Van V Vu

List of Publications by Year in descending order

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		201385	161609
80	3,327	27	54
papers	citations	h-index	g-index
0.5	0.5	0.5	2261
85	85	85	3361
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	Amyloid Oligomers: A Joint Experimental/Computational Perspective on Alzheimer's Disease, Parkinson's Disease, Type II Diabetes, and Amyotrophic Lateral Sclerosis. Chemical Reviews, 2021, 121, 2545-2647.	23.0	406
2	Cellulose Degradation by Polysaccharide Monooxygenases. Annual Review of Biochemistry, 2015, 84, 923-946.	5.0	246
3	Autodock Vina Adopts More Accurate Binding Poses but Autodock4 Forms Better Binding Affinity. Journal of Chemical Information and Modeling, 2020, 60, 204-211.	2.5	233
4	A family of starch-active polysaccharide monooxygenases. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 13822-13827.	3.3	222
5	Determinants of Regioselective Hydroxylation in the Fungal Polysaccharide Monooxygenases. Journal of the American Chemical Society, 2014, 136, 562-565.	6.6	198
6	Inhibition of Aggregation of Amyloid Peptides by Beta-Sheet Breaker Peptides and Their Binding Affinity. Journal of Physical Chemistry B, 2011 , 115 , 7433 - 7446 .	1.2	173
7	Computational Determination of Potential Inhibitors of SARS-CoV-2 Main Protease. Journal of Chemical Information and Modeling, 2020, 60, 5771-5780.	2.5	118
8	Human deoxyhypusine hydroxylase, an enzyme involved in regulating cell growth, activates O ₂ with a nonheme diiron center. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 14814-14819.	3.3	105
9	Curcumin Binds to AÎ 2 _{1â40} Peptides and Fibrils Stronger Than Ibuprofen and Naproxen. Journal of Physical Chemistry B, 2012, 116, 10165-10175.	1.2	85
10	Effect of the Tottori Familial Disease Mutation (D7N) on the Monomers and Dimers of A \hat{l}^2 ₄₀ and A \hat{l}^2 ₄₂ . ACS Chemical Neuroscience, 2013, 4, 1446-1457.	1.7	83
11	An Unusual Peroxo Intermediate of the Arylamine Oxygenase of the Chloramphenicol Biosynthetic Pathway. Journal of the American Chemical Society, 2015, 137, 1608-1617.	6.6	71
12	Fast and accurate determination of the relative binding affinities of small compounds to HIV-1 protease using non-equilibrium work. Journal of Computational Chemistry, 2016, 37, 2734-2742.	1.5	70
13	Benchmark of Popular Free Energy Approaches Revealing the Inhibitors Binding to SARS-CoV-2 Mpro. Journal of Chemical Information and Modeling, 2021, 61, 2302-2312.	2.5	66
14	Effective Estimation of Ligand-Binding Affinity Using Biased Sampling Method. ACS Omega, 2019, 4, 3887-3893.	1.6	52
15	Top-leads from natural products for treatment of Alzheimer's disease: docking and molecular dynamics study. Molecular Simulation, 2013, 39, 279-291.	0.9	50
16	Copper active site in polysaccharide monooxygenases. Coordination Chemistry Reviews, 2018, 368, 134-157.	9.5	47
17	Tetrameric Al 2 40 and Al 2 42 l 2 -Barrel Structures by Extensive Atomistic Simulations. I. In a Bilayer Mimicking a Neuronal Membrane. Journal of Physical Chemistry B, 2019, 123, 3643-3648.	1.2	42
18	Anti-arrhythmic Medication Propafenone a Potential Drug for Alzheimer's Disease Inhibiting Aggregation of Aβ: In Silico and in Vitro Studies. Journal of Chemical Information and Modeling, 2016, 56, 1344-1356.	2.5	41

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19	A mononuclear carboxylate-rich oxoiron(iv) complex: a structural and functional mimic of TauD intermediate â€̃J'. Chemical Science, 2012, 3, 1680.	3.7	40
20	In silico and in vitro characterization of anti-amyloidogenic activity of vitamin K3 analogues for Alzheimer's disease. Biochimica Et Biophysica Acta - General Subjects, 2013, 1830, 2960-2969.	1.1	38
21	Replica exchange molecular dynamics study of the amyloid beta (11–40) trimer penetrating a membrane. RSC Advances, 2017, 7, 7346-7357.	1.7	38
22	EGCG inhibits the oligomerization of amyloid beta (16-22) hexamer: Theoretical studies. Journal of Molecular Graphics and Modelling, 2017, 76, 1-10.	1.3	38
23	Replica exchange molecular dynamics study of the truncated amyloid beta (11–40) trimer in solution. Physical Chemistry Chemical Physics, 2017, 19, 1909-1919.	1.3	36
24	Characterization of Two Distinct Adducts in the Reaction of a Nonheme Diiron(II) Complex with O ₂ . Inorganic Chemistry, 2009, 48, 8325-8336.	1.9	33
25	Starch-degrading polysaccharide monooxygenases. Cellular and Molecular Life Sciences, 2016, 73, 2809-2819.	2.4	33
26	Tetrameric A $\hat{1}^2$ 40 and A $\hat{1}^2$ 42 $\hat{1}^2$ -Barrel Structures by Extensive Atomistic Simulations. II. In Aqueous Solution. Journal of Physical Chemistry B, 2019, 123, 6750-6756.	1.2	31
27	Substrate selectivity in starch polysaccharide monooxygenases. Journal of Biological Chemistry, 2019, 294, 12157-12166.	1.6	31
28	Oversampling Free Energy Perturbation Simulation in Determination of the Ligandâ€Binding Free Energy. Journal of Computational Chemistry, 2020, 41, 611-618.	1.5	30
29	Rapid prediction of possible inhibitors for SARS-CoV-2 main protease using docking and FPL simulations. RSC Advances, 2020, 10, 31991-31996.	1.7	30
30	Determination of the absolute binding free energies of HIV-1 protease inhibitors using non-equilibrium molecular dynamics simulations. Chemical Physics Letters, 2017, 676, 12-17.	1.2	27
31	Probable Transmembrane Amyloid α-Helix Bundles Capable of Conducting Ca ²⁺ Ions. Journal of Physical Chemistry B, 2019, 123, 2645-2653.	1.2	26
32	Estimation of the Binding Free Energy of AC1NX476 toÂHIVâ€1 Protease Wild Type and Mutations Using FreeÂEnergy Perturbation Method. Chemical Biology and Drug Design, 2015, 86, 546-558.	1.5	24
33	The Effects of A21G Mutation on Transmembrane Amyloid Beta (11–40) Trimer: An <i>In Silico</i> Study. Journal of Physical Chemistry B, 2017, 121, 8467-8474.	1.2	24
34	Prediction of AChE-ligand affinity using the umbrella sampling simulation. Journal of Molecular Graphics and Modelling, 2019, 93, 107441.	1.3	24
35	Active-Site Structure of a \hat{l}^2 -Hydroxylase in Antibiotic Biosynthesis. Journal of the American Chemical Society, 2011, 133, 6938-6941.	6.6	21
36	Oligomerization of Peptides LVEALYL and RGFFYT and Their Binding Affinity to Insulin. PLoS ONE, 2013, 8, e65358.	1.1	21

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37	X-ray absorption spectroscopic characterization of the diferric-peroxo intermediate of human deoxyhypusine hydroxylase in the presence of its substrate eIF5a. Journal of Biological Inorganic Chemistry, 2016, 21, 605-618.	1.1	21
38	Assessing potential inhibitors of SARS-CoV-2 main protease from available drugs using free energy perturbation simulations. RSC Advances, 2020, 10, 40284-40290.	1.7	21
39	Stability of AÎ 2 11â $^{\circ}$ 40 Trimers with Parallel and Antiparallel Î 2 -Sheet Organizations in a Membrane-Mimicking Environment by Replica Exchange Molecular Dynamics Simulation. Journal of Physical Chemistry B, 2020, 124, 617-626.	1.2	21
40	Binding of inhibitors to the monomeric and dimeric SARS-CoV-2 Mpro. RSC Advances, 2021, 11, 2926-2934.	1.7	19
41	Improving <scp>ligandâ€ranking</scp> of <scp>AutoDock</scp> Vina by changing the empirical parameters. Journal of Computational Chemistry, 2022, 43, 160-169.	1.5	19
42	Insights into the binding and covalent inhibition mechanism of PF-07321332 to SARS-CoV-2 M ^{pro} . RSC Advances, 2022, 12, 3729-3737.	1.7	19
43	Impact of A2T and D23N Mutations on Tetrameric AÎ ² 42 Barrel within a Dipalmitoylphosphatidylcholine Lipid Bilayer Membrane by Replica Exchange Molecular Dynamics. Journal of Physical Chemistry B, 2020, 124, 1175-1182.	1.2	18
44	Impact of the Astaxanthin, Betanin, and EGCG Compounds on Small Oligomers of Amyloid Aβ ₄₀ Peptide. Journal of Chemical Information and Modeling, 2020, 60, 1399-1408.	2.5	17
45	Adequate prediction for inhibitor affinity of $\hat{Al^2}$ sub>40 protofibril using the linear interaction energy method. RSC Advances, 2019, 9, 12455-12461.	1.7	16
46	How do magnetic, structural, and electronic criteria of aromaticity relate to HOMO – LUMO gap? An evaluation for graphene quantum dot and its derivatives. Chemical Physics, 2020, 539, 110951.	0.9	16
47	In silico studies of solvated F19W amyloid β (11–40) trimer. RSC Advances, 2017, 7, 42379-42386.	1.7	15
48	Fast pulling of ligand approach for the design of \hat{l}^2 -secretase 1 inhibitors. Chemical Physics Letters, 2017, 671, 142-146.	1.2	14
49	In vitroandin silicodetermination of glutaminyl cyclase inhibitors. RSC Advances, 2019, 9, 29619-29627.	1.7	14
50	Estimating the <scp>ligandâ€binding</scp> affinity via <scp>λâ€dependent</scp> umbrella sampling simulations. Journal of Computational Chemistry, 2021, 42, 117-123.	1.5	14
51	Effect of Cholesterol Molecules on Al 2 1-42 Wild-Type and Mutants Trimers. Molecules, 2022, 27, 1395.	1.7	13
52	Evaluation of the absolute affinity of neuraminidase inhibitor using steered molecular dynamics simulations. Journal of Molecular Graphics and Modelling, 2017, 77, 137-142.	1.3	12
53	Influence of various force fields in estimating the binding affinity of acetylcholinesterase inhibitors using fast pulling of ligand scheme. Chemical Physics Letters, 2018, 701, 65-71.	1.2	12
54	Interaction of carbohydrate binding module 20 with starch substrates. RSC Advances, 2019, 9, 24833-24842.	1.7	12

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55	Cholesterol Molecules Alter the Energy Landscape of Small Al^21â \in "42 Oligomers. Journal of Physical Chemistry B, 2021, 125, 2299-2307.	1.2	12
56	Conjugated polymers: A systematic investigation of their electronic and geometric properties using density functional theory and semi-empirical methods. Synthetic Metals, 2018, 246, 128-136.	2.1	11
57	Etersalate prevents the formations of $6 \mbox{Al}^2 16$ -22 oligomer: An in silico study. PLoS ONE, 2018, 13, e0204026.	1.1	11
58	Searching and designing potential inhibitors for SARS-CoV-2 Mpro from natural sources using atomistic and deep-learning calculations. RSC Advances, 2021, 11, 38495-38504.	1.7	11
59	Identifying Possible AChE Inhibitors from Drug-like Molecules via Machine Learning and Experimental Studies. ACS Omega, 2022, 7, 20673-20682.	1.6	11
60	Atomistic investigation of an lowa Amyloid- \hat{l}^2 trimer in aqueous solution. RSC Advances, 2018, 8, 41705-41712.	1.7	9
61	Fabrication of superhydrophobic surface using one-step chemical treatment. Surfaces and Interfaces, 2020, 21, 100673.	1.5	9
62	Systematic Investigation of the Structure, Stability, and Spin Magnetic Moment of $CrM < sub < i > n < i > c sub > Clusters (M = Cu, Ag, Au, and < i > n < i > c sub > Clusters (M = Cu, Ag, Au, and < i > n < i > c sub > Clusters (M = Cu, Ag, Au, and < i > n < i > c sub > Clusters (M = Cu, Ag, Au, and < i > n < i > c sub > Clusters (M = Cu, Ag, Au, and < i > n < i > c sub > Clusters (M = Cu, Ag, Au, and < i > n < i > c sub > Clusters (M = Cu, Ag, Au, and < i > n < i > c sub > Clusters (M = Cu, Ag, Au, and < i > n < sub > c sub > Clusters (M = Cu, Ag, Au, and < i > n < sub > c sub > Clusters (M = Cu, Ag, Au, and < i > n < sub > c sub > Clusters (M = Cu, Ag, Au, and < i > n < sub > c sub > Clusters (M = Cu, Ag, Au, and < i > n < sub > c sub > Clusters (M = Cu, Ag, Au, and < i > n < sub > c sub > Clusters (M = Cu, Ag, Au, and < i > n < sub > c sub > Clusters (M = Cu, Ag, Au, and < i > n < sub > c sub > Clusters (M = Cu, Ag, Au, and < i > n < sub > c sub > Clusters (M = Cu, Ag, Au, and < i > n < sub > c sub > c $	1.6	9
63	Unbinding ligands from SARS-CoV-2 Mpro via umbrella sampling simulations. Royal Society Open Science, 2022, 9, 211480.	1.1	9
64	Theoretical study of the interactions between the first transmembrane segment of NS2 protein and a POPC lipid bilayer. Biophysical Chemistry, 2016, 217, 1-7.	1.5	8
65	C-Terminal Plays as the Possible Nucleation of the Self-Aggregation of the S-Shape Aβ _{11–42} Tetramer in Solution: Intensive MD Study. ACS Omega, 2019, 4, 11066-11073.	1.6	8
66	Potential inhibitors for SARS-CoV-2 Mpro from marine compounds. RSC Advances, 2021, 11, 22206-22213.	1.7	8
67	Searching for AChE inhibitors from natural compounds by using machine learning and atomistic simulations. Journal of Molecular Graphics and Modelling, 2022, 115, 108230.	1.3	8
68	Effective estimation of the inhibitor affinity of HIV-1 protease <i>via</i> a modified LIE approach. RSC Advances, 2020, 10, 7732-7739.	1.7	7
69	Propafenone effects on the stable structures of \hat{Al}^2 16-22 system. Chemical Physics Letters, 2018, 696, 55-60.	1.2	6
70	The influences of E22Q mutant on solvated $3\text{A}\hat{1}^2$ 11-40 peptide: A REMD study. Journal of Molecular Graphics and Modelling, 2018, 83, 122-128.	1.3	6
71	Computational investigation of possible inhibitors of the winged-helix domain of MUS81. Journal of Molecular Graphics and Modelling, 2021, 103, 107771.	1.3	5
72	Marine derivatives prevent <i>w</i> MUS81 <i>iin silico</i> studies. Royal Society Open Science, 2021, 8, 210974.	1.1	5

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73	Umbrella Sampling-Based Method to Compute Ligand-Binding Affinity. Methods in Molecular Biology, 2022, 2385, 313-323.	0.4	5
74	Terahertz cut-wire-pair metamaterial absorber. Journal of Applied Physics, 2021, 130, .	1.1	4
75	Fine Tuning of the Copper Active Site in Polysaccharide Monooxygenases. Journal of Physical Chemistry B, 2020, 124, 1859-1865.	1.2	3
76	Impact of the Rat R5G, Y10F, and H13R Mutations on Tetrameric A \hat{l}^2 42 \hat{l}^2 -Barrel in a Lipid Bilayer Membrane Model. Journal of Physical Chemistry B, 2021, 125, 3105-3113.	1.2	3
77	Computational Investigations of the Transmembrane Italian-Mutant (E22K) $3A(eta_{11} - 40)$ in Aqueous Solution. Communications in Physics, 2018, 28, 265.	0.0	3
78	Thermodynamics and kinetics in antibody resistance of the 501Y.V2 SARS-CoV-2 variant. RSC Advances, 2021, 11, 33438-33446.	1.7	3
79	Solution structure of the reduced active site of a starch-active polysaccharide monooxygenase from Neurospora crassa. Vietnam Journal of Science Technology and Engineering, 2018, 60, 9-12.	0.1	2
80	501Y.V2 spike protein resists the neutralizing antibody in atomistic simulations. Computational Biology and Chemistry, 2022, 97, 107636.	1.1	1