

Michael J Kuiper

List of Publications by Year in descending order

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Version: 2024-02-01

37
papers

2,684
citations

304743

22
h-index

345221

36
g-index

40
all docs

40
docs citations

40
times ranked

3456
citing authors

#	ARTICLE	IF	CITATIONS
1	Live Virus Neutralisation of the 501Y.V1 and 501Y.V2 SARS-CoV-2 Variants following INO-4800 Vaccination of Ferrets. <i>Frontiers in Immunology</i> , 2021, 12, 694857.	4.8	9
2	Experimental and in silico evidence suggests vaccines are unlikely to be affected by D614G mutation in SARS-CoV-2 spike protein. <i>Npj Vaccines</i> , 2020, 5, 96.	6.0	56
3	The structure of the PA28 α 20S proteasome complex from <i>Plasmodium falciparum</i> and implications for proteostasis. <i>Nature Microbiology</i> , 2019, 4, 1990-2000.	13.3	31
4	The Structural Basis for a Transition State That Regulates Pore Formation in a Bacterial Toxin. <i>MBio</i> , 2019, 10, .	4.1	10
5	A structural basis for the amphiphilic character of alginates α Implications for membrane fouling. <i>Carbohydrate Polymers</i> , 2017, 164, 162-169.	10.2	26
6	Secondary Somatic Mutations Restoring <i>RAD51C</i> and <i>RAD51D</i> Associated with Acquired Resistance to the PARP Inhibitor Rucaparib in High-Grade Ovarian Carcinoma. <i>Cancer Discovery</i> , 2017, 7, 984-998.	9.4	310
7	Structural Basis for Receptor Recognition by the Human CD59-Responsive Cholesterol-Dependent Cytolysins. <i>Structure</i> , 2016, 24, 1488-1498.	3.3	34
8	The biological function of an insect antifreeze protein simulated by molecular dynamics. <i>ELife</i> , 2015, 4, .	6.0	85
9	An intermolecular electrostatic interaction controls the prepore-to-pore transition in a cholesterol-dependent cytolysin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 2204-2209.	7.1	44
10	Structural Studies of <i>Streptococcus pyogenes</i> Streptolysin O Provide Insights into the Early Steps of Membrane Penetration. <i>Journal of Molecular Biology</i> , 2014, 426, 785-792.	4.2	61
11	Manipulating the Lewis antigen specificity of the cholesterol-dependent cytolysin lectinolysin. <i>Frontiers in Immunology</i> , 2012, 3, 330.	4.8	8
12	Investigation of a predicted N-terminal amphipathic α -helix using atomistic molecular dynamics simulation of a complete prototype poliovirus virion. <i>Journal of Molecular Graphics and Modelling</i> , 2012, 38, 165-173.	2.4	18
13	BetaSearch: a new method for querying β^2 -residue motifs. <i>BMC Research Notes</i> , 2012, 5, 391.	1.4	1
14	Inner Ear Morphology Is Perturbed in Two Novel Mouse Models of Recessive Deafness. <i>PLoS ONE</i> , 2012, 7, e51284.	2.5	11
15	In silico modeling of the Menkes copper-translocating P-type ATPase 3rd metal binding domain predicts that phosphorylation regulates copper-binding. <i>BioMetals</i> , 2011, 24, 477-487.	4.1	6
16	The structural basis for membrane binding and pore formation by lymphocyte perforin. <i>Nature</i> , 2010, 468, 447-451.	27.8	364
17	Ice recrystallization inhibition proteins (IRIPs) and freeze tolerance in the cryophilic Antarctic hair grass <i>Deschampsia antarctica</i> E. Desv.. <i>Plant, Cell and Environment</i> , 2009, 32, 336-348.	5.7	69
18	Antifreeze protein from shorthorn sculpin: Identification of the ice-binding surface. <i>Protein Science</i> , 2009, 10, 2566-2576.	7.6	53

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19	The MACPF/CDC family of pore-forming toxins. <i>Cellular Microbiology</i> , 2008, 10, 1765-1774.	2.1	250
20	PConPyâ€”a Python module for generating 2D protein maps. <i>Bioinformatics</i> , 2008, 24, 2934-2935.	4.1	13
21	Ice recrystallisation inhibition proteins (IRIPs) and freeze tolerance in the cryophilic Antarctic hairgrass <i>Deschampsia antarctica</i> E. Desv.. <i>Plant, Cell and Environment</i> , 2008, 32, 336-48.	5.7	19
22	Insertion Sequence 1 of Muscle-specific Calpain, p94, Acts as an Internal Propeptide. <i>Journal of Biological Chemistry</i> , 2004, 279, 27656-27666.	3.4	48
23	New Simulation Model of Multicomponent Crystal Growth And Inhibition. <i>Chemistry - A European Journal</i> , 2004, 10, 1598-1605.	3.3	12
24	Partitioning of Fish and Insect Antifreeze Proteins into Ice Suggests They Bind with Comparable Affinityâ€”. <i>Biochemistry</i> , 2004, 43, 148-154.	2.5	33
25	Ligand specificity and developmental expression of RXR and ecdysone receptor in the migratory locust. <i>Journal of Insect Physiology</i> , 2003, 49, 1135-1144.	2.0	48
26	A New Model for Simulating 3-D Crystal Growth and Its Application to the Study of Antifreeze Proteins. <i>Journal of the American Chemical Society</i> , 2003, 125, 729-737.	13.7	39
27	Purification of antifreeze proteins by adsorption to ice. <i>Biochemical and Biophysical Research Communications</i> , 2003, 300, 645-648.	2.1	110
28	Three-dimensional simulation of ice growth in the presence of antifreeze proteins. <i>Canadian Journal of Physics</i> , 2003, 81, 39-45.	1.1	3
29	Antifreeze Protein Dimer. <i>Journal of Biological Chemistry</i> , 2003, 278, 38942-38947.	3.4	50
30	Structure and function of antifreeze proteins. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2002, 357, 927-935.	4.0	271
31	Structural variation in a novel zinc finger protein and investigation of its role in Hirschsprung disease. <i>Gene Function & Disease</i> , 2002, 3, 69-76.	0.3	3
32	Rational design of alpha-helical antifreeze peptides. <i>Chemical Biology and Drug Design</i> , 2002, 59, 1-8.	1.1	14
33	A Theoretical Model of a Plant Antifreeze Protein from <i>Lolium perenne</i> . <i>Biophysical Journal</i> , 2001, 81, 3560-3565.	0.5	85
34	Surviving winter with antifreeze proteins. , 2001, , 199-211.		6
35	Tobacco budworm dihydrofolate reductase is a promising target for insecticide discovery. <i>FEBS Journal</i> , 2000, 267, 394-403.	0.2	9
36	Structure-function relationships in spruce budworm antifreeze protein revealed by isoform diversity. <i>FEBS Journal</i> , 2000, 267, 6082-6088.	0.2	58

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37	Î²-Helix structure and ice-binding properties of a hyperactive antifreeze protein from an insect. Nature, 2000, 406, 325-328.	27.8	410