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	Machine learning and network medicine approaches for drug repositioning for COVID-19. Patterns, 2022, 3, 100396.	5.9	23
2	Unlike Chloroquine, Mefloquine Inhibits SARS-CoV-2 Infection in Physiologically Relevant Cells. Viruses, 2022, 14, 374.	3.3	12
3	Heterogeneous data integration methods for patient similarity networks. Briefings in Bioinformatics, 2022, 23, .	6.5	12
4	A Recommender System Approach for Predicting Effective Antivirals. , 2021, , .		0
5	Protein function prediction for newly sequenced organisms. Nature Machine Intelligence, 2021, 3, 1050-1060.	16.0	13
6	Predicting the frequencies of drug side effects. Nature Communications, 2020, 11, 4575.	12.8	54
7	The corrected gene proximity map for analyzing the 3D genome organization using Hi-C data. BMC Bioinformatics, 2020, 21, 222.	2.6	2
8	Network modeling of patients' biomolecular profiles for clinical phenotype/outcome prediction. Scientific Reports, 2020, 10, 3612.	3.3	11
9	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
10	Disease gene prediction for molecularly uncharacterized diseases. PLoS Computational Biology, 2019, 15, e1007078.	3.2	26
11	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
12	A Recommender System Approach for Predicting Drug Side Effects. , 2018, , .		18
13	Subclonal mutation selection in mouse lymphomagenesis identifies known cancer loci and suggests novel candidates. Nature Communications, 2018, 9, 2649.	12.8	3
14	Mining the biomedical literature to predict shared drug targets in DrugBank. , 2017, , .		0
15	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
16	Drug cocktail selection for the treatment of chagas disease: A multi-objective approach. , 2017, , .		0
17	mutation3D: Cancer Gene Prediction Through Atomic Clustering of Coding Variants in the Structural Proteome. Human Mutation, 2016, 37, 447-456.	2.5	94
18	Combining interactomes from multiple organisms: A case study on human-mouse. , 2016, , .		0

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19	A network medicine approach to quantify distance between hereditary disease modules on the interactome. Scientific Reports, 2016, 5, 17658.	3.3	17
20	Drug targets prediction using chemical similarity. , 2016, , .		5
21	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. Genome Biology, 2016, 17, 184.	8.8	308
22	Progressive promoter element combinations classify conserved orthogonal plant circadian gene expression modules. Journal of the Royal Society Interface, 2014, 11, 20140535.	3.4	4
23	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
24	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
25	A large-scale evaluation of computational protein function prediction. Nature Methods, 2013, 10, 221-227.	19.0	789
26	A Census of Human Soluble Protein Complexes. Cell, 2012, 150, 1068-1081.	28.9	781
27	GFam: a platform for automatic annotation of gene families. Nucleic Acids Research, 2012, 40, e152-e152.	14.5	3
28	Exploring the evolutionary path of plant MAPK networks. Trends in Plant Science, 2012, 17, 518-525.	8.8	94
29	Detecting overlapping protein complexes in protein-protein interaction networks. Nature Methods, 2012, 9, 471-472.	19.0	1,129
30	*OsWRKY22*, a monocot *WRKY* gene, plays a role in the resistance response to blast. Molecular Plant Pathology, 2012, 13, 828-841.	4.2	86
31	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
32	Statistical analysis of the genomic distribution and correlation of regulatory elements in the ENCODE regions. Genome Research, 2007, 17, 787-797.	5.5	56
33	Global landscape of protein complexes in the yeast Saccharomyces cerevisiae. Nature, 2006, 440, 637-643.	27.8	2,681
34	Predicting essential genes in fungal genomes. Genome Research, 2006, 16, 1126-1135.	5.5	109
35	Spectral clustering of protein sequences. Nucleic Acids Research, 2006, 34, 1571-1580.	14.5	147
36	Assessing the limits of genomic data integration for predicting protein networks. Genome Research, 2005, 15, 945-953.	5.5	182

#	Article	IF	Citations
37	Using the tree representation of terms to recognize matching with neural networks. Nonlinear Analysis: Theory, Methods & Applications, 1997, 30, 2925-2936.	1.1	0