Luigi Cerulo

List of Publications by Year in descending order

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	Identification of genetic determinants of breast cancer immune phenotypes by integrative genome-scale analysis. OncoImmunology, 2017, 6, e1253654.	4.6	146
2	An empirical study on the maintenance of source code clones. Empirical Software Engineering, 2010, 15, 1-34.	3.9	144
3	How Clones are Maintained: An Empirical Study. , 2007, , .		141
4	A metabolic function of FGFR3-TACC3 gene fusions in cancer. Nature, 2018, 553, 222-227.	27.8	137
5	Achievements and challenges in software reverse engineering. Communications of the ACM, 2011, 54, 142-151.	4.5	98
6	Learning gene regulatory networks from only positive and unlabeled data. BMC Bioinformatics, 2010, 11, 228.	2.6	90
7	Identifying Changed Source Code Lines from Version Repositories. , 2007, , .		68
8	An empirical study on the evolution of design patterns. , 2007, , .		61
9	Fine grained indexing of software repositories to support impact analysis. , 2006, , .		57
10	How changes affect software entropy: an empirical study. Empirical Software Engineering, 2014, 19, 1-38.	3.9	50
11	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
12	Using multivariate time series and association rules to detect logical change coupling: An empirical study. , 2010, , .		41
13	Ldiff: An enhanced line differencing tool. , 2009, , .		38
14	Tracking Your Changes: A Language-Independent Approach. IEEE Software, 2009, 26, 50-57.	1.8	38
15	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
16	Learning from bug-introducing changes to prevent fault prone code. , 2007, , .		35
17	An empirical study of the relationships between design pattern roles and class change proneness. , 2008, , .		33
18	Ensemble of Gene Signatures Identifies Novel Biomarkers in Colorectal Cancer Activated through PPARÎ³ and TNFÎ± Signaling. PLoS ONE, 2013, 8, e72638.	2.5	33

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19	RGBM: regularized gradient boosting machines for identification of the transcriptional regulators of discrete glioma subtypes. Nucleic Acids Research, 2018, 46, e39-e39.	14.5	32
20	A map of tumor–host interactions in glioma at single-cell resolution. GigaScience, 2020, 9, .	6.4	32
21	On the Use of Line Co-change for Identifying Crosscutting Concern Code. , 2006, , .		31
22	The life and death of statically detected vulnerabilities: An empirical study. Information and Software Technology, 2009, 51, 1469-1484.	4.4	31
23	Social interactions around cross-system bug fixings. , 2011, , .		31
24	Detection of long non–coding RNA homology, a comparative study on alignment and alignment–free metrics. BMC Bioinformatics, 2018, 19, 407.	2.6	31
25	An eclectic approach for change impact analysis. , 2010, , .		29
26	Detection of statistically significant network changes in complex biological networks. BMC Systems Biology, 2017, 11, 32.	3.0	29
27	How Long Does a Bug Survive? An Empirical Study. , 2011, , .		27
28	Identification of a Novel Gene Signature of ES Cells Self-Renewal Fluctuation through System-Wide Analysis. PLoS ONE, 2014, 9, e83235.	2.5	23
29	Emerging Insight into MAPK Inhibitors and Immunotherapy in Colorectal Cancer. Current Medicinal Chemistry, 2017, 24, 1383-1402.	2.4	23
30	Identification of long non-coding transcripts with feature selection: a comparative study. BMC Bioinformatics, 2017, 18, 187.	2.6	21
31	A Taxonomy of Information Retrieval Models and Tools. Journal of Computing and Information Technology, 2004, 12, 175.	0.3	20
32	VEGA: variational segmentation for copy number detection. Bioinformatics, 2010, 26, 3020-3027.	4.1	20
33	A review of COVID-19 biomarkers and drug targets: resources and tools. Briefings in Bioinformatics, 2021, 22, 701-713.	6.5	20
34	Mining candidate web services from legacy code. , 2008, , .		16
35	Deep learning predicts short non-coding RNA functions from only raw sequence data. PLoS Computational Biology, 2020, 16, e1008415.	3.2	16
36	An Exploratory Study of Factors Influencing Change Entropy. , 2010, , .		13

#	Article	IF	Citations
37	Loss of circadian rhythmicity in bdnf knockout zebrafish larvae. IScience, 2022, 25, 104054.	4.1	11
38	Selection of negative examples in learning gene regulatory networks. , 2009, , .		8
39	The Evolution and Decay of Statically Detected Source Code Vulnerabilities. , 2008, , .		7
40	On the Use of Process Trails to Understand Software Development. , 2006, , .		6
41	Relating the Evolution of Design Patterns and Crosscutting Concerns. , 2007, , .		6
42	A negative selection heuristic to predict new transcriptional targets. BMC Bioinformatics, 2013, 14, S3.	2.6	6
43	A visual approach to define XML to FO transformations. , 2002, , .		4
44	Irish: A Hidden Markov Model to detect coded information islands in free text. Science of Computer Programming, 2015, 105, 26-43.	1.9	4
45	Circulating microRNAs expression profile in newly diagnosed and imatinib treated chronic phase – chronic myeloid leukemia. Leukemia and Lymphoma, 2019, 60, 805-811.	1.3	4
46	Infer gene regulatory networks from time series data with formal methods. , 2013, , .		3
47	Where is bug resolution knowledge stored?. , 2006, , .		2
48	Adaptive one-class Gaussian processes allow accurate prioritization of oncology drug targets. Bioinformatics, 2021, 37, 1420-1427.	4.1	2
49	Wnt (canonical and non canonical) pathways in breast carcinoma with extensive vascular invasion and inflammatory breast carcinoma. Pathology Research and Practice, 2021, 219, 153347.	2.3	2
50	Labeling Negative Examples in Supervised Learning of New Gene Regulatory Connections. Lecture Notes in Computer Science, 2011, , 159-173.	1.3	0
51	Deep learning predicts short non-coding RNA functions from only raw sequence data. , 2020, 16, e1008415.		0
52	Deep learning predicts short non-coding RNA functions from only raw sequence data. , 2020, 16, e1008415.		0
53	Deep learning predicts short non-coding RNA functions from only raw sequence data. , 2020, 16, e1008415.		0
54	Deep learning predicts short non-coding RNA functions from only raw sequence data. , 2020, 16, e1008415.		0

#	ARTICLE	IF	CITATIONS
55	massiveGST: A Mann–Whitney–Wilcoxon Gene-Set Test Tool That Gives Meaning to Gene-Set Enrichment Analysis. Entropy, 2022, 24, 739.	2.2	0