Mohd Shahir Shamsir

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.

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	One gene, two diseases and three conformations: molecular dynamics simulations of mutants of human prion protein at room temperature and elevated temperatures. *Proteins: Structure, Function and Bioinformatics*, **2005**, 59, 275-90	4.2	37
94	Structural prediction of a novel chitinase from the psychrophilic Glaciozyma antarctica PI12 and an analysis of its structural properties and function. *Journal of Computer-Aided Molecular Design*, **2012**, 26, 947-61	4.2	36
93	Effects of Physiochemical Factors on Prokaryotic Biodiversity in Malaysian Circumneutral Hot Springs. *Frontiers in Microbiology*, **2017**, 8, 1252	5.7	34
92	Characterization of a glucose-tolerant glucosidase from Anoxybacillus sp. DT3-1. *Biotechnology for Biofuels*, **2016**, 9, 174	7.8	33
91	Crystal structure of Anoxybacillus amylase provides insights into maltose binding of a new glycosyl hydrolase subclass. *Scientific Reports*, **2016**, 6, 23126	4.9	27
90	Purification and characterization of a novel GH1 beta-glucosidase from Jeotgalibacillus malaysiensis. *International Journal of Biological Macromolecules*, **2018**, 115, 1094-1102	7.9	26
89	Sequence and structural investigation of a novel psychrophilic amylase from Glaciozyma antarctica PI12 for cold-adaptation analysis. *Journal of Molecular Modeling*, **2013**, 19, 3369-83	2	26
88	Structural and functional analysis of a novel psychrophilic mannanase from Glaciozyma antarctica PI12. *Journal of Computer-Aided Molecular Design*, **2014**, 28, 685-98	4.2	24
87	An expanded mammal mitogenome dataset from Southeast Asia. *GigaScience*, **2017**, 6, 1-8	7.6	20
86	Review: DNA Barcoding and Chromatography Fingerprints for the Authentication of Botanicals in Herbal Medicinal Products. *Evidence-based Complementary and Alternative Medicine*, **2017**, 2017, 1352948	3.3	19
85	Counting in the dark: non-intrusive laser scanning for population counting and identifying roosting bats. *Scientific Reports*, **2012**, 2, 524	4.9	18
84	Characterizing a Halo-Tolerant GH10 Xylanase from Strain RA and Its CBM-Truncated Variant. *International Journal of Molecular Sciences*, **2019**, 20,	6.3	17
83	Molecular Modelling and Functional Studies of the Non-Stereospecific Haloalkanoic Acid Dehalogenase (DehE) from Rhizobium SP. RC1 and its Association with 3-Chloropropionic Acid (Chlorinated Aliphatic Acid). *Biotechnology and Biotechnological Equipment*, **2013**, 27, 3725-3736	1.6	17
82	Beta-sheet containment by flanking prolines: molecular dynamic simulations of the inhibition of beta-sheet elongation by proline residues in human prion protein. *Biophysical Journal*, **2007**, 92, 2080-9	2.9	16
81	Model-aided atpE gene knockout strategy in Escherichia coli for enhanced succinic acid production from glycerol. *Journal of Biomolecular Structure and Dynamics*, **2016**, 34, 1705-16	3.6	12
80	Assessing product adulteration of Eurycoma longifolia (Tongkat Ali) herbal medicinal product using DNA barcoding and HPLC analysis. *Pharmaceutical Biology*, **2018**, 56, 368-377	3.8	12
79	Multi-template homology-based structural model of L-2-haloacid dehalogenase (DehL) from Rhizobium sp. RC1. *Journal of Biomolecular Structure and Dynamics*, **2017**, 35, 3285-3296	3.6	12

78	Functional features and protein network of human sperm-egg interaction. *Systems Biology in Reproductive Medicine*, **2014**, 60, 329-37	2.9	12
77	Structural prediction of a novel laminarinase from the psychrophilic Glaciozyma antarctica PI12 and its temperature adaptation analysis. *Journal of Molecular Modeling*, **2015**, 21, 63	2	11
76	Model-guided metabolic gene knockout of gnd for enhanced succinate production in Escherichia coli from glucose and glycerol substrates. *Computational Biology and Chemistry*, **2016**, 61, 130-7	3.6	11
75	An S188V mutation alters substrate specificity of non-stereospecific □haloalkanoic acid dehalogenase E (DehE). *PLoS ONE*, **2015**, 10, e0121687	3.7	11
74	Genome Analysis of a New Rhodothermaceae Strain Isolated from a Hot Spring. *Frontiers in Microbiology*, **2016**, 7, 1109	5.7	11
73	The role of alternative salt bridges in cold adaptation of a novel psychrophilic laminarinase. *Journal of Biomolecular Structure and Dynamics*, **2017**, 35, 1685-1692	3.6	10
72	In silico deletion of PtsG gene in Escherichia coli genome-scale model predicts increased succinate production from glycerol. *Journal of Biomolecular Structure and Dynamics*, **2015**, 33, 2380-9	3.6	10
71	Systematic Analysis of Protein Interaction Network Associated with Azoospermia. *International Journal of Molecular Sciences*, **2016**, 17,	6.3	10
70	Heterologous expression, purification and biochemical characterization of a new endo-1,4-□xylanase from Rhodothermaceae bacterium RA. *Protein Expression and Purification*, **2019**, 164, 105464	2	9
69	Insights into the stereospecificity of the d-specific dehalogenase from sp. RC1 toward d- and l-2-chloropropionate. *Biotechnology and Biotechnological Equipment*, **2014**, 28, 608-615	1.6	9
68	Psychrophilic enzymes: structural adaptation, pharmaceutical and industrial applications. *Applied Microbiology and Biotechnology*, **2021**, 105, 899-907	5.7	9
67	Assessing Bat Roosts Using the LiDAR System at Wind Cave Nature Reserve in Sarawak, Malaysian Borneo. *Acta Chiropterologica*, **2017**, 19, 199	1	8
66	Model-assisted formate dehydrogenase-O (fdoH) gene knockout for enhanced succinate production in Escherichia coli from glucose and glycerol carbon sources. *Journal of Biomolecular Structure and Dynamics*, **2016**, 34, 2305-16	3.6	8
65	Deciphering the catalytic amino acid residues of l-2-haloacid dehalogenase (DehL) from Rhizobium sp. RC1: An in silico analysis. *Computational Biology and Chemistry*, **2017**, 70, 125-132	3.6	8
64	Bioinformatics in Malaysia: hope, initiative, effort, reality, and challenges. *PLoS Computational Biology*, **2009**, 5, e1000457	5	8
63	Structure prediction, molecular dynamics simulation and docking studies of D-specific dehalogenase from Rhizobium sp. RC1. *International Journal of Molecular Sciences*, **2012**, 13, 15724-54	6.3	8
62	The first complete mitochondrial genome data of originating from Malaysia. *Data in Brief*, **2020**, 31, 105721	1.2	7
61	Construction and Analysis of the Cell Surface's Protein Network for Human Sperm-Egg Interaction. *ISRN Bioinformatics*, **2013**, 2013, 962760		6

60	Improved Differential Evolution Algorithm for Parameter Estimation to Improve the Production of Biochemical Pathway. *International Journal of Interactive Multimedia and Artificial Intelligence*, **2012**, 1, 22	3.8	6
59	Complete genome sequence of bacterium RA with cellulolytic and xylanolytic activities. *3 Biotech*, **2018**, 8, 376	2.8	6
58	Structural, functional and molecular dynamics analysis of the native and mutated actin to study its effect on congenital myopathy. *Journal of Biomolecular Structure and Dynamics*, **2017**, 35, 1608-1614	3.6	5
57	Global transcriptomic response of Anoxybacillus sp. SK 3-4 to aluminum exposure. *Journal of Basic Microbiology*, **2017**, 57, 151-161	2.7	5
56	Characterization of aluminum resistant Anoxybacillus sp. SK 3-4 isolated from a hot spring. *Journal of Basic Microbiology*, **2015**, 55, 514-9	2.7	5
55	GridMACS Portal: A Grid Web Portal for Molecular Dynamics Simulation Using GROMACS **2010**,		5
54	A Review on Modelling Methods, Pathway Simulation Software and Recent Development on Differential Evolution Algorithms for Metabolic Pathways in Systems Biology. *Current Bioinformatics*, **2014**, 9, 509-521	4.7	5
53	Identification of putative drug targets for human sperm-egg interaction defect using protein network approach. *BMC Systems Biology*, **2015**, 9, 37	3.5	4
52	Theoretical analyses on enantiospecificity of L-2-haloacid dehalogenase (DehL) from Rhizobium sp. RC1 towards 2-chloropropionic acid. *Journal of Molecular Graphics and Modelling*, **2019**, 92, 131-139	2.8	4
51	An overview of pathway prediction tools for synthetic design of microbial chemical factories. *AIMS Bioengineering*, **2015**, 2, 1-14	3.4	4
50	Model-driven in Silico glpC Gene Knockout Predicts Increased Succinate Production from Glycerol in Escherichia Coli. *AIMS Bioengineering*, **2015**, 2, 40-48	3.4	4
49	Evaluation of potential molecular interaction between quorum sensing receptor, LuxP and grouper fatty acids: in-silico screening and simulation. *PeerJ*, **2019**, 7, e6568	3.1	4
48	Genome sequence data of sp. strain CR14 isolated from mangrove forest at Tanjung Piai National Park, Malaysia. *Data in Brief*, **2020**, 30, 105658	1.2	3
47	Weighted voting-based consensus clustering for chemical structure databases. *Journal of Computer-Aided Molecular Design*, **2014**, 28, 675-84	4.2	3
46	Interactions of non-natural halogenated substrates with D-specific dehalogenase (DehD) mutants using studies. *Biotechnology and Biotechnological Equipment*, **2014**, 28, 949-957	1.6	3
45	Parameter Estimation by Using an Improved Bee Memory Differential Evolution Algorithm (IBMDE) to Simulate Biochemical Pathways. *Current Bioinformatics*, **2014**, 9, 65-75	4.7	3
44	Comparison of Different DNA Extraction Methods from Leaves and Roots of Eurycoma longifolia Plant. *Advanced Science Letters*, **2018**, 24, 3641-3645	0.1	3
43	Molecular Dynamics Simulations of the Temperature Induced Unfolding of Crambin Follow the Arrhenius Equation. *F1000Research*, **2015**, 4, 589	3.6	3

42	The complete mitochondrial genome data of the Common Rose butterfly, (Lepidoptera, Papilionoidea, Papilionidae) from Malaysia.. *Data in Brief*, **2022**, 40, 107740	1.2	3
41	Using Ant Colony Optimization (ACO) on Kinetic Modeling of the Acetoin Production in Lactococcus Lactis C7. *Studies in Computational Intelligence*, **2013**, 25-35	0.8	3
40	Deficiency in Sperm-Egg Protein Interaction as a Major Cause of Fertilization Failure. *Journal of Membrane Biology*, **2017**, 250, 133-144	2.3	2
39	Characterisation of a catalytic triad and reaction selectivity in the dual mechanism of the catalyse hydride transfer in xylitol phosphate dehydrogenase. *Journal of Molecular Graphics and Modelling*, **2020**, 97, 107548	2.8	2
38	Spatial occurrence of dengue fever and its relationship with land use in Selangor, Malaysia. *BMC Public Health*, **2014**, 14,	4.1	2
37	MHealth application: Mobile thalassemia patient management application **2014**,		2
36	CMD: A Database to Store the Bonding States of Cysteine Motifs with Secondary Structures. *Advances in Bioinformatics*, **2012**, 2012, 849830	5.5	2
35	Estimating Kinetic Parameters for Essential Amino Acid Production in Arabidopsis Thaliana by Using Particle Swarm Optimization. *Jurnal Teknologi (Sciences and Engineering)*, **2013**, 64,	1.2	2
34	A protein short motif search tool using amino acid sequence and their secondary structure assignment. *Bioinformation*, **2011**, 7, 304-6	1.1	2
33	Molecular identification and phylogenetic analysis of a complete mitogenome from Peninsular Malaysia. *Mitochondrial DNA Part B: Resources*, **2020**, 5, 3004-3006	0.5	2
32	Genome sequence of an uncharted halophilic bacterium Robertkochia marina with deciphering its phosphate-solubilizing ability. *Brazilian Journal of Microbiology*, **2021**, 52, 251-256	2.2	2
31	Development of a Haddon Matrix Framework for Higher Education Pandemic Preparedness: Scoping Review and Experiences of Malaysian Universities During the COVID-19 Pandemic. *Higher Education Policy*, **2021**, 1-40	1.5	2
30	Prediction of recombinant protein overexpression in Escherichia coli using a machine learning based model (RPOLP). *Computers in Biology and Medicine*, **2015**, 66, 330-6	7	1
29	Draft genome sequence of Parvularcula flava strain NH6-79, revealing its role as a cellulolytic enzymes producer. *Archives of Microbiology*, **2020**, 202, 2591-2597	3	1
28	Temperature adaptation analysis of a psychrophilic mannanase through structural, functional and molecular dynamics simulation. *Molecular Simulation*, **2018**, 44, 1270-1277	2	1
27	Molecular dynamics simulations suggest changes in electrostatic interactions as a potential mechanism through which serine phosphorylation inhibits DNA polymerase □activity. *Journal of Molecular Graphics and Modelling*, **2018**, 84, 236-241	2.8	1
26	USING AN IMPROVED BEE MEMORY DIFFERENTIAL EVOLUTION ALGORITHM FOR PARAMETER ESTIMATION TO SIMULATE BIOCHEMICAL PATHWAYS. *Journal of Biological Systems*, **2014**, 22, 101-121	1.6	1
25	Development and Deployment of an Ethnobotanical and Phytochemical Knowledge Database of Malaysia. *Jurnal Teknologi (Sciences and Engineering)*, **2013**, 64,	1.2	1

24	Comparison of Computational Tools for Protein-Protein Interaction (PPI) Mapping and Analysis. *Jurnal Teknologi (Sciences and Engineering)*, **2013**, 63,	1.2	1
23	Model-guided Metabolic Gene Knockout of pflA in Escherichia coli Increases Succinic Acid Production from Glycerol Carbon Source. *Current Metabolomics*, **2019**, 6, 201-206	1	1
22	Using an Improved Differential Evolution Algorithm for Parameter Estimation to Simulate Glycolysis Pathway. *Advances in Intelligent and Soft Computing*, **2012**, 709-716		1
21	Temporal changes of bat diversity in the urban habitat island of Batu Caves, Malaysia. *IOP Conference Series: Earth and Environmental Science*, **2021**, 736, 012051	0.3	1
20	The two mutations of actin-myosin interface and their effect on the dynamics, structures, and functions of skeletal muscle actin. *Journal of Biomolecular Structure and Dynamics*, **2019**, 37, 372-382	3.6	1
19	Characterization of the mitogenomes of long-tailed giant rat, and a comparative analysis with other species. *Mitochondrial DNA Part B: Resources*, **2021**, 6, 502-504	0.5	1
18	Molecular dynamics simulations suggest changes in electrostatic interactions as a potential mechanism through which serine phosphorylation inhibits DNA Polymerase β activity. *Journal of Molecular Graphics and Modelling*, **2018**, 79, 192	2.8	1
17	Structural and functional characterisation of HepTH1-5 peptide as a potential hepcidin replacement. *Journal of Biomolecular Structure and Dynamics*, **2021**, 1-24	3.6	1
16	Computer aided analysis of disease linked protein networks. *Bioinformation*, **2019**, 15, 513-522	1.1	0
15	Grid Jobs Scheduling Improvement Using Priority Rules and Backfilling. *Communications in Computer and Information Science*, **2011**, 401-415	0.3	0
14	The first complete mitochondrial genome data of Geoffroy's rousette, originating from Malaysia. *Mitochondrial DNA Part B: Resources*, **2020**, 5, 3262-3264	0.5	0
13	The first mitochondrial genome data of an old world fruit bat, from Malaysia. *Mitochondrial DNA Part B: Resources*, **2021**, 6, 53-55	0.5	0
12	Thermophiles and carbohydrate-active enzymes (CAZymes) in biofilm microbial consortia that decompose lignocellulosic plant litters at high temperatures.. *Scientific Reports*, **2022**, 12, 2850	4.9	0
11	An improved differential evolution algorithm for enhancing biochemical pathways simulation and production. *International Journal of Data Mining and Bioinformatics*, **2014**, 10, 424-39	0.5	
10	Development of a mobile application for amphibian species recognition. *IOP Conference Series: Earth and Environmental Science*, **2014**, 18, 012091	0.3	
9	Improving Molecular Dynamics Simulation Performance on Low-Cost Systems. *Computing in Science and Engineering*, **2013**, 15, 64-70	1.5	
8	birgHPC: creating instant computing clusters for bioinformatics and molecular dynamics. *Bioinformatics*, **2011**, 27, 1320-1	7.2	
7	Colour Number Coding Scheme for Human Blood Cell. *IFMBE Proceedings*, **2008**, 532-535	0.2	

6	Molecular Modeling and Simulation of Transketolase from Orthosiphon stamineus. *Current Computer-Aided Drug Design*, **2019**, 15, 308-317	1.4
5	Threonine Biosynthesis Pathway Simulation Using IBMDE with Parameter Estimation. *Lecture Notes in Computer Science*, **2013**, 191-200	0.9
4	Using Particle Swarm Optimization for Estimating Kinetics Parameters on Essential Amino Acid Production of Arabidopsis Thaliana. *Studies in Computational Intelligence*, **2013**, 51-61	0.8
3	Mitochondrial Barcodes of Three Malaysian Butterflies Originating from Taman Negara Endau Rompin Johor, Malaysia. *IOP Conference Series: Earth and Environmental Science*, **2021**, 736, 012053	0.3
2	Mitochondrial Barcodes of Dragonflies and Damselflies Originated from Taman Negara Endau Rompin, Johor, Malaysia. *IOP Conference Series: Earth and Environmental Science*, **2021**, 736, 012032	0.3
1	In silico analysis prediction of HepTH1-5 as a potential therapeutic agent by targeting tumour suppressor protein networks.. *Journal of Biomolecular Structure and Dynamics*, **2021**, 1-27	3.6