

# Ivica Letunic

## List of Publications by Year in descending order

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71  
papers

63,672  
citations

26567

56  
h-index

85405

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. <i>Nature</i> , 2002, 420, 520-562.	13.7	6,319
2	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-W245.	6.5	4,967
3	Interactive Tree Of Life (iTOL) v5: an online tool for phylogenetic tree display and annotation. <i>Nucleic Acids Research</i> , 2021, 49, W293-W296.	6.5	4,856
4	Interactive Tree Of Life (iTOL) v4: recent updates and new developments. <i>Nucleic Acids Research</i> , 2019, 47, W256-W259.	6.5	4,604
5	Interactive Tree Of Life (iTOL): an online tool for phylogenetic tree display and annotation. <i>Bioinformatics</i> , 2007, 23, 127-128.	1.8	2,609
6	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.	6.5	2,575
7	Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. <i>Nature</i> , 2004, 432, 695-716.	13.7	2,421
8	Pan-cancer analysis of whole genomes. <i>Nature</i> , 2020, 578, 82-93.	13.7	1,966
9	The Genome Sequence of the Malaria Mosquito <i>Anopheles gambiae</i> . <i>Science</i> , 2002, 298, 129-149.	6.0	1,859
10	InterPro: the integrative protein signature database. <i>Nucleic Acids Research</i> , 2009, 37, D211-D215.	6.5	1,712
11	Insights into social insects from the genome of the honeybee <i>Apis mellifera</i> . <i>Nature</i> , 2006, 443, 931-949.	13.7	1,648
12	20 years of the SMART protein domain annotation resource. <i>Nucleic Acids Research</i> , 2018, 46, D493-D496.	6.5	1,525
13	SMART: recent updates, new developments and status in 2015. <i>Nucleic Acids Research</i> , 2015, 43, D257-D260.	6.5	1,519
14	SMART 7: recent updates to the protein domain annotation resource. <i>Nucleic Acids Research</i> , 2012, 40, D302-D305.	6.5	1,462
15	The InterPro protein families and domains database: 20 years on. <i>Nucleic Acids Research</i> , 2021, 49, D344-D354.	6.5	1,385
16	Interactive Tree Of Life v2: online annotation and display of phylogenetic trees made easy. <i>Nucleic Acids Research</i> , 2011, 39, W475-W478.	6.5	1,361
17	InterPro in 2017 – beyond protein family and domain annotations. <i>Nucleic Acids Research</i> , 2017, 45, D190-D199.	6.5	1,358
18	InterPro in 2019: improving coverage, classification and access to protein sequence annotations. <i>Nucleic Acids Research</i> , 2019, 47, D351-D360.	6.5	1,291

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19	The InterPro protein families database: the classification resource after 15 years. <i>Nucleic Acids Research</i> , 2015, 43, D213-D221.	6.5	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.	3.5	1,174
21	The genome of the choanoflagellate <i>Monosiga brevicollis</i> and the origin of metazoans. <i>Nature</i> , 2008, 451, 783-788.	13.7	1,006
22	InterPro in 2011: new developments in the family and domain prediction database. <i>Nucleic Acids Research</i> , 2012, 40, D306-D312.	6.5	921
23	The SIDER database of drugs and side effects. <i>Nucleic Acids Research</i> , 2016, 44, D1075-D1079.	6.5	914
24	SMART: recent updates, new developments and status in 2020. <i>Nucleic Acids Research</i> , 2021, 49, D458-D460.	6.5	899
25	SMART 4.0: towards genomic data integration. <i>Nucleic Acids Research</i> , 2004, 32, 142D-144.	6.5	892
26	SMART 5: domains in the context of genomes and networks. <i>Nucleic Acids Research</i> , 2006, 34, D257-D260.	6.5	884
27	SMART 6: recent updates and new developments. <i>Nucleic Acids Research</i> , 2009, 37, D229-D232.	6.5	882
28	Immunity-Related Genes and Gene Families in <i>Anopheles gambiae</i> . <i>Science</i> , 2002, 298, 159-165.	6.0	845
29	A side effect resource to capture phenotypic effects of drugs. <i>Molecular Systems Biology</i> , 2010, 6, 343.	3.2	757
30	The InterPro Database, 2003 brings increased coverage and new features. <i>Nucleic Acids Research</i> , 2003, 31, 315-318.	6.5	640
31	Recent improvements to the SMART domain-based sequence annotation resource. <i>Nucleic Acids Research</i> , 2002, 30, 242-244.	6.5	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.	6.5	555
33	Comparative Genome and Proteome Analysis of <i>Anopheles gambiae</i> and <i>Drosophila melanogaster</i> . <i>Science</i> , 2002, 298, 149-159.	6.0	531
34	eggNOG v3.0: orthologous groups covering 1133 organisms at 41 different taxonomic ranges. <i>Nucleic Acids Research</i> , 2012, 40, D284-D289.	6.5	490
35	InterPro, progress and status in 2005. <i>Nucleic Acids Research</i> , 2004, 33, D201-D205.	6.5	478
36	New developments in the InterPro database. <i>Nucleic Acids Research</i> , 2007, 35, D224-D228.	6.5	444

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37	iPath2.0: interactive pathway explorer. <i>Nucleic Acids Research</i> , 2011, 39, W412-W415.	6.5	322
38	Statin therapy is associated with lower prevalence of gut microbiota dysbiosis. <i>Nature</i> , 2020, 581, 310-315.	13.7	283
39	Impact of Genome Reduction on Bacterial Metabolism and Its Regulation. <i>Science</i> , 2009, 326, 1263-1268.	6.0	267
40	Nonsense-mediated mRNA decay factors act in concert to regulate common mRNA targets. <i>Rna</i> , 2005, 11, 1530-1544.	1.6	226
41	Toward molecular trait-based ecology through integration of biogeochemical, geographical and metagenomic data. <i>Molecular Systems Biology</i> , 2011, 7, 473.	3.2	218
42	iPath: interactive exploration of biochemical pathways and networks. <i>Trends in Biochemical Sciences</i> , 2008, 33, 101-103.	3.7	216
43	iPath3.0: interactive pathways explorer v3. <i>Nucleic Acids Research</i> , 2018, 46, W510-W513.	6.5	210
44	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, 1374-1379.	3.3	177
45	InterPro: An integrated documentation resource for protein families, domains and functional sites. <i>Briefings in Bioinformatics</i> , 2002, 3, 225-235.	3.2	155
46	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, 9680-9684.	3.3	154
47	Common exon duplication in animals and its role in alternative splicing. <i>Human Molecular Genetics</i> , 2002, 11, 1561-1567.	1.4	140
48	proGenomes: a resource for consistent functional and taxonomic annotations of prokaryotic genomes. <i>Nucleic Acids Research</i> , 2017, 45, D529-D534.	6.5	131
49	Imidazole propionate is increased in diabetes and associated with dietary patterns and altered microbial ecology. <i>Nature Communications</i> , 2020, 11, 5881.	5.8	122
50	Alternative splicing and evolution. <i>BioEssays</i> , 2003, 25, 1031-1034.	1.2	119
51	PTMcode: a database of known and predicted functional associations between post-translational modifications in proteins. <i>Nucleic Acids Research</i> , 2012, 41, D306-D311.	6.5	116
52	Combinatorial, additive and dose-dependent drug-microbiome associations. <i>Nature</i> , 2021, 600, 500-505.	13.7	102
53	Microbiome and metabolome features of the cardiometabolic disease spectrum. <i>Nature Medicine</i> , 2022, 28, 303-314.	15.2	102
54	PTMcode v2: a resource for functional associations of post-translational modifications within and between proteins. <i>Nucleic Acids Research</i> , 2015, 43, D494-D502.	6.5	90

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55	Towards the biogeography of prokaryotic genes. <i>Nature</i> , 2022, 601, 252-256.	13.7	85
56	Visualization of multiple alignments, phylogenies and gene family evolution. <i>Nature Methods</i> , 2010, 7, S16-S25.	9.0	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.	3.3	72
58	Protein domain analysis in the era of complete genomes. <i>FEBS Letters</i> , 2002, 513, 129-134.	1.3	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.	6.5	60
60	Discovering Functional Novelty in Metagenomes: Examples from Light-Mediated Processes. <i>Journal of Bacteriology</i> , 2009, 191, 32-41.	1.0	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.	6.1	53
62	Landscape of mobile genetic elements and their antibiotic resistance cargo in prokaryotic genomes. <i>Nucleic Acids Research</i> , 2022, 50, 3155-3168.	6.5	34
63	4DXpress: a database for cross-species expression pattern comparisons. <i>Nucleic Acids Research</i> , 2007, 36, D847-D853.	6.5	33
64	metaTIGER: a metabolic evolution resource. <i>Nucleic Acids Research</i> , 2009, 37, D531-D538.	6.5	32
65	Metagenomic analysis of gut microbial communities from a Central Asian population. <i>BMJ Open</i> , 2018, 8, e021682.	0.8	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.	1.3	26
68	INSIDE NANO: a systems biology framework to contextualize the mechanism-of-action of engineered nanomaterials. <i>Scientific Reports</i> , 2019, 9, 179.	1.6	26
69	Genome and protein evolution in eukaryotes. <i>Current Opinion in Chemical Biology</i> , 2002, 6, 39-45.	2.8	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.	1.2	15
71	Computational Analysis of Modular Protein Architectures. , 2005, , 439-476.		2