Khairul Bariyyah Abd Halim

List of Publications by Year
in descending order

11 papers	215 citations	1163117 8 h-index	1281871 11 g-index
11 all docs	11 docs citations	11 times ranked	327 citing authors

#	Article	IF	Citations
1	Molecular docking and molecular dynamics simulations studies on Î²-glucosidase and xylanase Trichoderma asperellum to predict degradation order of cellulosic components in oil palm leaves for nanocellulose preparation. Journal of Biomolecular Structure and Dynamics, 2021, 39, 2628-2641.	3.5	24
2	Molecular docking and molecular dynamics simulations of a mutant Acinetobacter haemolyticus alkaline-stable lipase against tributyrin. Journal of Biomolecular Structure and Dynamics, 2021, 39, 2079-2091.	3.5	19
3	In silico mutation on a mutant lipase from Acinetobacter haemolyticus towards enhancing alkaline stability. Journal of Biomolecular Structure and Dynamics, 2020, 38, 4493-4507.	3.5	12
4	Substrate docking and molecular dynamic simulation for prediction of fungal enzymes from Trichoderma species-assisted extraction of nanocellulose from oil palm leaves. Journal of Biomolecular Structure and Dynamics, 2020, 38, 4246-4258.	3.5	7
5	The mechanistic role of active site residues in non-stereo haloacid dehalogenase E (DehE). Journal of Molecular Graphics and Modelling, 2019, 90, 219-225.	2.4	10
6	Interaction of monomeric Ebola VP40 protein with a plasma membrane: A coarse-grained molecular dynamics (CGMD) simulation study. Journal of Molecular Graphics and Modelling, 2018, 82, 137-144.	2.4	5
7	In silico study of carvone derivatives as potential neuraminidase inhibitors. Journal of Molecular Modeling, 2018, 24, 93.	1.8	9
8	Homology modeling and docking studies of a Î”9-fatty acid desaturase from a Cold-tolerantPseudomonassp. AMS8. PeerJ, 2018, 6, e4347.	2.0	11
9	Molecular Dynamic Simulation of Space and Earth-Grown Crystal Structures of Thermostable T1 Lipase Geobacillus zalihae Revealed a Better Structure. Molecules, 2017, 22, 1574.	3.8	25
10	Interactions of the EGFR juxtamembrane domain with PIP2-containing lipid bilayers: Insights from multiscale molecular dynamics simulations. Biochimica Et Biophysica Acta - General Subjects, 2015, 1850, 1017-1025.	2.4	66
11	Sidekick for Membrane Simulations: Automated Ensemble Molecular Dynamics Simulations of Transmembrane Helices. Journal of Chemical Theory and Computation, 2014, 10, 2165-2175.	5.3	27