

# Ivica Letunic

## List of Publications by Citations

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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	Initial sequencing and comparative analysis of the mouse genome. <i>Nature</i> , <b>2002</b> , 420, 520-62	50.4	5376
71	Interactive tree of life (iTOL) v3: an online tool for the display and annotation of phylogenetic and other trees. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, W242-5	20.1	3172
70	Interactive Tree Of Life (iTOL) v4: recent updates and new developments. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, W256-W259	20.1	2581
69	Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. <i>Nature</i> , <b>2004</b> , 432, 695-716	50.4	2143
68	Interactive Tree Of Life (iTOL): an online tool for phylogenetic tree display and annotation. <i>Bioinformatics</i> , <b>2007</b> , 23, 127-8	7.2	1778
67	The genome sequence of the malaria mosquito <i>Anopheles gambiae</i> . <i>Science</i> , <b>2002</b> , 298, 129-49	33.3	1622
66	Insights into social insects from the genome of the honeybee <i>Apis mellifera</i> . <i>Nature</i> , <b>2006</b> , 443, 931-49	50.4	1414
65	InterPro: the integrative protein signature database. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, D211-5	20.1	1379
64	SMART 7: recent updates to the protein domain annotation resource. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, D302-5	20.1	1226
63	SMART: recent updates, new developments and status in 2015. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, D257-60	20.1	1137
62	Interactive Tree Of Life v2: online annotation and display of phylogenetic trees made easy. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, W475-8	20.1	1116
61	InterPro in 2017-beyond protein family and domain annotations. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, D190-D199	20.1	970
60	The InterPro protein families database: the classification resource after 15 years. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, D213-21	20.1	954
59	20 years of the SMART protein domain annotation resource. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, D493-D496	20.1	884
58	The genome of the choanoflagellate <i>Monosiga brevicollis</i> and the origin of metazoans. <i>Nature</i> , <b>2008</b> , 451, 783-8	50.4	850
57	eggNOG 5.0: a hierarchical, functionally and phylogenetically annotated orthology resource based on 5090 organisms and 2502 viruses. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, D309-D314	20.1	850
56	InterPro in 2011: new developments in the family and domain prediction database. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, D306-12	20.1	844

55	Pan-cancer analysis of whole genomes. <i>Nature</i> , <b>2020</b> , 578, 82-93	50.4	840
54	InterPro in 2019: improving coverage, classification and access to protein sequence annotations. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, D351-D360	20.1	835
53	SMART 5: domains in the context of genomes and networks. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, D257-60	20.1	806
52	SMART 6: recent updates and new developments. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, D229-32	20.1	779
51	SMART 4.0: towards genomic data integration. <i>Nucleic Acids Research</i> , <b>2004</b> , 32, D142-4	20.1	764
50	Immunity-related genes and gene families in <i>Anopheles gambiae</i> . <i>Science</i> , <b>2002</b> , 298, 159-65	33.3	743
49	Interactive Tree Of Life (iTOL) v5: an online tool for phylogenetic tree display and annotation. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, W293-W296	20.1	635
48	A side effect resource to capture phenotypic effects of drugs. <i>Molecular Systems Biology</i> , <b>2010</b> , 6, 343	12.2	608
47	The InterPro Database, 2003 brings increased coverage and new features. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 315-8	20.1	556
46	Recent improvements to the SMART domain-based sequence annotation resource. <i>Nucleic Acids Research</i> , <b>2002</b> , 30, 242-4	20.1	535
45	The SIDER database of drugs and side effects. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, D1075-9	20.1	516
44	ELM server: A new resource for investigating short functional sites in modular eukaryotic proteins. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 3625-30	20.1	491
43	Comparative genome and proteome analysis of <i>Anopheles gambiae</i> and <i>Drosophila melanogaster</i> . <i>Science</i> , <b>2002</b> , 298, 149-59	33.3	455
42	InterPro, progress and status in 2005. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, D201-5	20.1	426
41	New developments in the InterPro database. <i>Nucleic Acids Research</i> , <b>2007</b> , 35, D224-8	20.1	397
40	eggNOG v3.0: orthologous groups covering 1133 organisms at 41 different taxonomic ranges. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, D284-9	20.1	387
39	The InterPro protein families and domains database: 20 years on. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, D344-D354	20.1	358
38	iPath2.0: interactive pathway explorer. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, W412-5	20.1	244

37	Impact of genome reduction on bacterial metabolism and its regulation. <i>Science</i> , <b>2009</b> , 326, 1263-8	33.3	229
36	Nonsense-mediated mRNA decay factors act in concert to regulate common mRNA targets. <i>Rna</i> , <b>2005</b> , 11, 1530-44	5.8	206
35	SMART: recent updates, new developments and status in 2020. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, D458-D460	46.0	193
34	iPath: interactive exploration of biochemical pathways and networks. <i>Trends in Biochemical Sciences</i> , <b>2008</b> , 33, 101-3	10.3	156
33	Quantifying environmental adaptation of metabolic pathways in metagenomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2009</b> , 106, 1374-9	11.5	148
32	InterPro: an integrated documentation resource for protein families, domains and functional sites. <i>Briefings in Bioinformatics</i> , <b>2002</b> , 3, 225-35	13.4	137
31	Toward molecular trait-based ecology through integration of biogeochemical, geographical and metagenomic data. <i>Molecular Systems Biology</i> , <b>2011</b> , 7, 473	12.2	129
30	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> , <b>2008</b> , 105, 9680-4	11.5	129
29	Common exon duplication in animals and its role in alternative splicing. <i>Human Molecular Genetics</i> , <b>2002</b> , 11, 1561-7	5.6	120
28	eggNOG-mapper v2: Functional Annotation, Orthology Assignments, and Domain Prediction at the Metagenomic Scale. <i>Molecular Biology and Evolution</i> , <b>2021</b> , 38, 5825-5829	8.3	116
27	Alternative splicing and evolution. <i>BioEssays</i> , <b>2003</b> , 25, 1031-4	4.1	115
26	Statin therapy is associated with lower prevalence of gut microbiota dysbiosis. <i>Nature</i> , <b>2020</b> , 581, 310-315	55.4	100
25	PTMcode: a database of known and predicted functional associations between post-translational modifications in proteins. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, D306-11	20.1	99
24	iPath3.0: interactive pathways explorer v3. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, W510-W513	20.1	94
23	proGenomes: a resource for consistent functional and taxonomic annotations of prokaryotic genomes. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, D529-D534	20.1	74
22	PTMcode v2: a resource for functional associations of post-translational modifications within and between proteins. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, D494-502	20.1	67
21	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> , <b>2007</b> , 104, 13913-8	11.5	66
20	Visualization of multiple alignments, phylogenies and gene family evolution. <i>Nature Methods</i> , <b>2010</b> , 7, S16-25	21.6	56

19	Discovering functional novelty in metagenomes: examples from light-mediated processes. <i>Journal of Bacteriology</i> , <b>2009</b> , 191, 32-41	3.5	50
18	Protein domain analysis in the era of complete genomes. <i>FEBS Letters</i> , <b>2002</b> , 513, 129-34	3.8	46
17	4DXpress: a database for cross-species expression pattern comparisons. <i>Nucleic Acids Research</i> , <b>2008</b> , 36, D847-53	20.1	31
16	metaTIGER: a metabolic evolution resource. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, D531-8	20.1	29
15	Imidazole propionate is increased in diabetes and associated with dietary patterns and altered microbial ecology. <i>Nature Communications</i> , <b>2020</b> , 11, 5881	17.4	29
14	Fast identification of folded human protein domains expressed in E. coli suitable for structural analysis. <i>BMC Structural Biology</i> , <b>2004</b> , 4, 4	2.7	25
13	eggNOG-mapper v2: Functional Annotation, Orthology Assignments, and Domain Prediction at the Metagenomic Scale		24
12	Metagenomic analysis of gut microbial communities from a Central Asian population. <i>BMJ Open</i> , <b>2018</b> , 8, e021682	3	23
11	Consistency of genome-based methods in measuring Metazoan evolution. <i>FEBS Letters</i> , <b>2005</b> , 579, 3355-368	3.8	22
10	proGenomes2: an improved database for accurate and consistent habitat, taxonomic and functional annotations of prokaryotic genomes. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, D621-D625	20.1	21
9	Genome and protein evolution in eukaryotes. <i>Current Opinion in Chemical Biology</i> , <b>2002</b> , 6, 39-45	9.7	19
8	INSIdE NANO: a systems biology framework to contextualize the mechanism-of-action of engineered nanomaterials. <i>Scientific Reports</i> , <b>2019</b> , 9, 179	4.9	18
7	Gene expression profiling of the rat superior olivary complex using serial analysis of gene expression. <i>European Journal of Neuroscience</i> , <b>2004</b> , 20, 3244-58	3.5	15
6	Combinatorial, additive and dose-dependent drug-microbiome associations. <i>Nature</i> , <b>2021</b> ,	50.4	11
5	Towards the biogeography of prokaryotic genes.. <i>Nature</i> , <b>2021</b> ,	50.4	8
4	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> , <b>2022</b> ,	19.2	5
3	Microbiome and metabolome features of the cardiometabolic disease spectrum.. <i>Nature Medicine</i> , <b>2022</b> ,	50.5	4
2	Computational Analysis of Modular Protein Architectures <b>2005</b> , 439-476		2

1 Computational Analysis of Modular Protein Architectures 439