

Lukasz Kozlowski

List of Publications by Year in descending order

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Version: 2024-02-01

20
papers

1,506
citations

516710

16
h-index

677142

22
g-index

27
all docs

27
docs citations

27
times ranked

2875
citing authors

#	ARTICLE	IF	CITATIONS
1	Proteome- <i>pI</i> 2.0: proteome isoelectric point database update. <i>Nucleic Acids Research</i> , 2022, 50, D1535-D1540.	14.5	18
2	IPC 2.0: prediction of isoelectric point and <i>pKa</i> dissociation constants. <i>Nucleic Acids Research</i> , 2021, 49, W285-W292.	14.5	67
3	Going to extremes – a metagenomic journey into the dark matter of life. <i>FEMS Microbiology Letters</i> , 2021, 368, .	1.8	16
4	Novel Lytic Enzyme of Prophage Origin from <i>Clostridium botulinum</i> E3 Strain Alaska E43 with Bactericidal Activity against Clostridial Cells. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9536.	4.1	5
5	A High-Throughput Screen for Transcription Activation Domains Reveals Their Sequence Features and Permits Prediction by Deep Learning. <i>Molecular Cell</i> , 2020, 78, 890-902.e6.	9.7	70
6	Structure and function of the Ts2631 endolysin of <i>Thermus scotoductus</i> phage ν B_Tsc2631 with unique N-terminal extension used for peptidoglycan binding. <i>Scientific Reports</i> , 2019, 9, 1261.	3.3	28
7	Proteome- <i>pI</i> : proteome isoelectric point database. <i>Nucleic Acids Research</i> , 2017, 45, D1112-D1116.	14.5	209
8	IPC – Isoelectric Point Calculator. <i>Biology Direct</i> , 2016, 11, 55.	4.6	308
9	MQAPsingle: A quasi single-model approach for estimation of the quality of individual protein structure models. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 1021-1028.	2.6	21
10	Sequence-specific cleavage of dsRNA by Mini-III RNase. <i>Nucleic Acids Research</i> , 2015, 43, 2864-2873.	14.5	28
11	Biochemical Characterization and Validation of a Catalytic Site of a Highly Thermostable Ts2631 Endolysin from the <i>Thermus scotoductus</i> Phage ν B_Tsc2631. <i>PLoS ONE</i> , 2015, 10, e0137374.	2.5	38
12	GDFuzz3D: a method for protein 3D structure reconstruction from contact maps, based on a non-Euclidean distance function. <i>Bioinformatics</i> , 2015, 31, 3499-3505.	4.1	33
13	Novel Highly Thermostable Endolysin from <i>Thermus scotoductus</i> MAT2119 Bacteriophage Ph2119 with Amino Acid Sequence Similarity to Eukaryotic Peptidoglycan Recognition Proteins. <i>Applied and Environmental Microbiology</i> , 2014, 80, 886-895.	3.1	35
14	Computational modeling of protein-RNA complex structures. <i>Methods</i> , 2014, 65, 310-319.	3.8	27
15	Female-specific gene expression in dioecious liverwort <i>Pellia endiviifolia</i> is developmentally regulated and connected to archegonia production. <i>BMC Plant Biology</i> , 2014, 14, 168.	3.6	5
16	CompaRNA: a server for continuous benchmarking of automated methods for RNA secondary structure prediction. <i>Nucleic Acids Research</i> , 2013, 41, 4307-4323.	14.5	105
17	Crohn's Disease Risk Alleles on the NOD2 Locus Have Been Maintained by Natural Selection on Standing Variation. <i>Molecular Biology and Evolution</i> , 2012, 29, 1569-1585.	8.9	21
18	Computational methods for prediction of protein-RNA interactions. <i>Journal of Structural Biology</i> , 2012, 179, 261-268.	2.8	112

#	ARTICLE	IF	CITATIONS
19	MetaDisorder: a meta-server for the prediction of intrinsic disorder in proteins. BMC Bioinformatics, 2012, 13, 111.	2.6	294
20	A novel homozygous p.Arg527Leu LMNA mutation in two unrelated Egyptian families causes overlapping mandibuloacral dysplasia and progeria syndrome. European Journal of Human Genetics, 2012, 20, 1134-1140.	2.8	31