

Ivica Letunic

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

72
papers

41,287
citations

53
h-index

74
g-index

74
ext. papers

54,417
ext. citations

20.2
avg, IF

8.61
L-index

#	Paper	IF	Citations
72	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 ,	19.2	5
71	Microbiome and metabolome features of the cardiometabolic disease spectrum.. <i>Nature Medicine</i> , 2022 ,	50.5	4
70	Combinatorial, additive and dose-dependent drug-microbiome associations. <i>Nature</i> , 2021 ,	50.4	11
69	Towards the biogeography of prokaryotic genes.. <i>Nature</i> , 2021 ,	50.4	8
68	SMART: recent updates, new developments and status in 2020. <i>Nucleic Acids Research</i> , 2021 , 49, D458-D460	46.0	193
67	Interactive Tree Of Life (iTOL) v5: an online tool for phylogenetic tree display and annotation. <i>Nucleic Acids Research</i> , 2021 , 49, W293-W296	20.1	635
66	The InterPro protein families and domains database: 20 years on. <i>Nucleic Acids Research</i> , 2021 , 49, D344-D354	43.4	358
65	eggNOG-mapper v2: Functional Annotation, Orthology Assignments, and Domain Prediction at the Metagenomic Scale. <i>Molecular Biology and Evolution</i> , 2021 , 38, 5825-5829	8.3	116
64	Statin therapy is associated with lower prevalence of gut microbiota dysbiosis. <i>Nature</i> , 2020 , 581, 310-315	55.4	100
63	Pan-cancer analysis of whole genomes. <i>Nature</i> , 2020 , 578, 82-93	50.4	840
62	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	20.1	21
61	Imidazole propionate is increased in diabetes and associated with dietary patterns and altered microbial ecology. <i>Nature Communications</i> , 2020 , 11, 5881	17.4	29
60	INSIDE NANO: a systems biology framework to contextualize the mechanism-of-action of engineered nanomaterials. <i>Scientific Reports</i> , 2019 , 9, 179	4.9	18
59	Interactive Tree Of Life (iTOL) v4: recent updates and new developments. <i>Nucleic Acids Research</i> , 2019 , 47, W256-W259	20.1	2581
58	eggNOG 5.0: a hierarchical, functionally and phylogenetically annotated orthology resource based on 5090 organisms and 2502 viruses. <i>Nucleic Acids Research</i> , 2019 , 47, D309-D314	20.1	850
57	InterPro in 2019: improving coverage, classification and access to protein sequence annotations. <i>Nucleic Acids Research</i> , 2019 , 47, D351-D360	20.1	835
56	20 years of the SMART protein domain annotation resource. <i>Nucleic Acids Research</i> , 2018 , 46, D493-D496	60.1	884

55	Metagenomic analysis of gut microbial communities from a Central Asian population. <i>BMJ Open</i> , 2018 , 8, e021682	3	23
54	iPath3.0: interactive pathways explorer v3. <i>Nucleic Acids Research</i> , 2018 , 46, W510-W513	20.1	94
53	InterPro in 2017-beyond protein family and domain annotations. <i>Nucleic Acids Research</i> , 2017 , 45, D190-D199	20.1	970
52	proGenomes: a resource for consistent functional and taxonomic annotations of prokaryotic genomes. <i>Nucleic Acids Research</i> , 2017 , 45, D529-D534	20.1	74
51	The SIDER database of drugs and side effects. <i>Nucleic Acids Research</i> , 2016 , 44, D1075-9	20.1	516
50	Interactive tree of life (iTOL) v3: an online tool for the display and annotation of phylogenetic and other trees. <i>Nucleic Acids Research</i> , 2016 , 44, W242-5	20.1	3172
49	The InterPro protein families database: the classification resource after 15 years. <i>Nucleic Acids Research</i> , 2015 , 43, D213-21	20.1	954
48	SMART: recent updates, new developments and status in 2015. <i>Nucleic Acids Research</i> , 2015 , 43, D257-60	20.1	1137
47	PTMcode v2: a resource for functional associations of post-translational modifications within and between proteins. <i>Nucleic Acids Research</i> , 2015 , 43, D494-502	20.1	67
46	PTMcode: a database of known and predicted functional associations between post-translational modifications in proteins. <i>Nucleic Acids Research</i> , 2013 , 41, D306-11	20.1	99
45	eggNOG v3.0: orthologous groups covering 1133 organisms at 41 different taxonomic ranges. <i>Nucleic Acids Research</i> , 2012 , 40, D284-9	20.1	387
44	SMART 7: recent updates to the protein domain annotation resource. <i>Nucleic Acids Research</i> , 2012 , 40, D302-5	20.1	1226
43	InterPro in 2011: new developments in the family and domain prediction database. <i>Nucleic Acids Research</i> , 2012 , 40, D306-12	20.1	844
42	Toward molecular trait-based ecology through integration of biogeochemical, geographical and metagenomic data. <i>Molecular Systems Biology</i> , 2011 , 7, 473	12.2	129
41	Interactive Tree Of Life v2: online annotation and display of phylogenetic trees made easy. <i>Nucleic Acids Research</i> , 2011 , 39, W475-8	20.1	1116
40	iPath2.0: interactive pathway explorer. <i>Nucleic Acids Research</i> , 2011 , 39, W412-5	20.1	244
39	Visualization of multiple alignments, phylogenies and gene family evolution. <i>Nature Methods</i> , 2010 , 7, S16-25	21.6	56
38	A side effect resource to capture phenotypic effects of drugs. <i>Molecular Systems Biology</i> , 2010 , 6, 343	12.2	608

37	metaTIGER: a metabolic evolution resource. <i>Nucleic Acids Research</i> , 2009 , 37, D531-8	20.1	29
36	Discovering functional novelty in metagenomes: examples from light-mediated processes. <i>Journal of Bacteriology</i> , 2009 , 191, 32-41	3.5	50
35	SMART 6: recent updates and new developments. <i>Nucleic Acids Research</i> , 2009 , 37, D229-32	20.1	779
34	InterPro: the integrative protein signature database. <i>Nucleic Acids Research</i> , 2009 , 37, D211-5	20.1	1379
33	Quantifying environmental adaptation of metabolic pathways in metagenomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 1374-9	11.5	148
32	Impact of genome reduction on bacterial metabolism and its regulation. <i>Science</i> , 2009 , 326, 1263-8	33.3	229
31	The genome of the choanoflagellate <i>Monosiga brevicollis</i> and the origin of metazoans. <i>Nature</i> , 2008 , 451, 783-8	50.4	850
30	iPath: interactive exploration of biochemical pathways and networks. <i>Trends in Biochemical Sciences</i> , 2008 , 33, 101-3	10.3	156
29	Evolution of the phospho-tyrosine signaling machinery in premetazoan lineages. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 9680-4	11.5	129
28	4DXpress: a database for cross-species expression pattern comparisons. <i>Nucleic Acids Research</i> , 2008 , 36, D847-53	20.1	31
27	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, 13913-8	11.5	66
26	New developments in the InterPro database. <i>Nucleic Acids Research</i> , 2007 , 35, D224-8	20.1	397
25	Interactive Tree Of Life (iTOL): an online tool for phylogenetic tree display and annotation. <i>Bioinformatics</i> , 2007 , 23, 127-8	7.2	1778
24	SMART 5: domains in the context of genomes and networks. <i>Nucleic Acids Research</i> , 2006 , 34, D257-60	20.1	806
23	Insights into social insects from the genome of the honeybee <i>Apis mellifera</i> . <i>Nature</i> , 2006 , 443, 931-49	50.4	1414
22	Nonsense-mediated mRNA decay factors act in concert to regulate common mRNA targets. <i>Rna</i> , 2005 , 11, 1530-44	5.8	206
21	Consistency of genome-based methods in measuring Metazoan evolution. <i>FEBS Letters</i> , 2005 , 579, 3355-58	5.8	22
20	InterPro, progress and status in 2005. <i>Nucleic Acids Research</i> , 2005 , 33, D201-5	20.1	426

19	Computational Analysis of Modular Protein Architectures 2005 , 439-476		2
18	SMART 4.0: towards genomic data integration. <i>Nucleic Acids Research</i> , 2004 , 32, D142-4	20.1	764
17	Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. <i>Nature</i> , 2004 , 432, 695-716	50.4	2143
16	Gene expression profiling of the rat superior olivary complex using serial analysis of gene expression. <i>European Journal of Neuroscience</i> , 2004 , 20, 3244-58	3.5	15
15	Fast identification of folded human protein domains expressed in E. coli suitable for structural analysis. <i>BMC Structural Biology</i> , 2004 , 4, 4	2.7	25
14	Alternative splicing and evolution. <i>BioEssays</i> , 2003 , 25, 1031-4	4.1	115
13	The InterPro Database, 2003 brings increased coverage and new features. <i>Nucleic Acids Research</i> , 2003 , 31, 315-8	20.1	556
12	ELM server: A new resource for investigating short functional sites in modular eukaryotic proteins. <i>Nucleic Acids Research</i> , 2003 , 31, 3625-30	20.1	491
11	Genome and protein evolution in eukaryotes. <i>Current Opinion in Chemical Biology</i> , 2002 , 6, 39-45	9.7	19
10	Initial sequencing and comparative analysis of the mouse genome. <i>Nature</i> , 2002 , 420, 520-62	50.4	5376
9	Comparative genome and proteome analysis of <i>Anopheles gambiae</i> and <i>Drosophila melanogaster</i> . <i>Science</i> , 2002 , 298, 149-59	33.3	455
8	Recent improvements to the SMART domain-based sequence annotation resource. <i>Nucleic Acids Research</i> , 2002 , 30, 242-4	20.1	535
7	InterPro: an integrated documentation resource for protein families, domains and functional sites. <i>Briefings in Bioinformatics</i> , 2002 , 3, 225-35	13.4	137
6	Common exon duplication in animals and its role in alternative splicing. <i>Human Molecular Genetics</i> , 2002 , 11, 1561-7	5.6	120
5	The genome sequence of the malaria mosquito <i>Anopheles gambiae</i> . <i>Science</i> , 2002 , 298, 129-49	33.3	1622
4	Protein domain analysis in the era of complete genomes. <i>FEBS Letters</i> , 2002 , 513, 129-34	3.8	46
3	Immunity-related genes and gene families in <i>Anopheles gambiae</i> . <i>Science</i> , 2002 , 298, 159-65	33.3	743
2	Computational Analysis of Modular Protein Architectures439		

1	eggNOG-mapper v2: Functional Annotation, Orthology Assignments, and Domain Prediction at the Metagenomic Scale	24
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