

Evangelos Christodoulou

List of Publications by Year in descending order

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Version: 2024-02-01

28
papers

2,769
citations

361413

20
h-index

526287

27
g-index

29
all docs

29
docs citations

29
times ranked

4686
citing authors

#	ARTICLE	IF	CITATIONS
1	HIV-1 restriction factor SAMHD1 is a deoxynucleoside triphosphate triphosphohydrolase. <i>Nature</i> , 2011, 480, 379-382.	27.8	707
2	Evolution of the receptor binding properties of the influenza A(H3N2) hemagglutinin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 21474-21479.	7.1	250
3	Structural basis of substrate discrimination and integrin binding by autotaxin. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 198-204.	8.2	247
4	LUBAC synthesizes linear ubiquitin chains via a thioester intermediate. <i>EMBO Reports</i> , 2012, 13, 840-846.	4.5	198
5	Inhibition of Autotaxin by Lysophosphatidic Acid and Sphingosine 1-Phosphate. <i>Journal of Biological Chemistry</i> , 2005, 280, 21155-21161.	3.4	178
6	Structural basis for ligase-specific conjugation of linear ubiquitin chains by HOIP. <i>Nature</i> , 2013, 503, 422-426.	27.8	174
7	Functional role of <scp>TRIM</scp> E3 ligase oligomerization and regulation of catalytic activity. <i>EMBO Journal</i> , 2016, 35, 1204-1218.	7.8	141
8	Structural basis of lentiviral subversion of a cellular protein degradation pathway. <i>Nature</i> , 2014, 505, 234-238.	27.8	115
9	Co-expression of protein complexes in prokaryotic and eukaryotic hosts: experimental procedures, database tracking and case studies. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 1232-1242.	2.5	113
10	Enabling high-throughput ligation-independent cloning and protein expression for the family of ubiquitin specific proteases. <i>Journal of Structural Biology</i> , 2011, 175, 113-119.	2.8	91
11	A cryptic RNA-binding domain mediates Syncrip recognition and exosomal partitioning of miRNA targets. <i>Nature Communications</i> , 2018, 9, 831.	12.8	86
12	The protein that binds to DNA base J in trypanosomatids has features of a thymidine hydroxylase. <i>Nucleic Acids Research</i> , 2007, 35, 2107-2115.	14.5	84
13	Chemical genetic identification of <scp>CDKL</scp> 5 substrates reveals its role in neuronal microtubule dynamics. <i>EMBO Journal</i> , 2018, 37, .	7.8	57
14	Molecular Determinants for Recognition of Divergent SAMHD1 Proteins by the Lentiviral Accessory Protein Vpx. <i>Cell Host and Microbe</i> , 2015, 17, 489-499.	11.0	51
15	The malaria parasite egress protease SUB1 is a calcium-dependent redox switch subtilisin. <i>Nature Communications</i> , 2014, 5, 3726.	12.8	43
16	High-resolution X-ray structure of the DNA-binding protein HU from the hyper-thermophilic <i>Thermotoga maritima</i> and the determinants of its thermostability. <i>Extremophiles</i> , 2003, 7, 111-122.	2.3	42
17	The structural basis for recognition of base J containing DNA by a novel DNA binding domain in JBP1. <i>Nucleic Acids Research</i> , 2011, 39, 5715-5728.	14.5	32
18	The thermostability of DNA-binding protein HU from mesophilic, thermophilic, and extreme thermophilic bacteria. <i>Extremophiles</i> , 2002, 6, 21-31.	2.3	28

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19	Mammalian cell expression, purification, crystallization and microcrystal data collection of autotaxin/ENPP2, a secreted mammalian glycoprotein. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1130-1135.	0.7	25
20	Ubiquitin activation is essential for schizont maturation in <i>Plasmodium falciparum</i> blood-stage development. <i>PLoS Pathogens</i> , 2020, 16, e1008640.	4.7	24
21	Overexpression, Purification, and Characterization of a Thermostable Chitinase (Chi40) from <i>Streptomyces thermoviolaceus</i> OPC-520. <i>Protein Expression and Purification</i> , 2001, 23, 97-105.	1.3	20
22	Thermodynamic analysis of the unfolding and stability of the dimeric DNA-binding protein HU from the hyperthermophilic eubacterium <i>Thermotoga maritima</i> and its E34D mutant. <i>FEBS Journal</i> , 2004, 271, 1497-1507.	0.2	20
23	Target highlights in CASP9: Experimental target structures for the critical assessment of techniques for protein structure prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 6-20.	2.6	19
24	The Biophysical Characterisation and SAXS Analysis of Human NLRP1 Uncover a New Level of Complexity of NLR Proteins. <i>PLoS ONE</i> , 2016, 11, e0164662.	2.5	12
25	The Arabidopsis (ASHH2) CW domain binds monomethylated K4 of the histone H3 tail through conformational selection. <i>FEBS Journal</i> , 2020, 287, 4458-4480.	4.7	4
26	Understanding heterologous protein overproduction under the T7 promoter: A practical exercise. <i>Biochemistry and Molecular Biology Education</i> , 2002, 30, 189-191.	1.2	3
27	Small Molecule Inhibitor Targeting CDT1/Geminin Protein Complex Promotes DNA Damage and Cell Death in Cancer Cells. <i>Frontiers in Pharmacology</i> , 2022, 13, 860682.	3.5	3
28	The distinct RNA-interaction modes of a small ZnF domain underlay TUT4(7) diverse action in miRNA regulation. <i>RNA Biology</i> , 2021, , 1-12.	3.1	0