

Pietro Hiram Guzzi

List of Publications by Year in descending order

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Version: 2024-02-01

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	Semantic similarity analysis of protein data: assessment with biological features and issues. <i>Briefings in Bioinformatics</i> , 2012, 13, 569-585.	3.2	236
2	Master Regulator Analysis of the SARS-CoV-2/Human Interactome. <i>Journal of Clinical Medicine</i> , 2020, 9, 982.	1.0	160
3	Non-coding RNAs in cancer: platforms and strategies for investigating the genomic "dark matter". <i>Journal of Experimental and Clinical Cancer Research</i> , 2020, 39, 117.	3.5	137
4	In Vitro and in Vivo Anti-tumor Activity of miR-221/222 Inhibitors in Multiple Myeloma. <i>Oncotarget</i> , 2013, 4, 242-255.	0.8	125
5	Protein-to-protein interactions. <i>ACM Computing Surveys</i> , 2010, 43, 1-36.	16.1	122
6	In Vivo Activity of MiR-34a Mimics Delivered by Stable Nucleic Acid Lipid Particles (SNALPs) against Multiple Myeloma. <i>PLoS ONE</i> , 2014, 9, e90005.	1.1	101
7	AlignNemo: A Local Network Alignment Method to Integrate Homology and Topology. <i>PLoS ONE</i> , 2012, 7, e38107.	1.1	97
8	Single nucleotide polymorphisms of ABCC5 and ABCG1 transporter genes correlate to irinotecan-associated gastrointestinal toxicity in colorectal cancer patients: A DMET microarray profiling study. <i>Cancer Biology and Therapy</i> , 2011, 12, 780-787.	1.5	79
9	Visualization of protein interaction networks: problems and solutions. <i>BMC Bioinformatics</i> , 2013, 14, S1.	1.2	70
10	A peroxisome proliferator-activated receptor gamma (<i>PPARG</i>) polymorphism is associated with zoledronic acid-related osteonecrosis of the jaw in multiple myeloma patients: analysis by DMET microarray profiling. <i>British Journal of Haematology</i> , 2011, 154, 529-533.	1.2	69
11	Survey of local and global biological network alignment: the need to reconcile the two sides of the same coin. <i>Briefings in Bioinformatics</i> , 2018, 19, bbw132.	3.2	69
12	DMET (Drug Metabolism Enzymes and Transporters): a pharmacogenomic platform for precision medicine. <i>Oncotarget</i> , 2016, 7, 54028-54050.	0.8	68
13	DMET-Analyzer: automatic analysis of Affymetrix DMET Data. <i>BMC Bioinformatics</i> , 2012, 13, 258.	1.2	66
14	DIETOS: A dietary recommender system for chronic diseases monitoring and management. <i>Computer Methods and Programs in Biomedicine</i> , 2018, 153, 93-104.	2.6	59
15	Improving the Robustness of Local Network Alignment: Design and Extensive Assessment of a Markov Clustering-Based Approach. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014, 11, 561-572.	1.9	56
16	DMET-Miner: Efficient discovery of association rules from pharmacogenomic data. <i>Journal of Biomedical Informatics</i> , 2015, 56, 273-283.	2.5	49
17	Sentiment analysis for mining texts and social networks data: Methods and tools. <i>Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery</i> , 2020, 10, e1333.	4.6	49
18	From Single Level Analysis to Multi-Omics Integrative Approaches: A Powerful Strategy towards the Precision Oncology. <i>High-Throughput</i> , 2018, 7, 33.	4.4	48

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19	Tractography in amyotrophic lateral sclerosis using a novel probabilistic tool: A study with tract-based reconstruction compared to voxel-based approach. <i>Journal of Neuroscience Methods</i> , 2014, 224, 79-87.	1.3	43
20	TM4-CS: An extension of the TM4 platform to manage Affymetrix binary data. <i>BMC Bioinformatics</i> , 2010, 11, 315.	1.2	42
21	Identification of polymorphic variants associated with erlotinib-related skin toxicity in advanced non-small cell lung cancer patients by DMET microarray analysis. <i>Cancer Chemotherapy and Pharmacology</i> , 2016, 77, 205-209.	1.1	42
22	Integrated analysis of microRNAs, transcription factors and target genes expression discloses a specific molecular architecture of hyperdiploid multiple myeloma. <i>Oncotarget</i> , 2015, 6, 19132-19147.	0.8	41
23	Predicting the response of the dental pulp to SARS-CoV2 infection: a transcriptome-wide effect cross-analysis. <i>Genes and Immunity</i> , 2020, 21, 360-363.	2.2	40
24	Structural genetics of circulating variants affecting the SARS-CoV-2 spike/human ACE2 complex. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 6545-6555.	2.0	40
25	Comparative analysis of nuclear estrogen receptor alpha and beta interactomes in breast cancer cells. <i>Molecular BioSystems</i> , 2011, 7, 667-676.	2.9	39
26	Data science in unveiling COVID-19 pathogenesis and diagnosis: evolutionary origin to drug repurposing. <i>Briefings in Bioinformatics</i> , 2021, 22, 855-872.	3.2	38
27	A large set of estrogen receptor interacting proteins identified by tandem affinity purification in hormone-responsive human breast cancer cell nuclei. <i>Proteomics</i> , 2011, 11, 159-165.	1.3	36
28	Extracting Cross-Ontology Weighted Association Rules from Gene Ontology Annotations. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2016, 13, 197-208.	1.9	36
29	M-Finder: Uncovering functionally associated proteins from interactome data integrated with GO annotations. <i>Proteome Science</i> , 2013, 11, S3.	0.7	34
30	Data mining and life sciences applications on the grid. <i>Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery</i> , 2013, 3, 216-238.	4.6	33
31	coreSNP: Parallel Processing of Microarray Data. <i>IEEE Transactions on Computers</i> , 2014, 63, 2961-2974.	2.4	32
32	An extensive assessment of network alignment algorithms for comparison of brain connectomes. <i>BMC Bioinformatics</i> , 2017, 18, 235.	1.2	32
33	Using ontologies for preprocessing and mining spectra data on the Grid. <i>Future Generation Computer Systems</i> , 2007, 23, 55-60.	4.9	30
34	Genetic variants associated with Fabry disease progression despite enzyme replacement therapy. <i>Oncotarget</i> , 2017, 8, 107558-107564.	0.8	30
35	Genetic variants associated with gastrointestinal symptoms in Fabry disease. <i>Oncotarget</i> , 2016, 7, 85895-85904.	0.8	30
36	Modeling multi-scale data via a network of networks. <i>Bioinformatics</i> , 2022, 38, 2544-2553.	1.8	30

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37	IMPRECO: Distributed prediction of protein complexes. <i>Future Generation Computer Systems</i> , 2010, 26, 434-440.	4.9	29
38	Parallel extraction of association rules from genomics data. <i>Applied Mathematics and Computation</i> , 2019, 350, 434-446.	1.4	28
39	Vestibular disorders in euthyroid patients with Hashimoto's thyroiditis: role of thyroid autoimmunity. <i>Clinical Endocrinology</i> , 2014, 81, 600-605.	1.2	26
40	AlignMCL: Comparative analysis of protein interaction networks through Markov clustering. , 2012, , .		25
41	Exploiting the molecular basis of age and gender differences in outcomes of SARS-CoV-2 infections. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 4092-4100.	1.9	23
42	Analysis of miRNA, mRNA, and TF interactions through network-based methods. <i>Eurasip Journal on Bioinformatics and Systems Biology</i> , 2015, 2015, 4.	1.4	22
43	Analyzing host-viral interactome of SARS-CoV-2 for identifying vulnerable host proteins during COVID-19 pathogenesis. <i>Infection, Genetics and Evolution</i> , 2021, 93, 104921.	1.0	21
44	Disease spreading modeling and analysis: a survey. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	20
45	Mining Association Rules from Gene Ontology and Protein Networks: Promises and Challenges.. <i>Procedia Computer Science</i> , 2014, 29, 1970-1980.	1.2	19
46	Methodologies and experimental platforms for generating and analysing microarray and mass spectrometry-based omics data to support P4 medicine. <i>Briefings in Bioinformatics</i> , 2016, 17, 553-561.	3.2	19
47	GoD: An R-package based on ontologies for prioritization of genes with respect to diseases. <i>Journal of Computational Science</i> , 2015, 9, 7-13.	1.5	18
48	L-HetNetAligner: A novel algorithm for Local Alignment of Heterogeneous Biological Networks. <i>Scientific Reports</i> , 2020, 10, 3901.	1.6	18
49	Using ontologies for querying and analysing protein-protein interaction data. <i>Procedia Computer Science</i> , 2010, 1, 997-1004.	1.2	17
50	Automatic summarisation and annotation of microarray data. <i>Soft Computing</i> , 2011, 15, 1505-1512.	2.1	17
51	Using GO-WAR for mining cross-ontology weighted association rules. <i>Computer Methods and Programs in Biomedicine</i> , 2015, 120, 113-122.	2.6	17
52	On the Analysis of Diseases and Their Related Geographical Data. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2017, 21, 228-237.	3.9	17
53	Parallel and distributed association rule mining in life science: A novel parallel algorithm to mine genomics data. <i>Information Sciences</i> , 2021, 575, 747-761.	4.0	17
54	Experiences on quantitative cardiac PET analysis. , 2016, , .		15

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55	OSAnalyzer: A Bioinformatics Tool for the Analysis of Gene Polymorphisms Enriched with Clinical Outcomes. <i>Microarrays (Basel, Switzerland)</i> , 2016, 5, 24.	1.4	14
56	GLAlign: A Novel Algorithm for Local Network Alignment. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 1958-1969.	1.9	14
57	Spatio-Temporal Resource Mapping for Intensive Care Units at Regional Level for COVID-19 Emergency in Italy. <i>International Journal of Environmental Research and Public Health</i> , 2020, 17, 3344.	1.2	14
58	A novel algorithm for finding top-k weighted overlapping densest connected subgraphs in dual networks. <i>Applied Network Science</i> , 2021, 6, 40.	0.8	14
59	Qualitative assessment of functional module detectors on microarray and RNASeq data. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2019, 8, 1.	1.2	12
60	Network for network concept offers new insights into host- SARS-CoV-2 protein interactions and potential novel targets for developing antiviral drugs. <i>Computers in Biology and Medicine</i> , 2022, 146, 105575.	3.9	12
61	DMETTM Genotyping: Tools for Biomarkers Discovery in the Era of Precision Medicine. <i>High-Throughput</i> , 2020, 9, 8.	4.4	11
62	Beyond COVID-19 pandemic: Topology-aware optimization of vaccination strategy for minimizing virus spreading. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 2664-2671.	1.9	11
63	PCN-Miner: an open-source extensible tool for the analysis of Protein Contact Networks. <i>Bioinformatics</i> , 2022, 38, 4235-4237.	1.8	11
64	Calculation of Intracoronary Pressure-Based Indexes with JLabChart. <i>Applied Sciences (Switzerland)</i> , 2022, 12, 3448.	1.3	10
65	Network building and analysis in connectomics studies: a review of algorithms, databases and technologies. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2019, 8, 1.	1.2	9
66	An experimental study of information content measurement of gene ontology terms. <i>International Journal of Machine Learning and Cybernetics</i> , 2018, 9, 427-439.	2.3	8
67	Design and Implementation of a Telecardiology System for Mobile Devices. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2015, 7, 266-274.	2.2	7
68	Micro-Analyzer: Automatic preprocessing of Affymetrix microarray data. <i>Computer Methods and Programs in Biomedicine</i> , 2013, 111, 402-409.	2.6	6
69	SL-GLAlign: improving local alignment of biological networks through simulated annealing. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2020, 9, 1.	1.2	6
70	A System for the Analysis of Snore Signals. <i>Procedia Computer Science</i> , 2011, 4, 1101-1108.	1.2	5
71	Improving annotation quality in gene ontology by mining cross-ontology weighted association rules. , 2014, , .		5
72	A Discussion on the Biological Relevance of Clustering Results. <i>Lecture Notes in Computer Science</i> , 2014, , 30-44.	1.0	5

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73	MODULA: A network module based local protein interaction network alignment method. , 2015, , .		5
74	Biological Network Inference from Microarray Data, Current Solutions, and Assessments. Methods in Molecular Biology, 2015, 1375, 155-167.	0.4	5
75	GIDAC: A prototype for bioimages annotation and clinical data integration. , 2016, , .		5
76	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
77	Extracting Dense and Connected Communities in Dual Networks: An Alignment Based Algorithm. IEEE Access, 2020, 8, 162279-162289.	2.6	5
78	Biases in information content measurement of gene ontology terms. , 2014, , .		4
79	Geoblood: A Web Based Tool for Geo-analysis of Biological Data. Procedia Computer Science, 2016, 98, 473-478.	1.2	4
80	Computational Methods for Detecting Functional Modules from Gene Regulatory Network. , 2016, , .		4
81	A Parallel Software Pipeline for DMET Microarray Genotyping Data Analysis. High-Throughput, 2018, 7, 17.	4.4	4
82	Using multiple network alignment for studying connectomes. Network Modeling Analysis in Health Informatics and Bioinformatics, 2019, 8, 1.	1.2	4
83	Regional Resource Assessment During the COVID-19 Pandemic in Italy: Modeling Study. JMIR Medical Informatics, 2021, 9, e18933.	1.3	4
84	Using dual-network-analyser for communities detecting in dual networks. BMC Bioinformatics, 2021, 22, 614.	1.2	4
85	Application of different classification techniques on brain morphological data. , 2013, , .		3
86	Using Network Alignment for Analysis of Connectomes. , 2016, , .		3
87	Using Multi Network Alignment for Analysis of Connectomes. Procedia Computer Science, 2017, 108, 1155-1164.	1.2	3
88	Performing local network alignment by ensembling global aligners. , 2017, , .		3
89	An Innovative Framework for Bioimage Annotation and Studies. Interdisciplinary Sciences, Computational Life Sciences, 2018, 10, 544-557.	2.2	3
90	Thresholding of Semantic Similarity Networks Using a Spectral Graph-Based Technique. Lecture Notes in Computer Science, 2014, , 201-213.	1.0	3

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91	Building and mining web-based questionnaires and surveys with SySQ. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2013, 5, 233-239.	2.2	2
92	Feature Selection Model for Diagnosis, Electronic Medical Records and Geographical Data Correlation. , 2016, , .		2
93	Chemical Characterization of Interacting Genes in Few Subnetworks of Alzheimerâ€™s Disease. , 2018, , .		2
94	Towards Heterogeneous Network Alignment: Design and Implementation of a Large-Scale Data Processing Framework. <i>Lecture Notes in Computer Science</i> , 2019, , 692-703.	1.0	2
95	Functional module extraction by ensembling the ensembles of selective module detectors. <i>International Journal of Computational Biology and Drug Design</i> , 2019, 12, 345.	0.3	2
96	An efficient and scalable SPARK preprocessing methodology for Genome Wide Association Studies. , 2020, , .		2
97	Top-k Connected Overlapping Densest Subgraphs in Dual Networks. <i>Studies in Computational Intelligence</i> , 2021, , 585-596.	0.7	2
98	The role of parallelism, web services and ontologies in bioinformatics and omics data management and analysis. <i>EMBnet Journal</i> , 2013, 19, 59.	0.2	2
99	A Novel Algorithm for Local Network Alignment Based on Network Embedding. <i>Applied Sciences (Switzerland)</i> , 2022, 12, 5403.	1.3	2
100	VeNet: A framework for the analysis of protein interaction networks through vector space embedding. , 2011, , .		1
101	CytoMCL: A Cytoscape plugin for fast clustering of protein interaction networks. , 2012, , .		1
102	OntoPIN: An ontology-annotated PPI database. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2013, 5, 187-195.	2.2	1
103	Towards the assessment of GRN algorithms based on (disease) ontology. , 2015, , .		1
104	LiSE: A Personal Booklet for Health Care Annotation. , 2015, , .		1
105	Using miRNA-Analyser for the Analysis of miRNA Data. <i>Microarrays (Basel, Switzerland)</i> , 2016, 5, 29.	1.4	1
106	Using Graphs to Relate Patientâ€™s Clinical and Geographical Data.. <i>Procedia Computer Science</i> , 2017, 110, 448-452.	1.2	1
107	Functional Enrichment Analysis Methods. , 2019, , 896-897.		1
108	An Extension of the TIGR M4 Suite to Preprocess and Visualize Affymetrix Binary Files. <i>Lecture Notes in Computer Science</i> , 2009, , 265-274.	1.0	1

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109	Semantic Similarities as Discriminative Features of Protein Complexes. <i>Current Bioinformatics</i> , 2013, 8, 347-356.	0.7	1
110	J-TM Align: Efficient Comparison of Protein Structure Based on TMAAlign. <i>Current Bioinformatics</i> , 2013, 8, 220-225.	0.7	1
111	Editorial (Hot Topic: Systematic Analysis of Biological Networks). <i>Current Bioinformatics</i> , 2013, 8, 275-275.	0.7	1
112	GO-WAR: A Tool for Mining Weighted Association Rules from Gene Ontology Annotations. <i>Lecture Notes in Computer Science</i> , 2015, , 3-18.	1.0	1
113	Using ontologies in PROTEUS for modeling proteomics data mining applications. <i>Studies in Health Technology and Informatics</i> , 2005, 112, 17-26.	0.2	1
114	SySQ: A Web-based system for survey and questionnaire management in medicine. , 2012, , .		0
115	Toward a Semantic Framework for the Querying, Mining and Visualization of Cancer Microenvironment Data. <i>Lecture Notes in Computer Science</i> , 2012, , 109-123.	1.0	0
116	Editorial: special issue on computational approaches for extracting knowledge from biological networks. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2013, 5, 165-166.	2.2	0
117	An Overview on Semantic Analysis of Proteomics Data. , 2013, , .		0
118	Modularity and community detection in Semantic Similarity Networks through Spectral Based Transformation and Markov Clustering. , 2013, , .		0
119	DMET-miner: Efficient learning of association rules from genotyping data for personalized medicine. , 2014, , .		0
120	A taxonomy for bioinformatics tools. , 2014, , .		0
121	Relating Clinical Diagnosis and Biological Analytes via EMRs Clustering. , 2014, , .		0
122	A web-based tool to analyze semantic similarity networks. , 2014, , .		0
123	Annotation and retrieval in protein interaction databases. <i>European Physical Journal Plus</i> , 2014, 129, 1.	1.2	0
124	Efficient learning of association rules from human phenotype ontology. , 2015, , .		0
125	Using SSN-Analyzer for analysis of semantic similarity networks. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2015, 4, 1.	1.2	0
126	ICT Solutions for Health Education Model. , 2015, , .		0

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127	High Performance Analysis of Omics Data: Experiences at University Magna Graecia of Catanzaro. , 2017, , .		0
128	Network based algorithms for module extraction from RNASeq data: A quantitative assessment. , 2017, , .		0
129	Integrative Bioinformatics of Transcriptome: Databases, Tools and Pipelines. , 2019, , 1099-1103.		0
130	Ontology-Based Annotation Methods. , 2019, , 867-869.		0
131	Mining Association Rules From Disease Ontology. , 2019, , .		0
132	Protein interaction networks. , 2020, , 133-166.		0
133	Brain connectome networks and analysis. , 2020, , 167-182.		0
134	Learning Association Rules for Pharmacogenomic Studies. Lecture Notes in Computer Science, 2018, , 1-15.	1.0	0
135	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
136	Towards Local Alignment of Multiple Networks. , 2019, , .		0
137	Learning Weighted Association Rules in Human Phenotype Ontology. Lecture Notes in Computer Science, 2020, , 245-256.	1.0	0
138	Parallel Learning of Weighted Association Rules in Human Phenotype Ontology. Lecture Notes in Computer Science, 2020, , 549-559.	1.0	0
139	A grid-based protein complex predictor. Studies in Health Technology and Informatics, 2008, 138, 116-24.	0.2	0
140	Omics sciences. , 2022, , 105-118.		0
141	Integrative bioinformatics. , 2022, , 129-136.		0
142	Biological networks analysis. , 2022, , 137-150.		0
143	Ontologies in bioinformatics. , 2022, , 119-128.		0