Ozlem Tastan Bishop

List of Publications by Year
in descending order

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89 papers	2,325 citations	279798 23 h-index	265206 42 g-index
105 all docs	105 docs citations	105 times ranked	3050 citing authors

#	Article	IF	Citations
1	Enabling the genomic revolution in Africa. Science, 2014, 344, 1346-1348.	12.6	361
2	MD-TASK: a software suite for analyzing molecular dynamics trajectories. Bioinformatics, 2017, 33, 2768-2771.	4.1	142
3	H3ABioNet, a sustainable pan-African bioinformatics network for human heredity and health in Africa. Genome Research, 2016, 26, 271-277.	5.5	94
4	Allosteric Modulation of Human Hsp90Î± Conformational Dynamics. Journal of Chemical Information and Modeling, 2018, 58, 383-404.	5.4	79
5	SANCDB: a South African natural compound database. Journal of Cheminformatics, 2015, 7, 29.	6.1	77
6	Integrated Computational Approaches and Tools for Allosteric Drug Discovery. International Journal of Molecular Sciences, 2020, 21, 847.	4.1	73
7	Structure Based Docking and Molecular Dynamic Studies of Plasmodial Cysteine Proteases against a South African Natural Compound and its Analogs. Scientific Reports, 2016, 6, 23690.	3.3	71
8	Perturbationâ€“Response Scanning Reveals Key Residues for Allosteric Control in Hsp70. Journal of Chemical Information and Modeling, 2017, 57, 1359-1374.	5.4	70
9	Comparison of the human and murine ATRX gene identifies highly conserved, functionally important domains. Mammalian Genome, 1998, 9, 400-403.	2.2	64
10	Impact of Early Pandemic Stage Mutations on Molecular Dynamics of SARS-CoV-2 M^{pro}. Journal of Chemical Information and Modeling, 2020, 60, 5080-5102.	5.4	62
11	Bioinformatics Education–Perspectives and Challenges out of Africa. Briefings in Bioinformatics, 2015, 16, 355-364.	6.5	61
12	GOBLET: The Global Organisation for Bioinformatics Learning, Education and Training. PLoS Computational Biology, 2015, 11, e1004143.	3.2	52
13	Development of Bioinformatics Infrastructure for Genomics Research. Global Heart, 2017, 12, 91.	2.3	47
14	PRIMO: An Interactive Homology Modeling Pipeline. PLoS ONE, 2016, 11, e0166698.	2.5	47
15	MODE-TASK: large-scale protein motion tools. Bioinformatics, 2018, 34, 3759-3763.	4.1	45
16	Ten simple rules for organizing a webinar series. PLoS Computational Biology, 2019, 15, e1006671.	3.2	43
17	Role of Structural Bioinformatics in Drug Discovery by Computational SNP Analysis. Global Heart, 2017, 12, 151.	2.3	38
18	Analysis of Protein Thermostability Enhancing Factors in Industrially ImportantThermusBacteria Species. Evolutionary Bioinformatics, 2013, 9, EBO.S12539.	1.2	33

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19	Discorhabdin N, a South African Natural Compound, for Hsp72 and Hsc70 Allosteric Modulation: Combined Study of Molecular Modeling and Dynamic Residue Network Analysis. Molecules, 2019, 24, 188.	3.8	31
20	Structure-Based Analysis of Single Nucleotide Variants in the Renin-Angiotensinogen Complex. Global Heart, 2017, 12, 121.	2.3	31
21	Codon-Anticodon Interaction at the P Site Is a Prerequisite for tRNA Interaction with the Small Ribosomal Subunit. Journal of Biological Chemistry, 2002, 277, 19095-19105.	3.4	29
22	The global distribution and diversity of protein vaccine candidate antigens in the highly virulent Streptococcus pnuemoniae serotype 1. Vaccine, 2017, 35, 972-980.	3.8	27
23	Modulation of Human Hsp90Î± Conformational Dynamics by Allosteric Ligand Interaction at the C-Terminal Domain. Scientific Reports, 2019, 9, 1600.	3.3	27
24	Understanding the Pyrimethamine Drug Resistance Mechanism via Combined Molecular Dynamics and Dynamic Residue Network Analysis. Molecules, 2020, 25, 904.	3.8	26
25	Plasmodium falciparumHsp70-x: a heat shock protein at the hostâ€“parasite interface. Journal of Biomolecular Structure and Dynamics, 2014, 32, 1766-1779.	3.5	25
26	Analysis of non-peptidic compounds as potential malarial inhibitors against Plasmodial cysteine proteases via integrated virtual screening workflow. Journal of Biomolecular Structure and Dynamics, 2016, 34, 2084-2101.	3.5	25
27	Human, vector and parasite Hsp90 proteins: A comparative bioinformatics analysis. FEBS Open Bio, 2015, 5, 916-927.	2.3	24
28	Improving fold resistance prediction of HIV-1 against protease and reverse transcriptase inhibitors using artificial neural networks. BMC Bioinformatics, 2017, 18, 369.	2.6	24
29	Characterizing early drug resistance-related events using geometric ensembles from HIV protease dynamics. Scientific Reports, 2018, 8, 17938.	3.3	24
30	Aminoacyl tRNA synthetases as malarial drug targets: a comparative bioinformatics study. Malaria Journal, 2019, 18, 34.	2.3	23
31	SANCDB: an update on South African natural compounds and their readily available analogs. Journal of Cheminformatics, 2021, 13, 37.	6.1	23
32	Identification of Novel Potential Inhibitors of Pteridine Reductase 1 in Trypanosoma brucei via Computational Structure-Based Approaches and in Vitro Inhibition Assays. Molecules, 2019, 24, 142.	3.8	21
33	Interacting motif networks located in hotspots associated with <scp>RNA</scp> release are conserved in Enterovirus capsids. FEBS Letters, 2017, 591, 1687-1701.	2.8	19
34	Unraveling the Motions behind Enterovirus 71ÂUncoating. Biophysical Journal, 2018, 114, 822-838.	0.5	19
35	Mechanism of Action of Non-Synonymous Single Nucleotide Variations Associated with Î±-Carbonic Anhydrase II Deficiency. Molecules, 2019, 24, 3987.	3.8	18
36	MDM-TASK-web: MD-TASK and MODE-TASK web server for analyzing protein dynamics. Computational and Structural Biotechnology Journal, 2021, 19, 5059-5071.	4.1	18

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37	A new approach to possible substrate binding mechanisms for nitrile hydratase. Biochemical and Biophysical Research Communications, 2006, 343, 319-325.	2.1	16
38	Bioinformatic characterization of type-specific sequence and structural features in auxiliary activity family 9 proteins. Biotechnology for Biofuels, 2016, 9, 239.	6.2	16
39	Polyphenols Epigallocatechin Gallate and Resveratrol, and Polyphenol-Functionalized Nanoparticles Prevent Enterovirus Infection through Clustering and Stabilization of the Viruses. Pharmaceutics, 2021, 13, 1182.	4.5	15
40	Study of protein complexes via homology modeling, applied to cysteine proteases and their protein inhibitors. Journal of Molecular Modeling, 2011, 17, 3163-3172.	1.8	14
41	Comparing sequence and structure of falcipains and human homologs at prodomain and catalytic active site for malarial peptide based inhibitor design. Malaria Journal, 2019, 18, 159.	2.3	14
42	Potential repurposing of four FDA approved compounds with antiplasmodial activity identified through proteome scale computational drug discovery and in vitro assay. Scientific Reports, 2021, 11, 1413.	3.3	14
43	Novel dynamic residue network analysis approaches to study allosteric modulation: SARS-CoV-2 Mpro and its evolutionary mutations as a case study. Computational and Structural Biotechnology Journal, 2021, 19, 6431-6455.	4.1	14
44	Anti-HIV-1 integrase potency of methylgallate from Alchornea cordifolia using in vitro and in silico approaches. Scientific Reports, 2019, 9, 4718.	3.3	13
45	AMBER force field parameters for the Zn (II) ions of the tunneling-fold enzymes GTP cyclohydrolase I and 6â€pyruvoyl tetrahydropterin synthase. Journal of Biomolecular Structure and Dynamics, 2021, 39, 5843-5860.	3.5	13
46	Human OMICs and Computational Biology Research in Africa: Current Challenges and Prospects. OMICS A Journal of Integrative Biology, 2021, 25, 213-233.	2.0	13
47	Determining the unbinding events and conserved motions associated with the pyrazinamide release due to resistance mutations of Mycobacterium tuberculosis pyrazinamidase. Computational and Structural Biotechnology Journal, 2020, 18, 1103-1120.	4.1	13
48	Allosteric pockets and dynamic residue network hubs of falcipain 2 in mutations including those linked to artemisinin resistance. Computational and Structural Biotechnology Journal, 2021, 19, 5647-5666.	4.1	13
49	Plasmodium falciparum Hop: Detailed analysis on complex formation with Hsp70 and Hsp90. Biochemical and Biophysical Research Communications, 2015, 456, 440-445.	2.1	12
50	The Development of Computational Biology in South Africa: Successes Achieved and Lessons Learnt. PLoS Computational Biology, 2016, 12, e1004395.	3.2	12
51	No evidence for association between APOL1 kidney disease risk alleles and Human African Trypanosomiasis in two Ugandan populations. PLoS Neglected Tropical Diseases, 2018, 12, e0006300.	3.0	12
52	Establishing Computational Approaches Towards Identifying Malarial Allosteric Modulators: A Case Study of Plasmodium falciparum Hsp70s. International Journal of Molecular Sciences, 2019, 20, 5574.	4.1	12
53	High Levels of Genetic Diversity within Nilo-Saharan Populations: Implications for Human Adaptation. American Journal of Human Genetics, 2020, 107, 473-486.	6.2	12
54	JMS: An Open Source Workflow Management System and Web-Based Cluster Front-End for High Performance Computing. PLoS ONE, 2015, 10, e0134273.	2.5	12

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55	Structural Characterization of Carbonic Anhydrase VIII and Effects of Missense Single Nucleotide Variations to Protein Structure and Function. International Journal of Molecular Sciences, 2020, 21, 2764.	4.1	11
56	Rearrangement of the 16S Precursor Subunits Is Essential for the Formation of the Active 20S Proteasome. Biophysical Journal, 2004, 87, 4098-4105.	0.5	10
57	How to establish a bioinformatics postgraduate degree programme--a case study from South Africa. Briefings in Bioinformatics, 2015, 16, 346-354.	6.5	10
58	Sequence and domain conservation of the coelacanth Hsp40 and Hsp90 chaperones suggests conservation of function. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2014, 322, 359-378.	1.3	9
59	Identification of Selective Novel Hits against Plasmodium falciparum Prolyl tRNA Synthetase Active Site and a Predicted Allosteric Site Using In Silico Approaches. International Journal of Molecular Sciences, 2020, 21, 3803.	4.1	9
60	Deciphering Isoniazid Drug Resistance Mechanisms on Dimeric Mycobacterium tuberculosis KatG via Post-molecular Dynamics Analyses Including Combined Dynamic Residue Network Metrics. ACS Omega, 2022, 7, 13313-13332.	3.5	9
61	Comparative structural bioinformatics analysis of Bacillus amyloliquefaciens chemotaxis proteins within Bacillus subtilis group. Applied Microbiology and Biotechnology, 2011, 92, 997-1008.	3.6	8
62	The evaluation and validation of copper (II) force field parameters of the Auxiliary Activity family 9 enzymes. Chemical Physics Letters, 2017, 678, 91-97.	2.6	8
63	HUMA: A platform for the analysis of genetic variation in humans. Human Mutation, 2018, 39, 40-51.	2.5	8
64	Allostery and Missense Mutations as Intermittently Linked Promising Aspects of Modern Computational Drug Discovery. Journal of Molecular Biology, 2022, 434, 167610.	4.2	8
65	Homology modeling and docking of AahII-Nanobody complexes reveal the epitope binding site on AahII scorpion toxin. Biochemical and Biophysical Research Communications, 2018, 496, 1025-1032.	2.1	7
66	The determination of CHARMM force field parameters for the Mg2+ containing HIV-1 integrase. Chemical Physics Letters, 2018, 711, 1-7.	2.6	7
67	South African Abietane Diterpenoids and Their Analogs as Potential Antimalarials: Novel Insights from Hybrid Computational Approaches. Molecules, 2019, 24, 4036.	3.8	6
68	Alpha-Carbonic Anhydrases from Hydrothermal Vent Sources as Potential Carbon Dioxide Sequestration Agents: In Silico Sequence, Structure and Dynamics Analyses. International Journal of Molecular Sciences, 2020, 21, 8066.	4.1	6
69	GTP Cyclohydrolase I as a Potential Drug Target: New Insights into Its Allosteric Modulation via Normal Mode Analysis. Journal of Chemical Information and Modeling, 2021, 61, 4701-4719.	5.4	6
70	Characterisation of plasmodial transketolases and identification of potential inhibitors: an in silico study. Malaria Journal, 2020, 19, 442.	2.3	5
71	X-ray Structure, Bioinformatics Analysis, and Substrate Specificity of a 6-Phospho-Î²-glucosidase Glycoside Hydrolase 1 Enzyme from Bacillus licheniformis. Journal of Chemical Information and Modeling, 2020, 60, 6392-6407.	5.4	5
72	Decoding the Molecular Effects of Atovaquone Linked Resistant Mutations on Plasmodium falciparum Cytb-ISP Complex in the Phospholipid Bilayer Membrane. International Journal of Molecular Sciences, 2021, 22, 2138.	4.1	5

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73	In Silico Investigation of Potential Applications of Gamma Carbonic Anhydrases as Catalysts of CO2 Biomineralization Processes: A Visit to the Thermophilic Bacteria Persephonella hydrogeniphila, Persephonella marina, Thermosulfidibacter takaii, and Thermus thermophilus. International Journal of Molecular Sciences, 2021, 22, 2861.	4.1	5
74	The generation and characterisation of neutralising antibodies against the Theilerâ€™s murine encephalomyelitis virus (TMEV) GDVII capsid reveals the potential binding site of the host cell co-receptor, heparan sulfate. Virus Research, 2018, 244, 153-163.	2.2	4
75	Oral Phyto-thymol ameliorates the stress induced IBS symptoms. Scientific Reports, 2020, 10, 13900.	3.3	4
76	The Structural Basis of Mycobacterium tuberculosis RpoB Drug-Resistant Clinical Mutations on Rifampicin Drug Binding. Molecules, 2022, 27, 885.	3.8	4
77	Subcellular localisation of Theiler's murine encephalomyelitis virus (TMEV) capsid subunit VP1 vis-Ã¡-vis host protein Hsp90. Virus Research, 2016, 222, 53-63.	2.2	3
78	Probing the Structural Dynamics of the Plasmodium falciparum Tunneling-Fold Enzyme 6-Pyruvoyl Tetrahydropterin Synthase to Reveal Allosteric Drug Targeting Sites. Frontiers in Molecular Biosciences, 2020, 7, 575196.	3.5	3
79	Computational Applications in Secondary Metabolite Discovery (CAiSMD): an online workshop. Journal of Cheminformatics, 2021, 13, 64.	6.1	3
80	Slipknot or Crystallographic Error: A Computational Analysis of the Plasmodium falciparum DHFR Structural Folds. International Journal of Molecular Sciences, 2022, 23, 1514.	4.1	3
81	The PINIT domain of PIAS3: structureâ€function analysis of its interaction with STAT3. Journal of Molecular Recognition, 2011, 24, 795-803.	2.1	2
82	The In Silico Prediction of Hotspot Residues that Contribute to the Structural Stability of Subunit Interfaces of a Picornavirus Capsid. Viruses, 2020, 12, 387.	3.3	2
83	Differences in Gluco and Galacto Substrate-Binding Interactions in a Dual 6PÎ²-Glucosidase/6PÎ²-Galactosidase Glycoside Hydrolase 1 Enzyme from Bacillus licheniformis. Journal of Chemical Information and Modeling, 2021, 61, 4554-4570.	5.4	2
84	Introducing DerivatizeME and its Application in the Augmentation of a Natural Product Library. Journal of Computational Biophysics and Chemistry, 2021, 20, 233-250.	1.7	1
85	Force Field Parameters for Fe2+4S2â^'4 Clusters of Dihydropyrimidine Dehydrogenase, the 5-Fluorouracil Cancer Drug Deactivation Protein: A Step towards In Silico Pharmacogenomics Studies. Molecules, 2021, 26, 2929.	3.8	1
86	Gamma Carbonic Anhydrases from Hydrothermal Vent Bacteria: Cases of Alternating Active Site Due to a Long Loop with Proton Shuttle Residue. Catalysts, 2021, 11, 1177.	3.5	1
87	Virtual screening andin vitrovalidation identifies the first reported inhibitors ofSalmonella entericaHPPK. RSC Medicinal Chemistry, 2021, 12, 1750-1756.	3.9	1
88	Establishment of â€œThe South African Bioinformatics Student Councilâ€•and Activity Highlights. EMBnet Journal, 0, 23, e903.	0.6	1
89	Characterization of RNAâ€”Protein Interactions by Phosphorothioate Footprinting and Its Applications to the Ribosome. Methods in Molecular Biology, 2008, 488, 129-151.	0.9	0