Alberto Paccanaro

List of Publications by Year
in descending order

37 papers	7,209 citations	394421 19 h-index	454955 30 g-index
39 all docs	39 docs citations	39 times ranked	10288 citing authors

#	Article	IF	Citations
1	Global landscape of protein complexes in the yeast Saccharomyces cerevisiae. Nature, 2006, 440, 637-643.	27.8	2,681
2	Detecting overlapping protein complexes in protein-protein interaction networks. Nature Methods, 2012, 9, 471-472.	19.0	1,129
3	A large-scale evaluation of computational protein function prediction. Nature Methods, 2013, 10, 221-227.	19.0	789
4	A Census of Human Soluble Protein Complexes. Cell, 2012, 150, 1068-1081.	28.9	781
5	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. Genome Biology, 2016, 17, 184.	8.8	308
6	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. Genome Biology, 2019, 20, 244.	8.8	261
7	Assessing the limits of genomic data integration for predicting protein networks. Genome Research, 2005, 15, 945-953.	5.5	182
8	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
9	Spectral clustering of protein sequences. Nucleic Acids Research, 2006, 34, 1571-1580.	14.5	147
10	Predicting essential genes in fungal genomes. Genome Research, 2006, 16, 1126-1135.	5.5	109
11	Exploring the evolutionary path of plant MAPK networks. Trends in Plant Science, 2012, 17, 518-525.	8.8	94
12	mutation3D: Cancer Gene Prediction Through Atomic Clustering of Coding Variants in the Structural Proteome. Human Mutation, 2016, 37, 447-456.	2.5	94
13	*OsWRKY22*, a monocot *WRKY* gene, plays a role in the resistance response to blast. Molecular Plant Pathology, 2012, 13, 828-841.	4.2	86
14	Statistical analysis of the genomic distribution and correlation of regulatory elements in the ENCODE regions. Genome Research, 2007, 17, 787-797.	5.5	56
15	Predicting the frequencies of drug side effects. Nature Communications, 2020, 11, 4575.	12.8	54
16	An extensive analysis of disease-gene associations using network integration and fast kernel-based gene prioritization methods. Artificial Intelligence in Medicine, 2014, 61, 63-78.	6.5	49
17	GOssTo: a stand-alone application and a web tool for calculating semantic similarities on the Gene Ontology. Bioinformatics, 2014, 30, 2235-2236.	4.1	44
18	Disease gene prediction for molecularly uncharacterized diseases. PLoS Computational Biology, 2019, 15, e1007078.	3.2	26

#	Article	IF	Citations
19	Machine learning and network medicine approaches for drug repositioning for COVID-19. Patterns, 2022, 3, 100396.	5.9	23
20	A Recommender System Approach for Predicting Drug Side Effects. , 2018, , .		18
21	A network medicine approach to quantify distance between hereditary disease modules on the interactome. Scientific Reports, 2016, 5, 17658.	3.3	17
22	Neurogenomic Signatures of Successes and Failures in Life-History Transitions in a Key Insect Pollinator. Genome Biology and Evolution, 2017, 9, 3059-3072.	2.5	14
23	Protein function prediction for newly sequenced organisms. Nature Machine Intelligence, 2021, 3, 1050-1060.	16.0	13
24	Unlike Chloroquine, Mefloquine Inhibits SARS-CoV-2 Infection in Physiologically Relevant Cells. Viruses, 2022, 14, 374.	3.3	12
25	Heterogeneous data integration methods for patient similarity networks. Briefings in Bioinformatics, 2022, 23, .	6.5	12
26	Network modeling of patients' biomolecular profiles for clinical phenotype/outcome prediction. Scientific Reports, 2020, 10, 3612.	3.3	11
27	Drug targets prediction using chemical similarity. , 2016, , .		5
28	Progressive promoter element combinations classify conserved orthogonal plant circadian gene expression modules. Journal of the Royal Society Interface, 2014, 11, 20140535.	3.4	4
29	LUMI-PCR: an Illumina platform ligation-mediated PCR protocol for integration site cloning, provides molecular quantitation of integration sites. Mobile DNA, 2020, 11, 7.	3.6	4
30	GFam: a platform for automatic annotation of gene families. Nucleic Acids Research, 2012, 40, e152-e152.	14.5	3
31	Subclonal mutation selection in mouse lymphomagenesis identifies known cancer loci and suggests novel candidates. Nature Communications, 2018, 9, 2649.	12.8	3
32	The corrected gene proximity map for analyzing the 3D genome organization using Hi-C data. BMC Bioinformatics, 2020, 21, 222.	2.6	2
33	Using the tree representation of terms to recognize matching with neural networks. Nonlinear Analysis: Theory, Methods & Applications, 1997, 30, 2925-2936.	1.1	0
34	Combining interactomes from multiple organisms: A case study on human-mouse. , 2016, , .		0
35	Mining the biomedical literature to predict shared drug targets in DrugBank. , 2017, , .		0
36	Drug cocktail selection for the treatment of chagas disease: A multi-objective approach. , 2017, , .		0

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37	A Recommender System Approach for Predicting Effective Antivirals. , 2021, , .		0