Usman Sumo Friend Tambunan

List of Publications by Year
in descending order

67 papers	642 citations	566801 15 h-index	676716 22 g-index
67 all docs	67 docs citations	67 times ranked	752 citing authors

#	Article	IF	Citations
1	Identification of DNA Methyltransferase-1 Inhibitor for Breast Cancer Therapy through Computational Fragment-Based Drug Design. Molecules, 2021, 26, 375.	1.7	6
2	Recent Progress and Challenges for Drug-Resistant Tuberculosis Treatment. Pharmaceutics, 2021, 13, 592.	2.0	20
3	Zika, chikungunya, and dengue viral infections in human peripheral blood mononuclear cells: cell susceptibility and gene expression. Medical Journal of Indonesia, 2020, 29, 129-35.	0.2	0
4	Identification of natural product compounds as NS5 RDRP inhibitor for dengue virus serotype 1-4 through in silico analysis. AIP Conference Proceedings, 2020, , .	0.3	1
5	Flexible molecular docking simulation of peptide compounds as inhibitor of GluI host protein for dengue fever therapy. AIP Conference Proceedings, 2020, , .	0.3	2
6	Role of Immunoinformatics in Accelerating Epitope-Based Vaccine Development against Dengue Virus. The Open Biochemistry Journal, 2020, 14, 9-18.	0.3	2
7	Inhibition of Primed Ebola Virus Glycoprotein by Peptide Compound Conjugated to HIV-1 Tat Peptide Through a Virtual Screening Approach. Lecture Notes in Computer Science, 2020, , 153-165.	1.0	0
8	Pharmacophore Modelling, Virtual Screening, and Molecular Docking Simulations of Natural Product Compounds as Potential Inhibitors of Ebola Virus Nucleoprotein. Lecture Notes in Computer Science, 2020, , 166-178.	1.0	0
9	Pharmacophore-based virtual screening and molecular docking simulation of terpenoid compounds as the inhibitor of sonic hedgehog protein for colorectal cancer therapy. IOP Conference Series: Materials Science and Engineering, 2019, 509, 012075.	0.3	2
10	Strategies of Tuberculosisâ€“HIV Vaccines Design using Immunoinformatic Approach. OnLine Journal of Biological Sciences, 2019, 19, 110-116.	0.2	2
11	Fragment-Based Drug Design to Discover Novel Inhibitor of Dipeptidyl Peptidase-4 (DPP-4) as a Potential Drug for Type 2 Diabetes Therapy. Lecture Notes in Computer Science, 2019, , 14-24.	1.0	0
12	Discovery of Novel Alpha-Amylase Inhibitors for Type II Diabetes Mellitus Through the Fragment-Based Drug Design. Lecture Notes in Computer Science, 2019, , 25-35.	1.0	0
13	In silico identification of potent inhibitors of heat shock protein 90 (Hsp90) from Indonesian natural product compounds as a novel approach to treat ebola virus disease. IOP Conference Series: Materials Science and Engineering, 2019, 509, 012082.	0.3	1
14	Discovery of biogenic-based compound as potential heat-shock protein 90 inhibitor through fragment-based drug design. IOP Conference Series: Materials Science and Engineering, 2019, 509, 012081.	0.3	1
15	Identification Novel Peptides Conjugated to HIV1 Tat Peptide to Inhibit Ebola Virus Entry by Targeting Niemann Pick C1 Protein. , 2019, , .		0
16	Screening of Potential Northern African Natural Product Compounds as Dengue Virus NS5 Methyltransferase Inhibitor: An in Silico Approach. , 2019, , .		3
17	In silico identification of 2-oxo-1,3-thiazolidine derivatives as novel inhibitor candidate of class II histone deacetylase (HDAC) in cervical cancer treatment. Arabian Journal of Chemistry, 2019, 12, 272-288.	2.3	10
18	Flexible docking-based molecular dynamics simulation of natural product compounds and Ebola virus Nucleocapsid (EBOV NP): a computational approach to discover new drug for combating Ebola. BMC Bioinformatics, 2018, 19, 419.	1.2	35

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19	Screening of Sonic Hedgehog (Shh) Inhibitors in the Hedgehog Signaling Pathway from Traditional Chinese Medicine (TCM) Database Through Structure-Based Pharmacophore Design. Lecture Notes in Computer Science, 2018, , 179-184.	1.0	3
20	Novel Inhibitors of T315I Mutant BCR-ABL1 Tyrosine Kinase for Chronic Myeloid Leukemia Disease Through Fragment-Based Drug Design. Lecture Notes in Computer Science, 2018, , 185-190.	1.0	2
21	EBOLA VIRAL PROTEIN 24 (VP24) INHIBITOR DISCOVERY BY IN SILICO FRAGMENT-BASED DESIGN. International Journal of GEOMATE, 2018, 15, .	0.1	6
22	Screening of commercial cyclic peptide conjugated to HIV-1 Tat peptide as inhibitor of N-terminal heptad repeat glycoprotein-2 ectodomain Ebola virus through in silico analysis. Journal of Molecular Graphics and Modelling, 2017, 74, 366-378.	1.3	18
23	Virtual screening of commercial cyclic peptides as NS2B-NS3 protease inhibitor of dengue virus serotype 2 through molecular docking simulation. IOP Conference Series: Materials Science and Engineering, 2017, 188, 012017.	0.3	4
24	Effects of gamma irradiation dose-rate on sterile male Aedesaegypti. AIP Conference Proceedings, 2017, , .	0.3	12
25	In silico design of fragment-based drug targeting host processing Î±-glucosidase i for dengue fever. IOP Conference Series: Materials Science and Engineering, 2017, 172, 012017.	0.3	12
26	Modification ofS-Adenosyl-<scp>l</scp>-Homocysteine as Inhibitor of Nonstructural Protein 5 Methyltransferase Dengue Virus Through Molecular Docking and Molecular Dynamics Simulation. Drug Target Insights, 2017, 11, 117739281770172.	0.9	25
27	VIRTUAL SCREENING OF COMMERCIAL CYCLIC PEPTIDES AS Î² -OG POCKET BINDER INHIBITOR IN DENGUE VIRUS SEROTYPE 2. International Journal of GEOMATE, 2017, 13, .	0.1	1
28	Exposing the Molecular Screening Method of Indonesian Natural Products Derivate as Drug Candidates for Cervical Cancer. Iranian Journal of Pharmaceutical Research, 2017, 16, 1113-1127.	0.3	3
29	DESIGNING DISULFIDE CYCLIC PEPTIDE AS FUSION INHIBITOR THAT TARGETS DENV ENVELOPE PROTEIN. Jurnal Teknologi (Sciences and Engineering), 2016, 78, .	0.3	1
30	Designing of Disulfide Cyclic Peptide for Inhibiting Polymerase A and B1 (PA_C-PB1_N) in H1N1 Virus using Molecular Simulation Approach. OnLine Journal of Biological Sciences, 2016, 16, 122-129.	0.2	2
31	In silico modification of Zn2+binding group of suberoylanilide hydroxamic acid (SAHA) by organoselenium compounds asHomo sapiensclass II HDAC inhibitor of cervical cancer. IOP Conference Series: Materials Science and Engineering, 2016, 107, 012054.	0.3	1
32	Vaccine Design for H5N1 Based on B- and T-cell Epitope Predictions. Bioinformatics and Biology Insights, 2016, 10, BBI.S38378.	1.0	14
33	Immunoinformatics Approach in Designing Epitope-based Vaccine against Meningitis-inducing Bacteria (Streptococcus pneumoniae, Neisseria meningitidis, and Haemophilus influenzae Type b). Drug Target Insights, 2016, 10, DTI.S38458.	0.9	32
34	Virtual screening of Indonesian flavonoid as neuraminidase inhibitor of influenza a subtype H5N1. IOP Conference Series: Materials Science and Engineering, 2016, 107, 012053.	0.3	7
35	Designing cyclopentapeptide inhibitor of neuraminidase H5N1 virus through molecular and pharmacology simulations. Tsinghua Science and Technology, 2015, 20, 431-440.	4.1	4
36	Screening Analogs of Î²-OG Pocket Binder as Fusion Inhibitor of Dengue Virus 2. Drug Target Insights, 2015, 9, DTI.S31566.	0.9	17

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37	1H, 13C and 15N backbone assignment of the EC-1 domain of human E-cadherin. Biomolecular NMR Assignments, 2015, 9, 31-35.	0.4	4
38	In silico modification of oseltamivir as neuraminidase inhibitor of influenza A virus subtype H1N1. Journal of Biomedical Research, 2015, 29, 150-9.	0.7	6
39	Utilization of Boron Compounds for the Modification of Suberoyl Anilide Hydroxamic Acid as Inhibitor of Histone Deacetylase Class II Homo sapiens. Advances in Bioinformatics, 2014, 2014, 1-10.	5.7	9
40	Computational design of drug candidates for influenza A virus subtype H1N1 by inhibiting the viral neuraminidase-1 enzyme. Acta Pharmaceutica, 2014, 64, 157-172.	0.9	10
41	Screening of commercial cyclic peptide as inhibitor NS5 methyltransferase of Dengue virus through Molecular Docking and Molecular Dynamics Simulation. Bioinformation, 2014, 10, 23-27.	0.2	21
42	Modification of Kampmann A5 as Potential Fusion Inhibitor of Dengue Virus using Molecular Docking and Molecular Dynamics Approach. Journal of Medical Sciences (Faisalabad, Pakistan), 2013, 13, 621-634.	0.0	4
43	Screening of Commercial Cyclic Peptides as Inhibitor Envelope Protein Dengue Virus (DENV) Through Molecular Docking and Molecular Dynamics. Pakistan Journal of Biological Sciences, 2013, 16, 1836-1848.	0.2	21
44	In Silico Molecular Interaction Studies of Suberoylanilide Hydroxamic Acid and Its Modified Compounds with Histones Deacetylase Class II <i>Homo sapiens</i> as Curative Measure towards Cervical Cancer. Engineering, 2013, 05, 203-206.	0.4	4
45	Molecular dynamics simulation of complex Histones Deacetylase (HDAC) Class II Homo Sapiens with suberoylanilide hydroxamic acid (SAHA) and its derivatives as inhibitors of cervical cancer. Bioinformation, 2013, 9, 696-700.	0.2	12
46	In silico Modification of (1R, 2R, 3R, 5S)-(-)- Isopinocampheylamine as Inhibitors of M2 Proton Channel in Influenza A Virus Subtype H1N1, using the Molecular Docking Approach. Trends in Bioinformatics, 2012, 5, 25-46.	0.3	5
47	Designing cyclopentapeptide inhibitor as potential antiviral drug for dengue virus ns5 methyltransferase. Bioinformation, 2012, 8, 348-352.	0.2	23
48	Enhancement of Drug Absorption through the Bloodâ^'Brain Barrier and Inhibition of Intercellular Tight Junction Resealing by E-Cadherin Peptides. Molecular Pharmaceutics, 2011, 8, 239-249.	2.3	44
49	Molecular Dynamics Simulation of DENV RNA-Dependent RNA-Polymerase with Potential Inhibitor of Disulfide Cyclic Peptide. OnLine Journal of Biological Sciences, 2011, 11, 48-62.	0.2	4
50	Modeling allosteric signal propagation using protein structure networks. BMC Bioinformatics, 2011, 12, S23.	1.2	20
51	In silico modification of suberoylanilide hydroxamic acid (SAHA) as potential inhibitor for class II histone deacetylase (HDAC). BMC Bioinformatics, 2011, 12, S23.	1.2	27
52	In silico Design of Drugs and Vaccines for Dengue Disease. Trends in Bioinformatics, 2011, 4, 1-9.	0.3	6
53	Identification of a better Homo sapiens Class II HDAC inhibitor through binding energy calculations and descriptor analysis. BMC Bioinformatics, 2010, 11, S16.	1.2	19
54	Design and Evaluation of Three Pair Primers for Exon 1 Amplification of Hyaluroglucosaminidase-1 Gene. OnLine Journal of Biological Sciences, 2010, 10, 66-72.	0.2	1

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55	Identification of sequence mutations affecting hemagglutinin specificity to sialic acid receptor in influenza A virus subtypes. Bioinformation, 2010, 5, 244-249.	0.2	10
56	Designing cyclic peptide inhibitor of dengue virus NS3-NS2B protease by using molecular docking approach. Bioinformation, 2010, 5, 250-254.	0.2	32
57	In Silico Analysis of Envelope Dengue Virus-2 and Envelope Dengue Virus-3 Protein as the Backbone of Dengue Virus Tetravalent Vaccine by Using Homology Modeling Method. OnLine Journal of Biological Sciences, 2009, 9, 6-16.	0.2	6
58	Structural Modifications of ICAMâ€1 Cyclic Peptides to Improve the Activity to Inhibit Heterotypic Adhesion of T cells. Chemical Biology and Drug Design, 2008, 72, 27-33.	1.5	10
59	Increasing paracellular porosity by E-cadherin peptides: discovery of bulge and groove regions in the EC1-domain of E-cadherin. Pharmaceutical Research, 2002, 19, 1170-1179.	1.7	51
60	Total synthesis of (Â±)-lauren-1-ene, the unique fenestrane diterpene. Tetrahedron Letters, 1987, 28, 2537-2540.	0.7	30
61	Total synthesis of (â^')-vitrenal and its biological activity. Tetrahedron Letters, 1986, 27, 1197-1200.	0.7	10
62	Bioinformatics Approach to Screening and Developing Drug against Ebola. , 0, , .		0
63	Virtual Screening Based on Pharmacophore to Discover Host ER Alpha-Glucosidase II Inhibitor for Dengue Therapy. Key Engineering Materials, 0, 840, 221-229.	0.4	1
64	Discovery of Novel Î±-Amylase Inhibitors as Type Two Diabetes Mellitus Therapy through Fragment-Based Drug Design. Key Engineering Materials, 0, 840, 237-244.	0.4	0
65	Discovery of Natural Product Compounds as Dengue Virus NS5 Methyltransferase Inhibitor Candidate through in Silico Method. Key Engineering Materials, 0, 840, 270-276.	0.4	1
66	Utilization of Flavonoid Compounds as HER2 Tyrosine Kinase Inhibitor in Breast Cancer Using Fragment-Based Drug Design. Key Engineering Materials, 0, 840, 230-236.	0.4	1
67	Screening of terpenoids as potential therapeutics against Zaire ebolavirus infection through pharmacophore-based drug design. F1000Research, 0, 8, 1040.	0.8	1