

Michael Kokkinidis

List of Publications by Year in descending order

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43
papers

1,322
citations

516710

16
h-index

345221

36
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44
all docs

44
docs citations

44
times ranked

1552
citing authors

#	ARTICLE	IF	CITATIONS
1	Structure of the ColE1 Rop protein at 1.7 Å... resolution. <i>Journal of Molecular Biology</i> , 1987, 196, 657-675.	4.2	312
2	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.	7.1	163
3	Playing the "Harp": Evolution of Our Understanding of <i>hrp/hrc</i> Genes. <i>Annual Review of Phytopathology</i> , 2010, 48, 347-370.	7.8	116
4	A correlation between the loss of hydrophobic core packing interactions and protein stability 1 Edited by A. R. Fersht. <i>Journal of Molecular Biology</i> , 1999, 285, 817-827.	4.2	67
5	Structure of HrcQB-C, a conserved component of the bacterial type III secretion systems. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 70-75.	7.1	62
6	Protein plasticity to the extreme: changing the topology of a 4- α -helical bundle with a single amino acid substitution. <i>Structure</i> , 1999, 7, 597-603.	3.3	54
7	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.	3.3	49
8	Restored heptad pattern continuity does not alter the folding of a four- α -helix bundle. <i>Nature Structural and Molecular Biology</i> , 1994, 1, 706-716.	8.2	39
9	Coiled-coils in type III secretion systems: structural flexibility, disorder and biological implications. <i>Cellular Microbiology</i> , 2009, 11, 719-729.	2.1	39
10	Evidence for a Coiled-coil Interaction Mode of Disordered Proteins from Bacterial Type III Secretion Systems. <i>Journal of Biological Chemistry</i> , 2008, 283, 34062-34068.	3.4	38
11	Relationships between sequence and structure for the four- α -helix bundle tertiary motif in proteins. <i>Protein Engineering, Design and Selection</i> , 1992, 5, 739-748.	2.1	33
12	Dimer-to-tetramer transformation: loop excision dramatically alters structure and stability of the ROP four α -helix bundle protein. <i>Journal of Molecular Biology</i> , 1998, 279, 987-1000.	4.2	33
13	Engineering the properties of a cold active enzyme through rational redesign of the active site. <i>FEBS Journal</i> , 2001, 268, 5074-5080.	0.2	31
14	Crystal structure of the BcZBP, a zinc-binding protein from <i>Bacillus cereus</i> . <i>FEBS Journal</i> , 2007, 274, 3044-3054.	4.7	28
15	Unusual α -Carbon Hydroxylation of Proline Promotes Active-Site Maturation. <i>Journal of the American Chemical Society</i> , 2017, 139, 5330-5337.	13.7	20
16	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
17	Loopless Rop: Structure and Dynamics of an Engineered Homotetrameric Variant of the Repressor of Primer Protein. <i>Biochemistry</i> , 2006, 45, 10905-10919.	2.5	17
18	Structural plasticity of 4- 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.	7.1	17

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19	Structural and Biochemical Characterization of a New Mg ²⁺ Binding Site Near Tyr94 in the Restriction Endonuclease PvuII. <i>Journal of Molecular Biology</i> , 2003, 331, 395-406.	4.2	16
20	Structure determination of a small protein through a 23-dimensional molecular-replacement search. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 709-718.	2.5	13
21	Structural polymorphism of a marginally stable 4- α -helical bundle. Images of a trapped molten globule?. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 56, 420-425.	2.6	13
22	Correlation between protein stability and crystal properties of designed ROP variants. <i>Proteins: Structure, Function and Bioinformatics</i> , 1993, 16, 214-216.	2.6	12
23	Purification, crystallization and preliminary X-ray diffraction studies of the PvuII endonuclease. <i>Journal of Molecular Biology</i> , 1991, 222, 451-453.	4.2	11
24	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.	2.3	10
25	Molecular Dynamics Simulations of BcZBP, A Deacetylase from <i>Bacillus cereus</i> : Active Site Loops Determine Substrate Accessibility and Specificity. <i>Journal of Chemical Theory and Computation</i> , 2009, 5, 3299-3311.	5.3	9
26	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.	1.8	9
27	Migration of Type III Secretion System Transcriptional Regulators Links Gene Expression to Secretion. <i>MBio</i> , 2018, 9, .	4.1	9
28	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.	3.9	8
29	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.	3.9	8
30	Probing Protein Folding with Sequence-Reversed α -Helical Bundles. <i>International Journal of Molecular Sciences</i> , 2021, 22, 1955.	4.1	8
31	The crystal structures of the synthetic C-terminal octa- and dodecapeptides of trichovirin. , 1999, 5, 83-95.		7
32	Side-chain conformations in 4- α -helical bundles. <i>Protein Engineering, Design and Selection</i> , 2001, 14, 321-328.	2.1	7
33	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.	4.1	7
34	GraphEnt: a maximum-entropy program with graphics capabilities. <i>Journal of Applied Crystallography</i> , 2000, 33, 982-985.	4.5	6
35	Purification, crystallization and preliminary X-ray diffraction analysis of a variant of the ColE1 Rop protein. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 432-434.	0.7	5
36	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.	4.1	5

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37	Meaningful refinement of polyalanine models using rigid-body simulated annealing: application to the structure determination of the A31P Rop mutant. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 1301-1308.	2.5	4
38	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 . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 203-205.	0.7	4
39	Probing the Structural Dynamics of the Catalytic Domain of Human Soluble Guanylate Cyclase. <i>Scientific Reports</i> , 2020, 10, 9488.	3.3	4
40	Î±-Helices in the Type III Secretion Effectors: A Prevalent Feature with Versatile Roles. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5412.	4.1	4
41	Protein Flexibility and Coiled-Coil Propensity: New Insights Into Type III and Other Bacterial Secretion Systems. , 2012, , .		2
42	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.	0.8	2
43	The benefit of the European User Community from transnational access to national radiation facilities. <i>Journal of Synchrotron Radiation</i> , 2014, 21, 638-639.	2.4	2