

# Marco Pellegrini

## List of Publications by Year in descending order

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Version: 2024-02-01

77  
papers

1,485  
citations

394421

19  
h-index

414414

32  
g-index

87  
all docs

87  
docs citations

87  
times ranked

1925  
citing authors

#	ARTICLE	IF	CITATIONS
1	STIMO: STILL and MOving video storyboard for the web scenario. <i>Multimedia Tools and Applications</i> , 2010, 46, 47-69.	3.9	214
2	Extraction and classification of dense communities in the web. , 2007, , .		143
3	Enhanced copy number variants detection from whole-exome sequencing data using EXCAVATOR2. <i>Nucleic Acids Research</i> , 2016, 44, gkw695.	14.5	75
4	Context-dependent miR-204 and miR-211 affect the biological properties of amelanotic and melanotic melanoma cells. <i>Oncotarget</i> , 2017, 8, 25395-25417.	1.8	64
5	miRandola 2017: a curated knowledge base of non-invasive biomarkers. <i>Nucleic Acids Research</i> , 2018, 46, D354-D359.	14.5	61
6	On the zone of a surface in a hyperplane arrangement. <i>Discrete and Computational Geometry</i> , 1993, 9, 177-186.	0.6	47
7	Extraction and classification of dense implicit communities in the Web graph. <i>ACM Transactions on the Web</i> , 2009, 3, 1-36.	2.5	45
8	TRStalker: an efficient heuristic for finding fuzzy tandem repeats. <i>Bioinformatics</i> , 2010, 26, i358-i366.	4.1	42
9	Ray shooting on triangles in 3-space. <i>Algorithmica</i> , 1993, 9, 471-494.	1.3	39
10	Protein complex prediction for large protein protein interaction networks with the Core&Peel method. <i>BMC Bioinformatics</i> , 2016, 17, 372.	2.6	38
11	Interplay Between Long Noncoding RNAs and MicroRNAs in Cancer. <i>Methods in Molecular Biology</i> , 2018, 1819, 75-92.	0.9	34
12	Fast Exact Computation of betweenness Centrality in Social Networks. , 2012, , .		33
13	SpeedHap: An Accurate Heuristic for the Single Individual SNP Haplotyping Problem with Many Gaps, High Reading Error Rate and Low Coverage. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2008, 5, 492-502.	3.0	28
14	VISTO. , 2007, , .		27
15	On counting pairs of intersecting segments and off-line triangle range searching. <i>Algorithmica</i> , 1997, 17, 380-398.	1.3	25
16	A knowledge base for the discovery of function, diagnostic potential and drug effects on cellular and extracellular miRNAs. <i>BMC Genomics</i> , 2014, 15, S4.	2.8	25
17	Ab initio detection of fuzzy amino acid tandem repeats in protein sequences. <i>BMC Bioinformatics</i> , 2012, 13, S8.	2.6	24
18	Cluster Generation and Labeling for Web Snippets: A Fast, Accurate Hierarchical Solution. <i>Internet Mathematics</i> , 2006, 3, 413-443.	0.7	23

#	ARTICLE	IF	CITATIONS
19	Tandem Repeats in Proteins: Prediction Algorithms and Biological Role. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 143.	4.1	23
20	MicroRNA 19a replacement partially rescues fin and cardiac defects in zebrafish model of Holt Oram syndrome. <i>Scientific Reports</i> , 2015, 5, 18240.	3.3	21
21	Discovering the miR-26a-5p Targetome in Prostate Cancer Cells. <i>Journal of Cancer</i> , 2017, 8, 2729-2739.	2.5	21
22	The miR-28-5p Targetome Discovery Identified SREBF2 as One of the Mediators of the miR-28-5p Tumor Suppressor Activity in Prostate Cancer Cells. <i>Cells</i> , 2020, 9, 354.	4.1	21
23	Finding stabbing lines in 3-space. <i>Discrete and Computational Geometry</i> , 1992, 8, 191-208.	0.6	20
24	Georoy: A location-aware enhancement to Viceroy peer-to-peer algorithm. <i>Computer Networks</i> , 2007, 51, 1998-2014.	5.1	20
25	A scalable algorithm for high-quality clustering of web snippets. , 2006, , .		18
26	Discovering miRNA Regulatory Networks in Holt Oram Syndrome Using a Zebrafish Model. <i>Frontiers in Bioengineering and Biotechnology</i> , 2016, 4, 60.	4.1	16
27	On Using Clustering Algorithms to Produce Video Abstracts for the Web Scenario. , 2008, , .		15
28	K-Boost: A Scalable Algorithm for High-Quality Clustering of Microarray Gene Expression Data. <i>Journal of Computational Biology</i> , 2009, 16, 859-873.	1.6	15
29	Counting Circular Arc Intersections. <i>SIAM Journal on Computing</i> , 1993, 22, 778-793.	1.0	14
30	On Numerical Approximation of Electrostatic Energy in 3D. <i>Journal of Computational Physics</i> , 1998, 146, 707-725.	3.8	13
31	<i>Dot2dot</i> : accurate whole-genome tandem repeats discovery. <i>Bioinformatics</i> , 2019, 35, 914-922.	4.1	13
32	Identification of BRAF 3' UTR Isoforms in Melanoma. <i>Journal of Investigative Dermatology</i> , 2015, 135, 1694-1697.	0.7	12
33	miR-182-5p is an evolutionarily conserved Tbx5 effector that impacts cardiac development and electrical activity in zebrafish. <i>Cellular and Molecular Life Sciences</i> , 2020, 77, 3215-3229.	5.4	12
34	On lines missing polyhedral sets in 3-space. <i>Discrete and Computational Geometry</i> , 1994, 12, 203-221.	0.6	10
35	Faster deterministic wakeup in multiple access channels. <i>Discrete Applied Mathematics</i> , 2007, 155, 898-903.	0.9	10
36	Tandem repeats discovery service (TReaDS) applied to finding novel cis-acting factors in repeat expansion diseases. <i>BMC Bioinformatics</i> , 2012, 13, S3.	2.6	10

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37	Systematic evaluation of the microRNAome through miR-CATCHv2.0 identifies positive and negative regulators of <i>BRAF</i> -X1 mRNA. <i>RNA Biology</i> , 2019, 16, 865-878.	3.1	10
38	Fetal cardiac growth is associated with in utero gut colonization. <i>Nutrition, Metabolism and Cardiovascular Diseases</i> , 2019, 29, 170-176.	2.6	10
39	A New Method for Discovering Disease-Specific MiRNA-Target Regulatory Networks. <i>PLoS ONE</i> , 2015, 10, e0122473.	2.5	9
40	The miRNA Pull Out Assay as a Method to Validate the miR-28-5p Targets Identified in Other Tumor Contexts in Prostate Cancer. <i>International Journal of Genomics</i> , 2017, 2017, 1-7.	1.6	9
41	A Census of Tandemly Repeated Polymorphic Loci in Genic Regions Through the Comparative Integration of Human Genome Assemblies. <i>Frontiers in Genetics</i> , 2018, 9, 155.	2.3	9
42	AMIC@: All Microarray Clusterings @ once. <i>Nucleic Acids Research</i> , 2008, 36, W315-W319.	14.5	8
43	Ray-shooting and isotopy classes of lines in 3-dimensional space. , 1991, , 20-31.		7
44	On Collision-Free Placements of Simplices and the Closest Pair of Lines in 3-Space. <i>SIAM Journal on Computing</i> , 1994, 23, 133-153.	1.0	7
45	The Prostate Cancer Cells Resistant to Docetaxel as in vitro Model for Discovering MicroRNAs Predictive of the Onset of Docetaxel Resistance. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1512.	4.1	7
46	Monte carlo approximation of form factors with error bounded a priori. <i>Discrete and Computational Geometry</i> , 1997, 17, 319-337.	0.6	6
47	A New Framework for Distilling Higher Quality Information from Health Data via Social Network Analysis. , 2013, , .		6
48	Finding disease modules for cancer and COVID-19 in gene co-expression networks with the Core&Peel method. <i>Scientific Reports</i> , 2020, 10, 17628.	3.3	6
49	FPF-SB: A Scalable Algorithm for Microarray Gene Expression Data Clustering. <i>Lecture Notes in Computer Science</i> , 2007, , 606-615.	1.3	6
50	A Fast and Accurate Heuristic for the Single Individual SNP Haplotyping Problem with Many Gaps, High Reading Error Rate and Low Coverage. <i>Lecture Notes in Computer Science</i> , 2007, , 49-60.	1.3	6
51	Drug repositioning by merging active subnetworks validated in cancer and COVID-19. <i>Scientific Reports</i> , 2021, 11, 19839.	3.3	6
52	Lower bounds on stabbing lines in 3-space. <i>Computational Geometry: Theory and Applications</i> , 1993, 3, 53-58.	0.5	5
53	On Point Location and Motion Planning among Simplices. <i>SIAM Journal on Computing</i> , 1996, 25, 1061-1081.	1.0	5
54	On computing the diameter of a point set in high dimensional Euclidean space. <i>Theoretical Computer Science</i> , 2002, 287, 501-514.	0.9	5

#	ARTICLE	IF	CITATIONS
55	Community Detection in Biological Networks. , 2019, , 978-987.		5
56	Identification of Disease-Related miRNA Networks Across Different Cancer Types Using SWIM. Methods in Molecular Biology, 2019, 1970, 169-181.	0.9	5
57	Circulating Noncoding RNAs as Clinical Biomarkers. , 2016, , 239-258.		4
58	On the Benefits of Keyword Spreading in Sponsored Search Auctions: An Experimental Analysis. Lecture Notes in Business Information Processing, 2010, , 158-171.	1.0	4
59	Editorial: Network Bioscience. Frontiers in Genetics, 2019, 10, 1160.	2.3	3
60	Accurate prediction of breast cancer survival through coherent voting networks with gene expression profiling. Scientific Reports, 2021, 11, 14645.	3.3	3
61	Electrostatic fields without singularities. Journal of the ACM, 1998, 45, 924-964.	2.2	2
62	Medium sized crawling made fast and easy through Lumbricus webis. , 2011, , .		2
63	MicroRNAs, Regulatory Networks, and Comorbidities: Decoding Complex Systems. Methods in Molecular Biology, 2017, 1580, 281-295.	0.9	2
64	Fast Exact and Approximate Computation of Betweenness Centrality in Social Networks. Lecture Notes in Social Networks, 2014, , 53-73.	0.1	2
65	From Literature to Knowledge: Exploiting PubMed to Answer Biomedical Questions in Natural Language. Lecture Notes in Computer Science, 2015, , 3-15.	1.3	2
66	Dynamic User-Defined Similarity Searching in Semi-Structured Text Retrieval. , 2008, , .		2
67	An Efficient Combinatorial Approach for Solving the DNA Motif Finding Problem. , 2009, , .		1
68	Alkaline Phosphatase-Positive Immortal Mouse Embryo Fibroblasts Are Cells in a Transitional Reprogramming State Induced to Face Environmental Stresses. Genetics & Epigenetics, 2015, 7, GEG.S27696.	2.5	1
69	CMStalker: A Combinatorial Tool for Composite Motif Discovery. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 1123-1136.	3.0	1
70	Faster Deterministic Wakeup in Multiple Access Channels. Lecture Notes in Computer Science, 2005, , 196-204.	1.3	1
71	CMF: A Combinatorial Tool to Find Composite Motifs. Lecture Notes in Computer Science, 2013, , 196-208.	1.3	1
72	Efficient IP table lookup via adaptive stratified trees with selective reconstructions. Journal of Experimental Algorithmics, 2008, 12, 1-28.	1.0	0

#	ARTICLE	IF	CITATIONS
73	Detecting fuzzy amino acid tandem repeats in protein sequences. , 2011, , .		0
74	Editorial: Repetitive Structures in Biological Sequences: Algorithms and Applications. Frontiers in Bioengineering and Biotechnology, 2016, 4, 66.	4.1	0
75	A Framework to Evaluate Information Quality in Public Administration Website. Pacific Asia Journal of the Association for Information Systems, 0, , 25-42.	0.7	0
76	CNVScan. , 2015, , .		0
77	A Transcriptional Study of Oncogenes and Tumor Suppressors Altered by Copy Number Variations in Ovarian Cancer. Smart Innovation, Systems and Technologies, 2020, , 159-169.	0.6	0