

Luigi Cerulo

List of Publications by Year in descending order

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Version: 2024-02-01

55
papers

1,804
citations

394421

19
h-index

501196

28
g-index

57
all docs

57
docs citations

57
times ranked

2302
citing authors

#	ARTICLE	IF	CITATIONS
1	Loss of circadian rhythmicity in bdnf knockout zebrafish larvae. <i>IScience</i> , 2022, 25, 104054.	4.1	11
2	massiveGST: A Mann-Whitney-Wilcoxon Gene-Set Test Tool That Gives Meaning to Gene-Set Enrichment Analysis. <i>Entropy</i> , 2022, 24, 739.	2.2	0
3	Adaptive one-class Gaussian processes allow accurate prioritization of oncology drug targets. <i>Bioinformatics</i> , 2021, 37, 1420-1427.	4.1	2
4	A review of COVID-19 biomarkers and drug targets: resources and tools. <i>Briefings in Bioinformatics</i> , 2021, 22, 701-713.	6.5	20
5	Wnt (canonical and non canonical) pathways in breast carcinoma with extensive vascular invasion and inflammatory breast carcinoma. <i>Pathology Research and Practice</i> , 2021, 219, 153347.	2.3	2
6	A map of tumor-host interactions in glioma at single-cell resolution. <i>GigaScience</i> , 2020, 9, .	6.4	32
7	Deep learning predicts short non-coding RNA functions from only raw sequence data. <i>PLoS Computational Biology</i> , 2020, 16, e1008415.	3.2	16
8	Deep learning predicts short non-coding RNA functions from only raw sequence data. , 2020, 16, e1008415.		0
9	Deep learning predicts short non-coding RNA functions from only raw sequence data. , 2020, 16, e1008415.		0
10	Deep learning predicts short non-coding RNA functions from only raw sequence data. , 2020, 16, e1008415.		0
11	Deep learning predicts short non-coding RNA functions from only raw sequence data. , 2020, 16, e1008415.		0
12	Circulating microRNAs expression profile in newly diagnosed and imatinib treated chronic phase acute chronic myeloid leukemia. <i>Leukemia and Lymphoma</i> , 2019, 60, 805-811.	1.3	4
13	RGBM: regularized gradient boosting machines for identification of the transcriptional regulators of discrete glioma subtypes. <i>Nucleic Acids Research</i> , 2018, 46, e39-e39.	14.5	32
14	A metabolic function of FGFR3-TACC3 gene fusions in cancer. <i>Nature</i> , 2018, 553, 222-227.	27.8	137
15	Detection of long non-coding RNA homology, a comparative study on alignment and alignment-free metrics. <i>BMC Bioinformatics</i> , 2018, 19, 407.	2.6	31
16	Identification of genetic determinants of breast cancer immune phenotypes by integrative genome-scale analysis. <i>Oncolmmunology</i> , 2017, 6, e1253654.	4.6	146
17	Detection of statistically significant network changes in complex biological networks. <i>BMC Systems Biology</i> , 2017, 11, 32.	3.0	29
18	Identification of long non-coding transcripts with feature selection: a comparative study. <i>BMC Bioinformatics</i> , 2017, 18, 187.	2.6	21

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19	Emerging Insight into MAPK Inhibitors and Immunotherapy in Colorectal Cancer. Current Medicinal Chemistry, 2017, 24, 1383-1402.	2.4	23
20	Systems biology analysis reveals NFAT5 as a novel biomarker and master regulator of inflammatory breast cancer. Journal of Translational Medicine, 2015, 13, 138.	4.4	38
21	Irish: A Hidden Markov Model to detect coded information islands in free text. Science of Computer Programming, 2015, 105, 26-43.	1.9	4
22	How changes affect software entropy: an empirical study. Empirical Software Engineering, 2014, 19, 1-38.	3.9	50
23	De novo reconstruction of gene regulatory networks from time series data, an approach based on formal methods. Methods, 2014, 69, 298-305.	3.8	44
24	Identification of a Novel Gene Signature of ES Cells Self-Renewal Fluctuation through System-Wide Analysis. PLoS ONE, 2014, 9, e83235.	2.5	23
25	A negative selection heuristic to predict new transcriptional targets. BMC Bioinformatics, 2013, 14, S3.	2.6	6
26	Infer gene regulatory networks from time series data with formal methods. , 2013, , .		3
27	Ensemble of Gene Signatures Identifies Novel Biomarkers in Colorectal Cancer Activated through PPAR β and TNF α Signaling. PLoS ONE, 2013, 8, e72638.	2.5	33
28	How Long Does a Bug Survive? An Empirical Study. , 2011, , .		27
29	Social interactions around cross-system bug fixings. , 2011, , .		31
30	Achievements and challenges in software reverse engineering. Communications of the ACM, 2011, 54, 142-151.	4.5	98
31	Labeling Negative Examples in Supervised Learning of New Gene Regulatory Connections. Lecture Notes in Computer Science, 2011, , 159-173.	1.3	0
32	An empirical study on the maintenance of source code clones. Empirical Software Engineering, 2010, 15, 1-34.	3.9	144
33	Learning gene regulatory networks from only positive and unlabeled data. BMC Bioinformatics, 2010, 11, 228.	2.6	90
34	An eclectic approach for change impact analysis. , 2010, , .		29
35	VEGA: variational segmentation for copy number detection. Bioinformatics, 2010, 26, 3020-3027.	4.1	20
36	An Exploratory Study of Factors Influencing Change Entropy. , 2010, , .		13

#	ARTICLE	IF	CITATIONS
37	Using multivariate time series and association rules to detect logical change coupling: An empirical study. , 2010, , .		41
38	Ldiff: An enhanced line differencing tool. , 2009, , .		38
39	The life and death of statically detected vulnerabilities: An empirical study. Information and Software Technology, 2009, 51, 1469-1484.	4.4	31
40	Tracking Your Changes: A Language-Independent Approach. IEEE Software, 2009, 26, 50-57.	1.8	38
41	Selection of negative examples in learning gene regulatory networks. , 2009, , .		8
42	Mining candidate web services from legacy code. , 2008, , .		16
43	An empirical study of the relationships between design pattern roles and class change proneness. , 2008, , .		33
44	The Evolution and Decay of Statically Detected Source Code Vulnerabilities. , 2008, , .		7
45	How Clones are Maintained: An Empirical Study. , 2007, , .		141
46	An empirical study on the evolution of design patterns. , 2007, , .		61
47	Learning from bug-introducing changes to prevent fault prone code. , 2007, , .		35
48	Identifying Changed Source Code Lines from Version Repositories. , 2007, , .		68
49	Relating the Evolution of Design Patterns and Crosscutting Concerns. , 2007, , .		6
50	On the Use of Process Trails to Understand Software Development. , 2006, , .		6
51	Fine grained indexing of software repositories to support impact analysis. , 2006, , .		57
52	Where is bug resolution knowledge stored?. , 2006, , .		2
53	On the Use of Line Co-change for Identifying Crosscutting Concern Code. , 2006, , .		31
54	A Taxonomy of Information Retrieval Models and Tools. Journal of Computing and Information Technology, 2004, 12, 175.	0.3	20

#	ARTICLE	IF	CITATIONS
55	A visual approach to define XML to FO transformations. , 2002, , .		4