

Ivica Letunic

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8885367/publications.pdf>

Version: 2024-02-01

71
papers

63,672
citations

26630
56
h-index

85541
71
g-index

74
all docs

74
docs citations

74
times ranked

75382
citing authors

#	ARTICLE	IF	CITATIONS
1	Initial sequencing and comparative analysis of the mouse genome. Nature, 2002, 420, 520-562.	27.8	6,319
2	Interactive tree of life (iTOL) v3: an online tool for the display and annotation of phylogenetic and other trees. Nucleic Acids Research, 2016, 44, W242-W245.	14.5	4,967
3	Interactive Tree Of Life (iTOL) v5: an online tool for phylogenetic tree display and annotation. Nucleic Acids Research, 2021, 49, W293-W296.	14.5	4,856
4	Interactive Tree Of Life (iTOL) v4: recent updates and new developments. Nucleic Acids Research, 2019, 47, W256-W259.	14.5	4,604
5	Interactive Tree Of Life (iTOL): an online tool for phylogenetic tree display and annotation. Bioinformatics, 2007, 23, 127-128.	4.1	2,609
6	eggNOG 5.0: a hierarchical, functionally and phylogenetically annotated orthology resource based on 5090 organisms and 2502 viruses. Nucleic Acids Research, 2019, 47, D309-D314.	14.5	2,575
7	Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. Nature, 2004, 432, 695-716.	27.8	2,421
8	Pan-cancer analysis of whole genomes. Nature, 2020, 578, 82-93.	27.8	1,966
9	The Genome Sequence of the Malaria Mosquito <i>Anopheles gambiae</i> . Science, 2002, 298, 129-149.	12.6	1,859
10	InterPro: the integrative protein signature database. Nucleic Acids Research, 2009, 37, D211-D215.	14.5	1,712
11	Insights into social insects from the genome of the honeybee <i>Apis mellifera</i> . Nature, 2006, 443, 931-949.	27.8	1,648
12	20 years of the SMART protein domain annotation resource. Nucleic Acids Research, 2018, 46, D493-D496.	14.5	1,525
13	SMART: recent updates, new developments and status in 2015. Nucleic Acids Research, 2015, 43, D257-D260.	14.5	1,519
14	SMART 7: recent updates to the protein domain annotation resource. Nucleic Acids Research, 2012, 40, D302-D305.	14.5	1,462
15	The InterPro protein families and domains database: 20 years on. Nucleic Acids Research, 2021, 49, D344-D354.	14.5	1,385
16	Interactive Tree Of Life v2: online annotation and display of phylogenetic trees made easy. Nucleic Acids Research, 2011, 39, W475-W478.	14.5	1,361
17	InterPro in 2017—beyond protein family and domain annotations. Nucleic Acids Research, 2017, 45, D190-D199.	14.5	1,358
18	InterPro in 2019: improving coverage, classification and access to protein sequence annotations. Nucleic Acids Research, 2019, 47, D351-D360.	14.5	1,291

#	ARTICLE	IF	CITATIONS
19	The InterPro protein families database: the classification resource after 15 years. <i>Nucleic Acids Research</i> , 2015, 43, D213-D221.	14.5	1,205
20	eggNOG-mapper v2: Functional Annotation, Orthology Assignments, and Domain Prediction at the Metagenomic Scale. <i>Molecular Biology and Evolution</i> , 2021, 38, 5825-5829.	8.9	1,174
21	The genome of the choanoflagellate <i>Monosiga brevicollis</i> and the origin of metazoans. <i>Nature</i> , 2008, 451, 783-788.	27.8	1,006
22	InterPro in 2011: new developments in the family and domain prediction database. <i>Nucleic Acids Research</i> , 2012, 40, D306-D312.	14.5	921
23	The SIDER database of drugs and side effects. <i>Nucleic Acids Research</i> , 2016, 44, D1075-D1079.	14.5	914
24	SMART: recent updates, new developments and status in 2020. <i>Nucleic Acids Research</i> , 2021, 49, D458-D460.	14.5	899
25	SMART 4.0: towards genomic data integration. <i>Nucleic Acids Research</i> , 2004, 32, 142D-144.	14.5	892
26	SMART 5: domains in the context of genomes and networks. <i>Nucleic Acids Research</i> , 2006, 34, D257-D260.	14.5	884
27	SMART 6: recent updates and new developments. <i>Nucleic Acids Research</i> , 2009, 37, D229-D232.	14.5	882
28	Immunity-Related Genes and Gene Families in <i>Anopheles gambiae</i> . <i>Science</i> , 2002, 298, 159-165.	12.6	845
29	A side effect resource to capture phenotypic effects of drugs. <i>Molecular Systems Biology</i> , 2010, 6, 343.	7.2	757
30	The InterPro Database, 2003 brings increased coverage and new features. <i>Nucleic Acids Research</i> , 2003, 31, 315-318.	14.5	640
31	Recent improvements to the SMART domain-based sequence annotation resource. <i>Nucleic Acids Research</i> , 2002, 30, 242-244.	14.5	613
32	ELM server: a new resource for investigating short functional sites in modular eukaryotic proteins. <i>Nucleic Acids Research</i> , 2003, 31, 3625-3630.	14.5	555
33	Comparative Genome and Proteome Analysis of <i>Anopheles gambiae</i> and <i>Drosophila melanogaster</i> . <i>Science</i> , 2002, 298, 149-159.	12.6	531
34	eggNOG v3.0: orthologous groups covering 1133 organisms at 41 different taxonomic ranges. <i>Nucleic Acids Research</i> , 2012, 40, D284-D289.	14.5	490
35	InterPro, progress and status in 2005. <i>Nucleic Acids Research</i> , 2004, 33, D201-D205.	14.5	478
36	New developments in the InterPro database. <i>Nucleic Acids Research</i> , 2007, 35, D224-D228.	14.5	444

#	ARTICLE	IF	CITATIONS
37	iPath2.0: interactive pathway explorer. Nucleic Acids Research, 2011, 39, W412-W415.	14.5	322
38	Statin therapy is associated with lower prevalence of gut microbiota dysbiosis. Nature, 2020, 581, 310-315.	27.8	283
39	Impact of Genome Reduction on Bacterial Metabolism and Its Regulation. Science, 2009, 326, 1263-1268.	12.6	267
40	Nonsense-mediated mRNA decay factors act in concert to regulate common mRNA targets. Rna, 2005, 11, 1530-1544.	3.5	226
41	Toward molecular trait-based ecology through integration of biogeochemical, geographical and metagenomic data. Molecular Systems Biology, 2011, 7, 473.	7.2	218
42	iPath: interactive exploration of biochemical pathways and networks. Trends in Biochemical Sciences, 2008, 33, 101-103.	7.5	216
43	iPath3.0: interactive pathways explorer v3. Nucleic Acids Research, 2018, 46, W510-W513.	14.5	210
44	Quantifying environmental adaptation of metabolic pathways in metagenomics. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 1374-1379.	7.1	177
45	InterPro: An integrated documentation resource for protein families, domains and functional sites. Briefings in Bioinformatics, 2002, 3, 225-235.	6.5	155
46	Evolution of the phospho-tyrosine signaling machinery in premetazoan lineages. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 9680-9684.	7.1	154
47	Common exon duplication in animals and its role in alternative splicing. Human Molecular Genetics, 2002, 11, 1561-1567.	2.9	140
48	proGenomes: a resource for consistent functional and taxonomic annotations of prokaryotic genomes. Nucleic Acids Research, 2017, 45, D529-D534.	14.5	131
49	Imidazole propionate is increased in diabetes and associated with dietary patterns and altered microbial ecology. Nature Communications, 2020, 11, 5881.	12.8	122
50	Alternative splicing and evolution. BioEssays, 2003, 25, 1031-1034.	2.5	119
51	PTMcode: a database of known and predicted functional associations between post-translational modifications in proteins. Nucleic Acids Research, 2012, 41, D306-D311.	14.5	116
52	Combinatorial, additive and dose-dependent drug-microbiome associations. Nature, 2021, 600, 500-505.	27.8	102
53	Microbiome and metabolome features of the cardiometabolic disease spectrum. Nature Medicine, 2022, 28, 303-314.	30.7	102
54	PTMcode v2: a resource for functional associations of post-translational modifications within and between proteins. Nucleic Acids Research, 2015, 43, D494-D502.	14.5	90

#	ARTICLE	IF	CITATIONS
55	Towards the biogeography of prokaryotic genes. <i>Nature</i> , 2022, 601, 252-256.	27.8	85
56	Visualization of multiple alignments, phylogenies and gene family evolution. <i>Nature Methods</i> , 2010, 7, S16-S25.	19.0	73
57	Quantitative assessment of protein function prediction from metagenomics shotgun sequences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 13913-13918.	7.1	72
58	Protein domain analysis in the era of complete genomes. <i>FEBS Letters</i> , 2002, 513, 129-134.	2.8	60
59	proGenomes2: an improved database for accurate and consistent habitat, taxonomic and functional annotations of prokaryotic genomes. <i>Nucleic Acids Research</i> , 2020, 48, D621-D625.	14.5	60
60	Discovering Functional Novelty in Metagenomes: Examples from Light-Mediated Processes. <i>Journal of Bacteriology</i> , 2009, 191, 32-41.	2.2	54
61	Impairment of gut microbial biotin metabolism and host biotin status in severe obesity: effect of biotin and prebiotic supplementation on improved metabolism. <i>Gut</i> , 2022, 71, 2463-2480.	12.1	53
62	Landscape of mobile genetic elements and their antibiotic resistance cargo in prokaryotic genomes. <i>Nucleic Acids Research</i> , 2022, 50, 3155-3168.	14.5	34
63	4DXpress: a database for cross-species expression pattern comparisons. <i>Nucleic Acids Research</i> , 2007, 36, D847-D853.	14.5	33
64	metaTIGER: a metabolic evolution resource. <i>Nucleic Acids Research</i> , 2009, 37, D531-D538.	14.5	32
65	Metagenomic analysis of gut microbial communities from a Central Asian population. <i>BMJ Open</i> , 2018, 8, e021682.	1.9	31
66	Fast identification of folded human protein domains expressed in <i>E. coli</i> suitable for structural analysis. <i>BMC Structural Biology</i> , 2004, 4, 4.	2.3	29
67	Consistency of genome-based methods in measuring Metazoan evolution. <i>FEBS Letters</i> , 2005, 579, 3355-3361.	2.8	26
68	INSIDE NANO: a systems biology framework to contextualize the mechanism-of-action of engineered nanomaterials. <i>Scientific Reports</i> , 2019, 9, 179.	3.3	26
69	Genome and protein evolution in eukaryotes. <i>Current Opinion in Chemical Biology</i> , 2002, 6, 39-45.	6.1	21
70	Gene expression profiling of the rat superior olivary complex using serial analysis of gene expression. <i>European Journal of Neuroscience</i> , 2004, 20, 3244-3258.	2.6	15
71	Computational Analysis of Modular Protein Architectures. , 2005, , 439-476.		2