

# Constantina Bakolitsa

## List of Publications by Year in descending order

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34  
papers

1,167  
citations

623188

14  
h-index

395343

33  
g-index

34  
all docs

34  
docs citations

34  
times ranked

1680  
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural basis for vinculin activation at sites of cell adhesion. <i>Nature</i> , 2004, 430, 583-586.	13.7	356
2	Crystal Structure of the Vinculin Tail Suggests a Pathway for Activation. <i>Cell</i> , 1999, 99, 603-613.	13.5	183
3	Exploration of Uncharted Regions of the Protein Universe. <i>PLoS Biology</i> , 2009, 7, e1000205.	2.6	123
4	Correlated firing among major ganglion cell types in primate retina. <i>Journal of Physiology</i> , 2011, 589, 75-86.	1.3	65
5	Structure of the $\hat{I}^3$ -D-glutamyl-L-diamino acid endopeptidase YkfC from <i>Bacillus cereus</i> in complex with L-Ala- $\hat{I}^3$ -D-Glu: insights into substrate recognition by NlpC/P60 cysteine peptidases. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1354-1364.	0.7	64
6	Structure of the $\hat{I}^{\pm}$ -Actinin-Vinculin Head Domain Complex Determined by Cryo-electron Microscopy. <i>Journal of Molecular Biology</i> , 2006, 357, 562-573.	2.0	36
7	TOPSAN: use of a collaborative environment for annotating, analyzing and disseminating data on JCSC and PSI structures. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1143-1147.	0.7	33
8	Bacterial Pleckstrin Homology Domains: A Prokaryotic Origin for the PH Domain. <i>Journal of Molecular Biology</i> , 2010, 396, 31-46.	2.0	32
9	Structure of a membrane-attack complex/perforin (MACPF) family protein from the human gut symbiont <i>Bacteroides thetaiotaomicron</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1297-1305.	0.7	30
10	Structural and Functional Characterizations of SsgB, a Conserved Activator of Developmental Cell Division in Morphologically Complex Actinomycetes. <i>Journal of Biological Chemistry</i> , 2009, 284, 25268-25279.	1.6	23
11	The structure of SSO2064, the first representative of Pfam family PF01796, reveals a novel two-domain zinc-ribbon OB-fold architecture with a potential acyl-CoA-binding role. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1160-1166.	0.7	20
12	TOPSAN: a collaborative annotation environment for structural genomics. <i>BMC Bioinformatics</i> , 2010, 11, 426.	1.2	19
13	Structure of the first representative of Pfam family PF09410 (DUF2006) reveals a structural signature of the calycin superfamily that suggests a role in lipid metabolism. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1153-1159.	0.7	18
14	TOPSAN: a dynamic web database for structural genomics. <i>Nucleic Acids Research</i> , 2011, 39, D494-D496.	6.5	17
15	The crystal structure of a bacterial Sufu-like protein defines a novel group of bacterial proteins that are similar to the N-terminal domain of human Sufu. <i>Protein Science</i> , 2010, 19, 2131-2140.	3.1	12
16	Structure of BT_3984, a member of the SusD/RagB family of nutrient-binding molecules. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1274-1280.	0.7	11
17	Two-wavelength MAD phasing and radiation damage: a case study. <i>Journal of Synchrotron Radiation</i> , 2005, 12, 285-291.	1.0	10
18	The structure of the first representative of Pfam family PF06475 reveals a new fold with possible involvement in glycolipid metabolism. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1211-1217.	0.7	10

#	ARTICLE	IF	CITATIONS
19	CAGI SickKids challenges: Assessment of phenotype and variant predictions derived from clinical and genomic data of children with undiagnosed diseases. <i>Human Mutation</i> , 2019, 40, 1373-1391.	1.1	10
20	Assessment of predicted enzymatic activity of <i>N</i> -acetylglucosaminidase variants of unknown significance for CAGI 2016. <i>Human Mutation</i> , 2019, 40, 1519-1529.	1.1	10
21	The structure of Jann_2411 (DUF1470) from <i>Jannaschia</i> sp. at 1.45 Å resolution reveals a new fold (the ABATE domain) and suggests its possible role as a transcription regulator. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1198-1204.	0.7	9
22	A conserved fold for fimbrial components revealed by the crystal structure of a putative fimbrial assembly protein (BT1062) from <i>Bacteroides thetaiotaomicron</i> at 2.2 Å resolution. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1281-1286.	0.7	9
23	Crystal structure of an orphan protein (TM0875) from <i>Thermotoga maritima</i> at 2.00 Å resolution reveals a new fold. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 56, 607-610.	1.5	8
24	The structure of the first representative of Pfam family PF09836 reveals a two-domain organization and suggests involvement in transcriptional regulation. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1174-1181.	0.7	8
25	The structure of BVU2987 from <i>Bacteroides vulgatus</i> reveals a superfamily of bacterial periplasmic proteins with possible inhibitory function. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1265-1273.	0.7	8
26	Structures of the first representatives of Pfam family PF06938 (DUF1285) reveal a new fold with repeated structural motifs and possible involvement in signal transduction. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1218-1225.	0.7	8
27	Structures of three members of Pfam PF02663 (FmdE) implicated in microbial methanogenesis reveal a conserved $\beta^2$ core domain and an auxiliary C-terminal treble-clef zinc finger. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1335-1346.	0.7	8
28	LUD, a new protein domain associated with lactate utilization. <i>BMC Bioinformatics</i> , 2013, 14, 341.	1.2	8
29	Assessing computational predictions of the phenotypic effect of cystathionine $\beta$ -synthase variants. <i>Human Mutation</i> , 2019, 40, 1530-1545.	1.1	5
30	The structure of KPN03535 (gi 152972051), a novel putative lipoprotein from <i>Klebsiella pneumoniae</i> , reveals an OB-fold. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1254-1260.	0.7	3
31	Structure of LP2179, the first representative of Pfam family PF08866, suggests a new fold with a role in amino-acid metabolism. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1205-1210.	0.7	3
32	Structures of the first representatives of Pfam family PF06684 (DUF1185) reveal a novel variant of the <i>Bacillus</i> chorismate mutase fold and suggest a role in amino-acid metabolism. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1182-1189.	0.7	3
33	Structure of the first representative of Pfam family PF04016 (DUF364) reveals enolase and Rossmann-like folds that combine to form a unique active site with a possible role in heavy-metal chelation. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1167-1173.	0.7	3
34	Structure of <i>Bacteroides thetaiotaomicron</i> BT2081 at 2.05 Å resolution: the first structural representative of a new protein family that may play a role in carbohydrate metabolism. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1287-1296.	0.7	2