

Michael Kokkinidis

List of Publications by Year in descending order

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43
papers

1,322
citations

586496

16
h-index

388640

36
g-index

44
all docs

44
docs citations

44
times ranked

1745
citing authors

#	ARTICLE	IF	CITATIONS
1	Crystal structure of glutamate dehydrogenase 2, a positively selected novel human enzyme involved in brain biology and cancer pathophysiology. <i>Journal of Neurochemistry</i> , 2021, 157, 802-815.	2.1	8
2	Probing Protein Folding with Sequence-Reversed α -Helical Bundles. <i>International Journal of Molecular Sciences</i> , 2021, 22, 1955.	1.8	8
3	α -Helices in the Type III Secretion Effectors: A Prevalent Feature with Versatile Roles. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5412.	1.8	4
4	Structure and Thermal Stability of wtRop and RM6 Proteins through All-Atom Molecular Dynamics Simulations and Experiments. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5931.	1.8	7
5	Probing the Structural Dynamics of the Catalytic Domain of Human Soluble Guanylate Cyclase. <i>Scientific Reports</i> , 2020, 10, 9488.	1.6	4
6	Catalytic activity regulation through post-translational modification: the expanding universe of protein diversity. <i>Advances in Protein Chemistry and Structural Biology</i> , 2020, 122, 97-125.	1.0	10
7	Dynamic Characterization of the Human Heme Nitric Oxide/Oxygen (HNOX) Domain under the Influence of Diatomic Gaseous Ligands. <i>International Journal of Molecular Sciences</i> , 2019, 20, 698.	1.8	5
8	Migration of Type III Secretion System Transcriptional Regulators Links Gene Expression to Secretion. <i>MBio</i> , 2018, 9, .	1.8	9
9	Unusual α -Carbon Hydroxylation of Proline Promotes Active-Site Maturation. <i>Journal of the American Chemical Society</i> , 2017, 139, 5330-5337.	6.6	20
10	Expression, purification and crystallization of a protein resulting from the inversion of the amino-acid sequence of a helical bundle. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2017, 73, 51-53.	0.4	2
11	HrpG and HrpV proteins from the Type III secretion system of <i>Erwinia amylovora</i> form a stable heterodimer. <i>FEMS Microbiology Letters</i> , 2015, 362, 1-8.	0.7	9
12	Side-chain interactions in the regulatory domain of human glutamate dehydrogenase determine basal activity and regulation. <i>Journal of Neurochemistry</i> , 2015, 133, 73-82.	2.1	8
13	Structural plasticity of α -helical bundles exemplified by the puzzle-like molecular assembly of the Rop protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 11049-11054.	3.3	17
14	The benefit of the European User Community from transnational access to national radiation facilities. <i>Journal of Synchrotron Radiation</i> , 2014, 21, 638-639.	1.0	2
15	Structure determination through homology modelling and torsion-angle simulated annealing: application to a polysaccharide deacetylase from <i>Bacillus cereus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 276-283.	2.5	19
16	Phylogenetic analysis of a gene cluster encoding an additional, rhizobial-like type III secretion system that is narrowly distributed among <i>Pseudomonas syringae</i> strains. <i>BMC Microbiology</i> , 2012, 12, 188.	1.3	49
17	α -Protein Flexibility and Coiled-Coil Propensity: New Insights Into Type III and Other Bacterial Secretion Systems. , 2012, , .		2
18	Controlling the enzymatic activity of a restriction enzyme by light. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 1361-1366.	3.3	163

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19	Playing the "Harp": Evolution of Our Understanding of <i>hrp/hrc</i> Genes. Annual Review of Phytopathology, 2010, 48, 347-370.	3.5	116
20	Coiled-coils in type III secretion systems: structural flexibility, disorder and biological implications. Cellular Microbiology, 2009, 11, 719-729.	1.1	39
21	Molecular Dynamics Simulations of BcZBP, A Deacetylase from Bacillus cereus: Active Site Loops Determine Substrate Accessibility and Specificity. Journal of Chemical Theory and Computation, 2009, 5, 3299-3311.	2.3	9
22	Purification, crystallization and preliminary X-ray analysis of the peptidoglycan <i>N</i> -acetylglucosamine deacetylase BC1960 from <i>Bacillus cereus</i> in the presence of its substrate (GlcNAc) ₆ . Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 203-205.	0.7	4
23	Purification, crystallization and preliminary X-ray diffraction analysis of a variant of the ColE1 Rop protein. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 432-434.	0.7	5
24	Evidence for a Coiled-coil Interaction Mode of Disordered Proteins from Bacterial Type III Secretion Systems. Journal of Biological Chemistry, 2008, 283, 34062-34068.	1.6	38
25	Crystal structure of the BcZBP, a zinc-binding protein from Bacillus cereus. FEBS Journal, 2007, 274, 3044-3054.	2.2	28
26	Loopless Rop: Structure and Dynamics of an Engineered Homotetrameric Variant of the Repressor of Primer Protein. Biochemistry, 2006, 45, 10905-10919.	1.2	17
27	Structure of HrcQB-C, a conserved component of the bacterial type III secretion systems. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 70-75.	3.3	62
28	Structural polymorphism of a marginally stable 4-helical bundle. Images of a trapped molten globule?. Proteins: Structure, Function and Bioinformatics, 2004, 56, 420-425.	1.5	13
29	Structure determination of a small protein through a 23-dimensional molecular-replacement search. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 709-718.	2.5	13
30	Structural and Biochemical Characterization of a New Mg ²⁺ Binding Site Near Tyr94 in the Restriction Endonuclease PvuII. Journal of Molecular Biology, 2003, 331, 395-406.	2.0	16
31	Engineering the properties of a cold active enzyme through rational redesign of the active site. FEBS Journal, 2001, 268, 5074-5080.	0.2	31
32	Side-chain conformations in 4-helical bundles. Protein Engineering, Design and Selection, 2001, 14, 321-328.	1.0	7
33	GraphEnt: a maximum-entropy program with graphics capabilities. Journal of Applied Crystallography, 2000, 33, 982-985.	1.9	6
34	Meaningful refinement of polyalanine models using rigid-body simulated annealing: application to the structure determination of the A31P Rop mutant. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 1301-1308.	2.5	4
35	Protein plasticity to the extreme: changing the topology of a 4-helical bundle with a single amino acid substitution. Structure, 1999, 7, 597-603.	1.6	54
36	The crystal structures of the synthetic C-terminal octa- and dodecapeptides of trichovirin. , 1999, 5, 83-95.		7

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37	A correlation between the loss of hydrophobic core packing interactions and protein stability 1 Edited by A. R. Fersht. Journal of Molecular Biology, 1999, 285, 817-827.	2.0	67
38	Dimer-to-tetramer transformation: loop excision dramatically alters structure and stability of the ROP four α -helix bundle protein. Journal of Molecular Biology, 1998, 279, 987-1000.	2.0	33
39	Restored heptad pattern continuity does not alter the folding of a four- α -helix bundle. Nature Structural and Molecular Biology, 1994, 1, 706-716.	3.6	39
40	Correlation between protein stability and crystal properties of designed ROP variants. Proteins: Structure, Function and Bioinformatics, 1993, 16, 214-216.	1.5	12
41	Relationships between sequence and structure for the four- α -helix bundle tertiary motif in proteins. Protein Engineering, Design and Selection, 1992, 5, 739-748.	1.0	33
42	Purification, crystallization and preliminary X-ray diffraction studies of the PvuII endonuclease. Journal of Molecular Biology, 1991, 222, 451-453.	2.0	11
43	Structure of the ColE1 Rop protein at 1.7 Å... resolution. Journal of Molecular Biology, 1987, 196, 657-675.	2.0	312