Pierangelo Veltri

List of Publications by Year
in descending order

154 papers	1,790 citations	304743 22 h-index	361022 35 g-index
160 all docs	160 docs citations	160 times ranked	1554 citing authors

#	Article	IF	Citations
1	Pattern Discovery in Multilayer Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 741-752.	3.0	13
2	Calculation of Intracoronary Pressure-Based Indexes with JLabChart. Applied Sciences (Switzerland), 2022, 12, 3448.	2.5	10
3	A Novel Algorithm for Local Network Alignment Based on Network Embedding. Applied Sciences (Switzerland), 2022, 12, 5403.	2.5	2
4	PCN-Miner: an open-source extensible tool for the analysis of Protein Contact Networks. Bioinformatics, 2022, 38, 4235-4237.	4.1	11
5	Exploiting the molecular basis of age and gender differences in outcomes of SARS-CoV-2 infections. Computational and Structural Biotechnology Journal, 2021, 19, 4092-4100.	4.1	23
6	Data science in unveiling COVID-19 pathogenesis and diagnosis: evolutionary origin to drug repurposing. Briefings in Bioinformatics, 2021, 22, 855-872.	6.5	38
7	Regional Resource Assessment During the COVID-19 Pandemic in Italy: Modeling Study. JMIR Medical Informatics, 2021, 9, e18933.	2.6	4
8	In vitro CSC-derived cardiomyocytes exhibit the typical microRNA-mRNA blueprint of endogenous cardiomyocytes. Communications Biology, 2021, 4, 1146.	4.4	15
9	Clinical data annotation for parotid neoplasia management. , 2021, , .		3
10	Guest Editorial Innovative Data Analysis Methods for Biomedicine. IEEE Journal of Biomedical and Health Informatics, 2021, 25, 4066-4067.	6.3	0
11	Using dual-network-analyser for communities detecting in dual networks. BMC Bioinformatics, 2021, 22, 614.	2.6	4
12	Annotations for clinical data enrichment. , 2021, , .		1
13	A framework for clinical data integration and annotation for decision support. , 2021, , .		0
14	A Tool for clinical data annotation of parotid neoplasia. , 2021, , .		0
15	Model and Application to Support the Coronary Artery Diseases (CAD): Development and Testing. Interdisciplinary Sciences, Computational Life Sciences, 2020, 12, 50-58.	3.6	6
16	Melanoma Detection by Means of Multiple Instance Learning. Interdisciplinary Sciences, Computational Life Sciences, 2020, 12, 24-31.	3.6	42
17	Reduction in Global Myocardial Glucose Metabolism in Subjects With 1-Hour Postload Hyperglycemia and Impaired Glucose Tolerance. Diabetes Care, 2020, 43, 669-676.	8.6	25
18	Spatio-Temporal Resource Mapping for Intensive Care Units at Regional Level for COVID-19 Emergency in Italy. International Journal of Environmental Research and Public Health, 2020, 17, 3344.	2.6	14

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19	Atrial myxomas arise from multipotent cardiac stem cells. European Heart Journal, 2020, 41, 4332-4345.	2.2	51
20	Information Retrieval in Life Sciences. , 2019, , 1104-1108.		1
21	On discovering relevant features for tongue colored image analysis. , 2019, , .		5
22	Towards Heterogeneous Network Alignment: Design and Implementation of a Large-Scale Data Processing Framework. Lecture Notes in Computer Science, 2019, , 692-703.	1.3	2
23	Mathematical Theories in the Era of Big Data. Mathematical Problems in Engineering, 2019, 2019, 1-2.	1.1	0
24	Functional module extraction by ensembling the ensembles of selective module detectors. International Journal of Computational Biology and Drug Design, 2019, 12, 345.	0.3	2
25	H-Ferritin Affects Cisplatin-Induced Cytotoxicity in Ovarian Cancer Cells through the Modulation of ROS. Oxidative Medicine and Cellular Longevity, 2019, 2019, 1-13.	4.0	41
26	Using Dual Networks for the Integration of Clinical and Biological Data.. , 2019, , .		0
27	On the reliability of measurements for a stent positioning simulation system. International Journal of Medical Informatics, 2019, 123, 23-28.	3.3	16
28	Methodologies of speech analysis for neurodegenerative diseases evaluation. International Journal of Medical Informatics, 2019, 122, 45-54.	3.3	34
29	On the Usefulness of Pre-Processing Step in Melanoma Detection Using Multiple Instance Learning. Lecture Notes in Computer Science, 2019, , 374-382.	1.3	22
30	Melanoma detection using color and texture features in computer vision systems. Advances in Science, Technology and Engineering Systems, 2019, 4, 16-22.	0.5	28
31	Kitcre knock-in mice fail to fate-map cardiac stem cells. Nature, 2018, 555, E1-E5.	27.8	79
32	An Innovative Framework for Bioimage Annotation and Studies. Interdisciplinary Sciences, Computational Life Sciences, 2018, 10, 544-557.	3.6	3
33	On the Classification of EEG Signal by Using an SVM Based Algorithm. Smart Innovation, Systems and Technologies, 2018, , 271-278.	0.6	15
34	Image pre-processing in computer vision systems for melanoma detection. , 2018, , .		26
35	INTEGRO: an algorithm for data-integration and disease-gene association. , 2018, , .		10
36	Features for Melanoma Lesions Characterization in Computer Vision Systems. , 2018, , .		18

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37	On the use of mining techniques to analyse human papilloma virus dataset. , 2018, , .		1
38	Deep Learning Techniques for Electronic Health Record Analysis. , 2018, , .		30
39	Tracking agricultural products for wellness care. , 2018, , .		4
40	A Voice-Aware System for Vocal Wellness. , 2018, , .		0
41	Software Tools for Medical Imaging Extended Abstract. Communications in Computer and Information Science, 2018, , 297-304.	0.5	3
42	SL-GLAlign. , 2018, , .		0
43	Modeling and application of aorta coarctation: support system for pre-operative decision. , 2018, , .		1
44	VOTA - A Vocal Tract and Training Analysis Tool. , 2018, , .		2
45	A framework for the decomposition and features extraction from lung DICOM images. , 2018, , .		10
46	On Blood Viscosity and Its Correlation with Biological Parameters. Lecture Notes in Computer Science, 2018, , 347-353.	1.3	1
47	Database Community and Health Related Data: Experiences Through the Last Decade. Studies in Big Data, 2018, , 473-487.	1.1	0
48	On the Analysis of Diseases and Their Related Geographical Data. IEEE Journal of Biomedical and Health Informatics, 2017, 21, 228-237.	6.3	17
49	Parallel and Cloud-Based Analysis of Omics Data: Modelling and Simulation in Medicine. , 2017, , .		5
50	Vocal signal analysis in patients affected by Multiple Sclerosis. Procedia Computer Science, 2017, 108, 1205-1214.	2.0	17
51	Using Graphs to Relate Patient's Clinical and Geographical Data.. Procedia Computer Science, 2017, 110, 448-452.	2.0	1
52	On the use of Networks in Biomedicine. Procedia Computer Science, 2017, 110, 498-503.	2.0	19
53	Adult cardiac stem cells are multipotent and robustly myogenic: c-kit expression is necessary but not sufficient for their identification. Cell Death and Differentiation, 2017, 24, 2101-2116.	11.2	131
54	An extensive assessment of network alignment algorithms for comparison of brain connectomes. BMC Bioinformatics, 2017, 18, 235.	2.6	32

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55	Associating Genomics and Clinical Information by Means of Semantic Based Ranking. , 2017, , .		0
56	Signal Analysis for Voice Evaluation in Parkinson's Disease. , 2017, , .		14
57	Development of a DSS for cardiovascular prevention and rehabilitation. , 2017, , .		0
58	Network based algorithms for module extraction from RNASeq data: A quantitative assessment. , 2017, , .		0
59	On a recent algorithm for multiple instance learning. Preliminary applications in image classification. , 2017, , .		15
60	Development and testing of the application based on coronary artery diseases (CAD). , 2017, , .		1
61	mEEG: A system for electroencephalogram data management and analysis. , 2017, , .		3
62	Data mining techniques for vestibular data classification. International Journal of Internet Technology and Secured Transactions, 2017, 7, 51.	0.4	2
63	On the Use of Voice Signals for Studying Sclerosis Disease. Computers, 2017, 6, 30.	3.3	0
64	A Multi-Task Framework for Monitoring Health Conditions via Attention-based Recurrent Neural Networks. AMIA ... Annual Symposium proceedings, 2017, 2017, 1665-1674.	0.2	8
65	Using miRNA-Analyzer for the Analysis of miRNA Data. Microarrays (Basel, Switzerland), 2016, 5, 29.	1.4	1
66	Experiences on quantitative cardiac PET analysis. , 2016, , .		15
67	On the identification of long non-coding RNAs from RNA-seq. , 2016, , .		4
68	G-quadruplex Structure Prediction and integration in the GenData2020 data model. , 2016, , .		1
69	High-performance data structures for de novo assembly of genomes. , 2016, , .		2
70	GIDAC: A prototype for bioimages annotation and clinical data integration. , 2016, , .		5
71	Microfluidic device for continuous single cells analysis via Raman spectroscopy enhanced by integrated plasmonic nanodimers. Optics Express, 2016, 24, A180.	3.4	38
72	Applying Mining Techniques to Analyze Vestibular Data. Procedia Computer Science, 2016, 98, 467-472.	2.0	4

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73	Geoblood: A Web Based Tool for Geo-analysis of Biological Data. Procedia Computer Science, 2016, 98, 473-478.	2.0	4
74	Computational Methods for Detecting Functional Modules from Gene Regulatory Network. , 2016, , .		4
75	Feature Selection Model for Diagnosis, Electronic Medical Records and Geographical Data Correlation. , 2016, , .		2
76	A New ICT Based Model for Wellness and Health Care. Smart Innovation, Systems and Technologies, 2016, , 243-252.	0.6	0
77	Using SSN-Analyzer for analysis of semantic similarity networks. Network Modeling Analysis in Health Informatics and Bioinformatics, 2015, 4, 1.	2.1	0
78	An m-health system for the estimation of voice disorders. , 2015, , .		12
79	MODULA: A network module based local protein interaction network alignment method. , 2015, , .		5
80	LiSE: A Personal Booklet for Health Care Annotation. , 2015, , .		1
81	Management and Analysis of Biological and Clinical Data: How Computer Science May Support Biomedical and Clinical Research. Physics Procedia, 2015, 62, 29-35.	1.2	3
82	A framework for the atrial fibrillation prediction in electrophysiological studies. Computer Methods and Programs in Biomedicine, 2015, 120, 65-76.	4.7	23
83	ICT Solutions for Health Education Model. , 2015, , .		0
84	Intelligent healthcare informatics in big data era. Artificial Intelligence in Medicine, 2015, 65, 75-77.	6.5	32
85	A noise-aware methodology for a Mobile Voice Screening application. , 2015, , .		3
86	Methods and Techniques for miRNA Data Analysis. Methods in Molecular Biology, 2015, 1375, 11-23.	0.9	4
87	Design and Implementation of a Telecardiology System for Mobile Devices. Interdisciplinary Sciences, Computational Life Sciences, 2015, 7, 266-274.	3.6	7
88	Voice signal features analysis and classification. , 2015, , .		7
89	Study on Squeaking Hip Analysis. , 2014, , .		0
90	Relating Clinical Diagnosis and Biological Analytes via EMRs Clustering. , 2014, , .		0

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91	A system for ubiquitous distributed acquisition of voice alteration samples through a mobile application. , 2014, , .		3
92	A system for geoanalysis of clinical and geographical data. , 2014, , .		1
93	An R-based tool for miRNA data analysis and correlation with clinical ontologies. , 2014, , .		0
94	Hippocampal BOLD response during category learning predicts subsequent performance on transfer generalization. Human Brain Mapping, 2014, 35, 3122-3131.	3.6	6
95	Assessment of G-quadruplex Prediction Tools. , 2014, , .		2
96	Toward an accurate prediction of inter-residue distances in proteins using 2D recursive neural networks. BMC Bioinformatics, 2014, 15, 6.	2.6	51
97	Annotation and retrieval in protein interaction databases. European Physical Journal Plus, 2014, 129, 1.	2.6	0
98	An Architecture for Integrating Genetic and Clinical Data. Procedia Computer Science, 2014, 29, 1959-1969.	2.0	1
99	Thresholding of Semantic Similarity Networks Using a Spectral Graph-Based Technique. Lecture Notes in Computer Science, 2014, , 201-213.	1.3	3
100	Biological Databases. , 2014, , 431-440.		2
101	OntoPIN: An ontology-annotated PPI database. Interdisciplinary Sciences, Computational Life Sciences, 2013, 5, 187-195.	3.6	1
102	Methodologies for the analysis and classification of PET neuroimages. Network Modeling Analysis in Health Informatics and Bioinformatics, 2013, 2, 191-208.	2.1	17
103	AutoSPET: An SPM plugin to automatize neuroimages PET analysis. Interdisciplinary Sciences, Computational Life Sciences, 2013, 5, 225-232.	3.6	3
104	Modularity and community detection in Semantic Similarity Networks trough Spectral Based Transformation and Markov Clustering. , 2013, , .		0
105	Using open data in health care and tourism. , 2013, , .		1
106	Protein Structure Metapredictors. , 2013, , 1781-1785.		1
107	Distributed Data Management. , 2013, , 603-604.		0
108	J-TM Align: Efficient Comparison of Protein Structure Based on TMAlign. Current Bioinformatics, 2013, 8, 220-225.	1.5	1

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109	Studying neonatal TSH distribution by using GIS. , 2012, , .		4
110	A system for acquiring and management of ECG signals by using mobile devices. , 2012, , .		1
111	Health risk assessment of zoonotic infections agents through plant products in areas with high livestock pressure. , 2012, , .		2
112	Unraveling multiple miRNA-mRNA associations through a graph-based approach. , 2012, , .		1
113	A time series approach for clustering mass spectrometry data. Journal of Computational Science, 2012, 3, 344-355.	2.9	31
114	VeNet: A framework for the analysis of protein interaction networks through vector space embedding. , 2011, , .		1
115	A peroxisome proliferatorâ€activated receptor gamma (<i>PPARG</i>) polymorphism is associated with zoledronic acidâ€related osteonecrosis of the jaw in multiple myeloma patients: analysis by DMET microarray profiling. British Journal of Haematology, 2011, 154, 529-533.	2.5	69
116	Automatic summarisation and annotation of microarray data. Soft Computing, 2011, 15, 1505-1512.	3.6	17
117	A System for the Analysis of Snore Signals. Procedia Computer Science, 2011, 4, 1101-1108.	2.0	5
118	Experimental evaluation of OntoPIN. , 2011, , .		1
119	Using semantic similarity to detect features in yeast protein complexes. , 2011, , .		0
120	Protein-to-protein interactions. ACM Computing Surveys, 2010, 43, 1-36.	23.0	122
121	Using ontologies for querying and analysing protein-protein interaction data. Procedia Computer Science, 2010, 1, 997-1004.	2.0	17
122	IMPRECO: Distributed prediction of protein complexes. Future Generation Computer Systems, 2010, 26, 434-440.	7.5	29
123	Experimental comparison of biclustering algorithms for PPI networks. , 2010, , .		2
124	Using RDF for managing protein-protein interaction data. , 2010, , .		2
125	Using ontologies for annotating and retrieving protein-protein interactions data. , 2009, , .		2
126	Cartesio: A Software Tool for Pre-implant Stent Analyses. Lecture Notes in Computer Science, 2009, , 810-818.	1.3	1

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127	MaSDA: A system for analyzing mass spectrometry data. Computer Methods and Programs in Biomedicine, 2009, 95, S12-S21.	4.7	3
128	Improving protein secondary structure predictions by prediction fusion. Information Fusion, 2009, 10, 217-232.	19.1	15
129	StiMaRe: A software tool supporting visual stimuli definition and analysis in magnetic resonance. , 2009, , .		0
130	A device for stent designing in emodynamic surgery room. , 2009, , .		0
131	An Extension of the TIGR M4 Suite to Preprocess and Visualize Affymetrix Binary Files. Lecture Notes in Computer Science, 2009, , 265-274.	1.3	1
132	Management and Analysis of Mass Spectrometry Proteomics Data on the Grid. , 2009, , 206-227.		0
133	Experimental Evaluation of Protein Secondary Structure Predictors. Lecture Notes in Computer Science, 2009, , 848-857.	1.3	0
134	SIGMCC: A system for sharing meta patient records in a Peer-to-Peer environment. Future Generation Computer Systems, 2008, 24, 222-234.	7.5	28
135	MSPtool: A Versatile Tool for Mass Spectrometry Data Preprocessing. , 2008, , .		2
136	A proteomics approach to identify changes in protein profiles in serum of Familial Adenomatous Polyposis patients. Cancer Letters, 2008, 272, 40-52.	7.2	22
137	myMCL: A Web Portal for Protein Complexes Prediction. , 2008, , .		1
138	A Tool for the Semiautomatic Acquisition of the Morphological Data of Blood Vessel Networks. , 2008, , .		2
139	IMPRECO: A Tool for Improving the Prediction of Protein Complexes. Lecture Notes in Computer Science, 2008, , 148-157.	1.3	0
140	Semantic extraction and adaptive delivery of multimedia contents for the cultural assets. , 2007, , .		0
141	Algorithms and tools for analysis and management of mass spectrometry data. Briefings in Bioinformatics, 2007, 9, 144-155.	6.5	17
142	A Grid Environment for High-Throughput Proteomics. IEEE Transactions on Nanobioscience, 2007, 6, 117-123.	3.3	8
143	MS-Analyzer: preprocessing and data mining services for proteomics applications on the Grid. Concurrency Computation Practice and Experience, 2007, 19, 2047-2066.	2.2	16
144	The EIPeptiDi tool: enhancing peptide discovery in ICAT-based LC MS/MS experiments. BMC Bioinformatics, 2007, 8, 255.	2.6	10

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145	SpecDB: A Database for Storing and Managing Mass Spectrometry Proteomics Data. Lecture Notes in Computer Science, 2006, , 236-245.	1.3	1
146	PROTEIN SECONDARY STRUCTURE PREDICTION: HOW TO IMPROVE ACCURACY BY INTEGRATION. , 2006, , .		1
147	A General Architecture for Grid-Based PSE Toolkits. Lecture Notes in Computer Science, 2006, , 656-664.	1.3	4
148	Studying the XML Web: Gathering Statistics from an XML Sample. World Wide Web, 2005, 8, 413-438.	4.0	42
149	MS-Analyzer: Intelligent Preprocessing, Management, and Data Mining Analysis of Mass Spectrometry Data on the Grid. , 2005, , .		3
150	Using Views to Query XML Documents. , 2005, , 729-735.		1
151	PROTEUS: a Bioinformatics Problem Solving Environment on Grids. Parallel Processing Letters, 2004, 14, 217-237.	0.6	15
152	The XML web. , 2003, , .		70
153	Views in a large-scale XML repository. VLDB Journal, 2002, 11, 238-255.	4.1	37
154	Metabolic Syndrome Is Associated With Impaired Insulin-Stimulated Myocardial Glucose Metabolic Rate in Individuals With Type 2 Diabetes: A Cardiac Dynamic 18F-FDG-PET Study. Frontiers in Cardiovascular Medicine, 0, 9, .	2.4	10