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List of Publications by Year in descending order

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Version: 2024-02-01

27
papers

10,670
citations

567281

15
h-index

552781

26
g-index

27
all docs

27
docs citations

27
times ranked

20068
citing authors

#	ARTICLE	IF	CITATIONS
1	Evolutionary Diversification of Host-Targeted Bartonella Effectors Proteins Derived from a Conserved FicTA Toxin-Antitoxin Module. <i>Microorganisms</i> , 2021, 9, 1645.	3.6	5
2	SWISS-MODEL: homology modelling of protein structures and complexes. <i>Nucleic Acids Research</i> , 2018, 46, W296-W303.	14.5	8,474
3	The SWISS-MODEL Repository's new features and functionality. <i>Nucleic Acids Research</i> , 2017, 45, D313-D319.	14.5	1,227
4	A computational protocol to evaluate the effects of protein mutants in the kinase gatekeeper position on the binding of ATP substrate analogues. <i>BMC Research Notes</i> , 2017, 10, 104.	1.4	7
5	Common sequence variants affect molecular function more than rare variants?. <i>Scientific Reports</i> , 2017, 7, 1608.	3.3	20
6	The BID Domain of Type IV Secretion Substrates Forms a Conserved Four-Helix Bundle Topped with a Hook. <i>Structure</i> , 2017, 25, 203-211.	3.3	15
7	StrÃmme Syndrome Is a Ciliary Disorder Caused by Mutations in <i>CENPF</i> . <i>Human Mutation</i> , 2016, 37, 359-363.	2.5	27
8	Synthesis of empty african horse sickness virus particles. <i>Virus Research</i> , 2016, 213, 184-194.	2.2	17
9	The SIB Swiss Institute of Bioinformatics's resources: focus on curated databases. <i>Nucleic Acids Research</i> , 2016, 44, D27-D37.	14.5	64
10	Insight into Neutral and Disease-Associated Human Genetic Variants through Interpretable Predictors. <i>PLoS ONE</i> , 2015, 10, e0120729.	2.5	2
11	Determination of common genetic variants within the non-structural proteins of foot-and-mouth disease viruses isolated in sub-Saharan Africa. <i>Veterinary Microbiology</i> , 2015, 177, 106-122.	1.9	6
12	Genetic heterogeneity in the leader and P1-coding regions of foot-and-mouth disease virus serotypes A and O in Africa. <i>Archives of Virology</i> , 2014, 159, 947-61.	2.1	11
13	The Catalytic Site Atlas 2.0: cataloging catalytic sites and residues identified in enzymes. <i>Nucleic Acids Research</i> , 2014, 42, D485-D489.	14.5	168
14	PDBsum additions. <i>Nucleic Acids Research</i> , 2014, 42, D292-D296.	14.5	279
15	Amino Acid Changes in Disease-Associated Variants Differ Radically from Variants Observed in the 1000 Genomes Project Dataset. <i>PLoS Computational Biology</i> , 2013, 9, e1003382.	3.2	54
16	LigSearch: a knowledge-based web server to identify likely ligands for a protein target. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2395-2402.	2.5	2
17	Analysis of SAT Type Foot-And-Mouth Disease Virus Capsid Proteins and the Identification of Putative Amino Acid Residues Affecting Virus Stability. <i>PLoS ONE</i> , 2013, 8, e61612.	2.5	21
18	Current challenges in genome annotation through structural biology and bioinformatics. <i>Current Opinion in Structural Biology</i> , 2012, 22, 594-601.	5.7	14

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19	1,000 structures and more from the MCSG. BMC Structural Biology, 2011, 11, 2.	2.3	14
20	Predicting antigenic sites on the foot-and-mouth disease virus capsid of the South African Territories types using virus neutralization data. Journal of General Virology, 2011, 92, 2297-2309.	2.9	40
21	Mapping of amino acid residues responsible for adhesion of cell culture-adapted foot-and-mouth disease SAT type viruses. Virus Research, 2010, 153, 82-91.	2.2	40
22	In silico Discovery of Chemotherapeutic Agents. , 2010, , 279-304.		0
23	Sequence-Based Prediction for Vaccine Strain Selection and Identification of Antigenic Variability in Foot-and-Mouth Disease Virus. PLoS Computational Biology, 2010, 6, e1001027.	3.2	63
24	The Malarial Drug Target Plasmodium falciparum 1-Deoxy-D-Xylulose-5- Phosphate Reductoisomerase (PfDXR): Development of a 3-D Model for Identification of Novel, Structural and Functional Features and for Inhibitor Screening (Supplementary Information). Protein and Peptide Letters, 2010, 17, 109-120.	0.9	14
25	Discovery: an interactive resource for the rational selection and comparison of putative drug target proteins in malaria. Malaria Journal, 2009, 8, 178.	2.3	9
26	Structure-Function Study of a Plasmodium falciparum Hsp70 Using Three Dimensional Modelling and in Vitro Analyses. Protein and Peptide Letters, 2008, 15, 1117-1125.	0.9	55
27	Elucidation of sulfadoxine resistance with structural models of the bifunctional Plasmodium falciparum dihydropterin pyrophosphokinaseâ€“dihydropteroate synthase. Bioorganic and Medicinal Chemistry, 2006, 14, 4433-4443.	3.0	22