Pietro Hiram Guzzi

List of Publications by Year
in descending order

143 papers	2,978 citations	147726 31 h-index	189801 50 g-index
156 all docs	156 docs citations	156 times ranked	2762 citing authors

#	Article	IF	Citations
1	Structural genetics of circulating variants affecting the SARS-CoV-2 spike/human ACE2 complex. Journal of Biomolecular Structure and Dynamics, 2022, 40, 6545-6555.	2.0	40
2	Calculation of Intracoronary Pressure-Based Indexes with JLabChart. Applied Sciences (Switzerland), 2022, 12, 3448.	1.3	10
3	Modeling multi-scale data via a network of networks. Bioinformatics, 2022, 38, 2544-2553.	1.8	30
4	Network for network concept offers new insights into host- SARS-CoV-2 protein interactions and potential novel targets for developing antiviral drugs. Computers in Biology and Medicine, 2022, 146, 105575.	3.9	12
5	Omics sciences. , 2022, , 105-118.		0
6	Integrative bioinformatics. , 2022, , 129-136.		0
7	Biological networks analysis. , 2022, , 137-150.		0
8	Ontologies in bioinformatics. , 2022, , 119-128.		0
9	Beyond COVID-19 pandemic: Topology-aware optimization of vaccination strategy for minimizing virus spreading. Computational and Structural Biotechnology Journal, 2022, 20, 2664-2671.	1.9	11
10	A Novel Algorithm for Local Network Alignment Based on Network Embedding. Applied Sciences (Switzerland), 2022, 12, 5403.	1.3	2
11	Disease spreading modeling and analysis: a survey. Briefings in Bioinformatics, 2022, 23, .	3.2	20
12	PCN-Miner: an open-source extensible tool for the analysis of Protein Contact Networks. Bioinformatics, 2022, 38, 4235-4237.	1.8	11
13	Parallel and distributed association rule mining in life science: A novel parallel algorithm to mine genomics data. Information Sciences, 2021, 575, 747-761.	4.0	17
14	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.	1.9	23
15	Data science in unveiling COVID-19 pathogenesis and diagnosis: evolutionary origin to drug repurposing. Briefings in Bioinformatics, 2021, 22, 855-872.	3.2	38
16	Regional Resource Assessment During the COVID-19 Pandemic in Italy: Modeling Study. JMIR Medical Informatics, 2021, 9, e18933.	1.3	4
17	A novel algorithm for finding top-k weighted overlapping densest connected subgraphs in dual networks. Applied Network Science, 2021, 6, 40.	0.8	14
18	Analyzing host-viral interactome of SARS-CoV-2 for identifying vulnerable host proteins during COVID-19 pathogenesis. Infection, Genetics and Evolution, 2021, 93, 104921.	1.0	21

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19	Top-k Connected Overlapping Densest Subgraphs in Dual Networks. Studies in Computational Intelligence, 2021, , 585-596.	0.7	2
20	Using dual-network-analyser for communities detecting in dual networks. BMC Bioinformatics, 2021, 22, 614.	1.2	4
21	Sentiment analysis for mining texts and social networks data: Methods and tools. Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery, 2020, 10, e1333.	4.6	49
22	SL-GLAlign: improving local alignment of biological networks through simulated annealing. Network Modeling Analysis in Health Informatics and Bioinformatics, 2020, 9, 1.	1.2	6
23	Predicting the response of the dental pulp to SARS-CoV2 infection: a transcriptome-wide effect cross-analysis. Genes and Immunity, 2020, 21, 360-363.	2.2	40
24	Extracting Dense and Connected Communities in Dual Networks: An Alignment Based Algorithm. IEEE Access, 2020, 8, 162279-162289.	2.6	5
25	Protein interaction networks. , 2020, , 133-166.		0
26	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.	1.2	14
27	An efficient and scalable SPARK preprocessing methodology for Genome Wide Association Studies. , 2020, , .		2
28	Non-coding RNAs in cancer: platforms and strategies for investigating the genomic â€œdark matterâ€. Journal of Experimental and Clinical Cancer Research, 2020, 39, 117.	3.5	137
29	Brain connectome networks and analysis. , 2020, , 167-182.		0
30	L-HetNetAligner: A novel algorithm for Local Alignment of Heterogeneous Biological Networks. Scientific Reports, 2020, 10, 3901.	1.6	18
31	Master Regulator Analysis of the SARS-CoV-2/Human Interactome. Journal of Clinical Medicine, 2020, 9, 982.	1.0	160
32	DMETTM Genotyping: Tools for Biomarkers Discovery in the Era of Precision Medicine. High-Throughput, 2020, 9, 8.	4.4	11
33	Learning Weighted Association Rules in Human Phenotype Ontology. Lecture Notes in Computer Science, 2020, , 245-256.	1.0	0
34	Parallel Learning of Weighted Association Rules in Human Phenotype Ontology. Lecture Notes in Computer Science, 2020, , 549-559.	1.0	0
35	Functional Enrichment Analysis Methods. , 2019, , 896-897.		1
36	Integrative Bioinformatics of Transcriptome: Databases, Tools and Pipelines. , 2019, , 1099-1103.		0

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37	Ontology-Based Annotation Methods. , 2019, , 867-869.		0
38	Using multiple network alignment for studying connectomes. Network Modeling Analysis in Health Informatics and Bioinformatics, 2019, 8, 1.	1.2	4
39	Towards Heterogeneous Network Alignment: Design and Implementation of a Large-Scale Data Processing Framework. Lecture Notes in Computer Science, 2019, , 692-703.	1.0	2
40	Network building and analysis in connectomics studies: a review of algorithms, databases and technologies. Network Modeling Analysis in Health Informatics and Bioinformatics, 2019, 8, 1.	1.2	9
41	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
42	Mining Association Rules From Disease Ontology. , 2019, , .		0
43	Qualitative assessment of functional module detectors on microarray and RNASeq data. Network Modeling Analysis in Health Informatics and Bioinformatics, 2019, 8, 1.	1.2	12
44	Parallel extraction of association rules from genomics data. Applied Mathematics and Computation, 2019, 350, 434-446.	1.4	28
45	GLAlign: A Novel Algorithm for Local Network Alignment. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1958-1969.	1.9	14
46	Functional module extraction by ensembling the ensembles of selective module detectors. International Journal of Computational Biology and Drug Design, 2019, 12, 345.	0.3	0
47	Towards Local Alignment of Multiple Networks. , 2019, , .		0
48	Survey of local and global biological network alignment: the need to reconcile the two sides of the same coin. Briefings in Bioinformatics, 2018, 19, bbw132.	3.2	69
49	An experimental study of information content measurement of gene ontology terms. International Journal of Machine Learning and Cybernetics, 2018, 9, 427-439.	2.3	8
50	An Innovative Framework for Bioimage Annotation and Studies. Interdisciplinary Sciences, Computational Life Sciences, 2018, 10, 544-557.	2.2	3
51	DIETOS: A dietary recommender system for chronic diseases monitoring and management. Computer Methods and Programs in Biomedicine, 2018, 153, 93-104.	2.6	59
52	Chemical Characterization of Interacting Genes in Few Subnetworks of Alzheimer's Disease. , 2018, , .		2
53	From Single Level Analysis to Multi-Omics Integrative Approaches: A Powerful Strategy towards the Precision Oncology. High-Throughput, 2018, 7, 33.	4.4	48
54	A Parallel Software Pipeline for DMET Microarray Genotyping Data Analysis. High-Throughput, 2018, 7, 17.	4.4	4

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55	Learning Association Rules for Pharmacogenomic Studies. Lecture Notes in Computer Science, 2018, , 1-15.	1.0	0
56	On the Analysis of Diseases and Their Related Geographical Data. IEEE Journal of Biomedical and Health Informatics, 2017, 21, 228-237.	3.9	17
57	Using Graphs to Relate Patientâ€™s Clinical and Geographical Data.. Procedia Computer Science, 2017, 110, 448-452.	1.2	1
58	Using Multi Network Alignment for Analysis of Connectomes. Procedia Computer Science, 2017, 108, 1155-1164.	1.2	3
59	An extensive assessment of network alignment algorithms for comparison of brain connectomes. BMC Bioinformatics, 2017, 18, 235.	1.2	32
60	High Performance Analysis of Omics Data: Experiences at University Magna Graecia of Catanzaro. , 2017, , .		0
61	Network based algorithms for module extraction from RNASeq data: A quantitative assessment. , 2017, , .		0
62	Performing local network alignment by ensembling global aligners. , 2017, , .		3
63	Genetic variants associated with Fabry disease progression despite enzyme replacement therapy. Oncotarget, 2017, 8, 107558-107564.	0.8	30
64	DMETâ„¢ (Drug Metabolism Enzymes and Transporters): a pharmacogenomic platform for precision medicine. Oncotarget, 2016, 7, 54028-54050.	0.8	68
65	OSAnalyzer: A Bioinformatics Tool for the Analysis of Gene Polymorphisms Enriched with Clinical Outcomes. Microarrays (Basel, Switzerland), 2016, 5, 24.	1.4	14
66	Using miRNA-Analyzer for the Analysis of miRNA Data. Microarrays (Basel, Switzerland), 2016, 5, 29.	1.4	1
67	Experiences on quantitative cardiac PET analysis. , 2016, , .		15
68	Using Network Alignment for Analysis of Connectomes. , 2016, , .		3
69	GIDAC: A prototype for bioimages annotation and clinical data integration. , 2016, , .		5
70	Geoblood: A Web Based Tool for Geo-analysis of Biological Data. Procedia Computer Science, 2016, 98, 473-478.	1.2	4
71	Computational Methods for Detecting Functional Modules from Gene Regulatory Network. , 2016, , .		4
72	Feature Selection Model for Diagnosis, Electronic Medical Records and Geographical Data Correlation. , 2016, , .		2

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73	Identification of polymorphic variants associated with erlotinib-related skin toxicity in advanced non-small cell lung cancer patients by DMET microarray analysis. Cancer Chemotherapy and Pharmacology, 2016, 77, 205-209.	1.1	42
74	Experimental treatment of multiple myeloma in the era of precision medicine. Expert Review of Precision Medicine and Drug Development, 2016, 1, 37-51.	0.4	5
75	Extracting Cross-Ontology Weighted Association Rules from Gene Ontology Annotations. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2016, 13, 197-208.	1.9	36
76	Methodologies and experimental platforms for generating and analysing microarray and mass spectrometry-based omics data to support P4 medicine. Briefings in Bioinformatics, 2016, 17, 553-561.	3.2	19
77	Genetic variants associated with gastrointestinal symptoms in Fabry disease. Oncotarget, 2016, 7, 85895-85904.	0.8	30
78	Efficient learning of association rules from human phenotype ontology. , 2015, , .		0
79	Towards the assessment of GRN algorithms based on (disease) ontology. , 2015, , .		1
80	Using SSN-Analyzer for analysis of semantic similarity networks. Network Modeling Analysis in Health Informatics and Bioinformatics, 2015, 4, 1.	1.2	0
81	Analysis of miRNA, mRNA, and TF interactions through network-based methods. Eurasip Journal on Bioinformatics and Systems Biology, 2015, 2015, 4.	1.4	22
82	MODULA: A network module based local protein interaction network alignment method. , 2015, , .		5
83	LiSE: A Personal Booklet for Health Care Annotation. , 2015, , .		1
84	GoD: An R-package based on ontologies for prioritization of genes with respect to diseases. Journal of Computational Science, 2015, 9, 7-13.	1.5	18
85	Using GO-WAR for mining cross-ontology weighted association rules. Computer Methods and Programs in Biomedicine, 2015, 120, 113-122.	2.6	17
86	DMET-Miner: Efficient discovery of association rules from pharmacogenomic data. Journal of Biomedical Informatics, 2015, 56, 273-283.	2.5	49
87	Biological Network Inference from Microarray Data, Current Solutions, and Assessments. Methods in Molecular Biology, 2015, 1375, 155-167.	0.4	5
88	ICT Solutions for Health Education Model. , 2015, , .		0
89	Design and Implementation of a Telecardiology System for Mobile Devices. Interdisciplinary Sciences, Computational Life Sciences, 2015, 7, 266-274.	2.2	7
90	Integrated analysis of microRNAs, transcription factors and target genes expression discloses a specific molecular architecture of hyperdiploid multiple myeloma. Oncotarget, 2015, 6, 19132-19147.	0.8	41

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91	GO-WAR: A Tool for Mining Weighted Association Rules from Gene Ontology Annotations. Lecture Notes in Computer Science, 2015, , 3-18.	1.0	1
92	Improving annotation quality in gene ontology by mining cross-ontology weighted association rules. , 2014, , .		5
93	DMET-miner: Efficient learning of association rules from genotyping data for personalized medicine. , 2014, , .		0
94	A taxonomy for bioinformatics tools. , 2014, , .		0
95	Biases in information content measurement of gene ontology terms. , 2014, , .		4
96	Relating Clinical Diagnosis and Biological Analytes via EMRs Clustering. , 2014, , .		0
97	A web-based tool to analyze semantic similarity networks. , 2014, , .		0
98	coreSNP: Parallel Processing of Microarray Data. IEEE Transactions on Computers, 2014, 63, 2961-2974.	2.4	32
99	Tractography in amyotrophic lateral sclerosis using a novel probabilistic tool: A study with tract-based reconstruction compared to voxel-based approach. Journal of Neuroscience Methods, 2014, 224, 79-87.	1.3	43
100	Annotation and retrieval in protein interaction databases. European Physical Journal Plus, 2014, 129, 1.	1.2	0
101	Improving the Robustness of Local Network Alignment: Design and Extensive Assessment of a Markov Clustering-Based Approach. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2014, 11, 561-572.	1.9	56
102	Vestibular disorders in euthyroid patients with Hashimoto's thyroiditis: role of thyroid autoimmunity. Clinical Endocrinology, 2014, 81, 600-605.	1.2	26
103	A Discussion on the Biological Relevance of Clustering Results. Lecture Notes in Computer Science, 2014, , 30-44.	1.0	5
104	Mining Association Rules from Gene Ontology and Protein Networks: Promises and Challenges.. Procedia Computer Science, 2014, 29, 1970-1980.	1.2	19
105	Thresholding of Semantic Similarity Networks Using a Spectral Graph-Based Technique. Lecture Notes in Computer Science, 2014, , 201-213.	1.0	3
106	In Vivo Activity of MiR-34a Mimics Delivered by Stable Nucleic Acid Lipid Particles (SNALPs) against Multiple Myeloma. PLoS ONE, 2014, 9, e90005.	1.1	101
107	Visualization of protein interaction networks: problems and solutions. BMC Bioinformatics, 2013, 14, S1.	1.2	70
108	OntoPIN: An ontology-annotated PPI database. Interdisciplinary Sciences, Computational Life Sciences, 2013, 5, 187-195.	2.2	1

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109	Editorial: special issue on computational approaches for extracting knowledge from biological networks. Interdisciplinary Sciences, Computational Life Sciences, 2013, 5, 165-166.	2.2	0
110	Building and mining web-based questionnaires and surveys with SySQ. Interdisciplinary Sciences, Computational Life Sciences, 2013, 5, 233-239.	2.2	2
111	Application of different classification techniques on brain morphological data. , 2013, , .		3
112	Data mining and life sciences applications on the grid. Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery, 2013, 3, 216-238.	4.6	33
113	Micro-Analyzer: Automatic preprocessing of Affymetrix microarray data. Computer Methods and Programs in Biomedicine, 2013, 111, 402-409.	2.6	6
114	M-Finder: Uncovering functionally associated proteins from interactome data integrated with GO annotations. Proteome Science, 2013, 11, S3.	0.7	34
115	An Overview on Semantic Analysis of Proteomics Data. , 2013, , .		0
116	Modularity and community detection in Semantic Similarity Networks trough Spectral Based Transformation and Markov Clustering. , 2013, , .		0
117	The role of parallelism, web services and ontologies in bioinformatics and omics data management and analysis. EMBnet Journal, 2013, 19, 59.	0.2	2
118	In Vitro and in Vivo Anti-tumor Activity of miR-221/222 Inhibitors in Multiple Myeloma. Oncotarget, 2013, 4, 242-255.	0.8	125
119	Semantic Similarities as Discriminative Features of Protein Complexes. Current Bioinformatics, 2013, 8, 347-356.	0.7	1
120	J-TM Align: Efficient Comparison of Protein Structure Based on TMAlign. Current Bioinformatics, 2013, 8, 220-225.	0.7	1
121	Editorial (Hot Topic:Systematic Analysis of Biological Networks). Current Bioinformatics, 2013, 8, 275-275.	0.7	1
122	SySQ: A Web-based system for survey and questionnaire management in medicine. , 2012, , .		0
123	AlignMCL: Comparative analysis of protein interaction networks through Markov clustering. , 2012, , .		25
124	CytoMCL: A Cytoscape plugin for fast clustering of protein interaction networks. , 2012, , .		1
125	Toward a Semantic Framework for the Querying, Mining and Visualization of Cancer Microenvironment Data. Lecture Notes in Computer Science, 2012, , 109-123.	1.0	0
126	Semantic similarity analysis of protein data: assessment with biological features and issues. Briefings in Bioinformatics, 2012, 13, 569-585.	3.2	236

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127	DMET-Analyzer: automatic analysis of Affymetrix DMET Data. BMC Bioinformatics, 2012, 13, 258.	1.2	66
128	AlignNemo: A Local Network Alignment Method to Integrate Homology and Topology. PLoS ONE, 2012, 7, e38107.	1.1	97
129	VeNet: A framework for the analysis of protein interaction networks through vector space embedding. , 2011, , .		1
130	Comparative analysis of nuclear estrogen receptor alpha and beta interactomes in breast cancer cells. Molecular BioSystems, 2011, 7, 667-676.	2.9	39
131	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.	1.2	69
132	Automatic summarisation and annotation of microarray data. Soft Computing, 2011, 15, 1505-1512.	2.1	17
133	A System for the Analysis of Snore Signals. Procedia Computer Science, 2011, 4, 1101-1108.	1.2	5
134	A large set of estrogen receptor Î²â€interacting proteins identified by tandem affinity purification in hormoneâ€responsive human breast cancer cell nuclei. Proteomics, 2011, 11, 159-165.	1.3	36
135	Single nucleotide polymorphisms of ABCC5 and ABCG1 transporter genes correlate to irinotecan-associated gastrointestinal toxicity in colorectal cancer patients: A DMET microarray profiling study. Cancer Biology and Therapy, 2011, 12, 780-787.	1.5	79
136	Protein-to-protein interactions. ACM Computing Surveys, 2010, 43, 1-36.	16.1	122
137	Î¼-CS: An extension of the TM4 platform to manage Affymetrix binary data. BMC Bioinformatics, 2010, 11, 315.	1.2	42
138	Using ontologies for querying and analysing protein-protein interaction data. Procedia Computer Science, 2010, 1, 997-1004.	1.2	17
139	IMPRECO: Distributed prediction of protein complexes. Future Generation Computer Systems, 2010, 26, 434-440.	4.9	29
140	An Extension of the TIGR M4 Suite to Preprocess and Visualize Affymetrix Binary Files. Lecture Notes in Computer Science, 2009, , 265-274.	1.0	1
141	A grid-based protein complex predictor. Studies in Health Technology and Informatics, 2008, 138, 116-24.	0.2	0
142	Using ontologies for preprocessing and mining spectra data on the Grid. Future Generation Computer Systems, 2007, 23, 55-60.	4.9	30
143	Using ontologies in PROTEUS for modeling proteomics data mining applications. Studies in Health Technology and Informatics, 2005, 112, 17-26.	0.2	1