase from the psychrophilic <i>Glaciozyma antarctica</i> PI12 and an analysis of its structural properties and function. <i>Journal of Computer-Aided Molecular Design</i> , 2012 , 26, 947-61	4.2	36
13	CMD: A Database to Store the Bonding States of Cysteine Motifs with Secondary Structures. <i>Advances in Bioinformatics</i> , 2012 , 2012, 849830	5.5	2
12	Structure prediction, molecular dynamics simulation and docking studies of D-specific dehalogenase from <i>Rhizobium</i> sp. RC1. <i>International Journal of Molecular Sciences</i> , 2012 , 13, 15724-54	6.3	8
11	Counting in the dark: non-intrusive laser scanning for population counting and identifying roosting bats. <i>Scientific Reports</i> , 2012 , 2, 524	4.9	18
10	Improved Differential Evolution Algorithm for Parameter Estimation to Improve the Production of Biochemical Pathway. <i>International Journal of Interactive Multimedia and Artificial Intelligence</i> , 2012 , 1, 22	3.8	6
9	Using an Improved Differential Evolution Algorithm for Parameter Estimation to Simulate Glycolysis Pathway. <i>Advances in Intelligent and Soft Computing</i> , 2012 , 709-716		1
8	birgHPC: creating instant computing clusters for bioinformatics and molecular dynamics. <i>Bioinformatics</i> , 2011 , 27, 1320-1	7.2	
7	A protein short motif search tool using amino acid sequence and their secondary structure assignment. <i>Bioinformation</i> , 2011 , 7, 304-6	1.1	2

6	Grid Jobs Scheduling Improvement Using Priority Rules and Backfilling. <i>Communications in Computer and Information Science</i> , 2011 , 401-415	0.3	0
5	GridMACS Portal: A Grid Web Portal for Molecular Dynamics Simulation Using GROMACS 2010 ,		5
4	Bioinformatics in Malaysia: hope, initiative, effort, reality, and challenges. <i>PLoS Computational Biology</i> , 2009 , 5, e1000457	5	8
3	Colour Number Coding Scheme for Human Blood Cell. <i>IFMBE Proceedings</i> , 2008 , 532-535	0.2	
2	Beta-sheet containment by flanking prolines: molecular dynamic simulations of the inhibition of beta-sheet elongation by proline residues in human prion protein. <i>Biophysical Journal</i> , 2007 , 92, 2080-9	2.9	16
1	One gene, two diseases and three conformations: molecular dynamics simulations of mutants of human prion protein at room temperature and elevated temperatures. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 59, 275-90	4.2	37