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List of Publications by Year
in descending order

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14 papers	39,626 citations	623574 14 h-index	996849 15 g-index
17 all docs	17 docs citations	17 times ranked	60686 citing authors

#	Article	IF	Citations
1	The STRING database in 2021: customizable proteinâ€“protein networks, and functional characterization of user-uploaded gene/measurement sets. Nucleic Acids Research, 2021, 49, D605-D612.	6.5	4,274
2	GUNC: detection of chimerism and contamination in prokaryotic genomes. Genome Biology, 2021, 22, 178.	3.8	94
3	Pathogenic impact of transcript isoform switching in 1,209 cancer samples covering 27 cancer types using an isoform-specific interaction network. Scientific Reports, 2020, 10, 14453.	1.6	27
4	Analysis of the Human Kinome and Phosphatome by Mass Cytometry Reveals Overexpression-Induced Effects on Cancer-Related Signaling. Molecular Cell, 2019, 74, 1086-1102.e5.	4.5	32
5	Tree reconciliation combined with subsampling improves large scale inference of orthologous group hierarchies. BMC Bioinformatics, 2019, 20, 228.	1.2	1
6	STRING v11: proteinâ€“protein association networks with increased coverage, supporting functional discovery in genome-wide experimental datasets. Nucleic Acids Research, 2019, 47, D607-D613.	6.5	12,237
7	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.	6.5	2,575
8	Fast Genome-Wide Functional Annotation through Orthology Assignment by eggNOG-Mapper. Molecular Biology and Evolution, 2017, 34, 2115-2122.	3.5	2,156
9	The STRING database in 2017: quality-controlled proteinâ€“protein association networks, made broadly accessible. Nucleic Acids Research, 2017, 45, D362-D368.	6.5	6,303
10	Standardized benchmarking in the quest for orthologs. Nature Methods, 2016, 13, 425-430.	9.0	198
11	WeGET: predicting new genes for molecular systems by weighted co-expression. Nucleic Acids Research, 2016, 44, D567-D573.	6.5	35
12	eggNOG 4.5: a hierarchical orthology framework with improved functional annotations for eukaryotic, prokaryotic and viral sequences. Nucleic Acids Research, 2016, 44, D286-D293.	6.5	1,937
13	Version 4.0 of PaxDb: Protein abundance data, integrated across model organisms, tissues, and cellâ€•lines. Proteomics, 2015, 15, 3163-3168.	1.3	493
14	STRING v10: proteinâ€“protein interaction networks, integrated over the tree of life. Nucleic Acids Research, 2015, 43, D447-D452.	6.5	9,029