

NCG 4.0: the network of cancer genes in the era of mass cancer genomes

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Algorithms for network-based identification of differential regulators from transcriptome data: a systematic evaluation. <i>Science China Life Sciences</i> , 2014, 57, 1090-1102.	4.9	7
2	Deep sequencing of the X chromosome reveals the proliferation history of colorectal adenomas. <i>Genome Biology</i> , 2014, 15, 437.	8.8	1
3	Massive gene amplification drives paediatric hepatocellular carcinoma caused by bile salt export pump deficiency. <i>Nature Communications</i> , 2014, 5, 3850.	12.8	49
4	Network analysis reveals a stress-affected common gene module among seven stress-related diseases/systems which provides potential targets for mechanism research. <i>Scientific Reports</i> , 2015, 5, 12939.	3.3	8
5	Computational methods and resources for the interpretation of genomic variants in cancer. <i>BMC Genomics</i> , 2015, 16, S7.	2.8	18
6	Identification and validation of potential prognostic lncRNA biomarkers for predicting survival in patients with multiple myeloma. <i>Journal of Experimental and Clinical Cancer Research</i> , 2015, 34, 102.	8.6	207
7	FARE-CAFE: a database of functional and regulatory elements of cancer-associated fusion events. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav086.	3.0	11
8	Personalized targeted therapy for esophageal squamous cell carcinoma. <i>World Journal of Gastroenterology</i> , 2015, 21, 7648.	3.3	43
9	Evaluation and integration of cancer gene classifiers: identification and ranking of plausible drivers. <i>Scientific Reports</i> , 2015, 5, 10204.	3.3	18
10	Human cancer databases (Review). <i>Oncology Reports</i> , 2015, 33, 3-18.	2.6	69
11	Foamy viral vector integration sites in SCID-repopulating cells after MGMP140K-mediated in vivo selection. <i>Gene Therapy</i> , 2015, 22, 591-595.	4.5	14
12	Practical aspects of NGS-based pathways analysis for personalized cancer science and medicine. <i>Oncotarget</i> , 2016, 7, 52493-52516.	1.8	15
13	Characterization of long non-coding RNA-associated ceRNA network to reveal potential prognostic lncRNA biomarkers in human ovarian cancer. <i>Oncotarget</i> , 2016, 7, 12598-12611.	1.8	218
14	GeneSCF: a real-time based functional enrichment tool with support for multiple organisms. <i>BMC Bioinformatics</i> , 2016, 17, 365.	2.6	87
15	Predicting miRNA Targets by Integrating Gene Regulatory Knowledge with Expression Profiles. <i>PLoS ONE</i> , 2016, 11, e0152860.	2.5	15
16	Discovering potential cancer driver genes by an integrated network-based approach. <i>Molecular BioSystems</i> , 2016, 12, 2921-2931.	2.9	27
17	A comparison of foamy and lentiviral vector genotoxicity in SCID-repopulating cells shows foamy vectors are less prone to clonal dominance. <i>Molecular Therapy - Methods and Clinical Development</i> , 2016, 3, 16048.	4.1	13
18	Characterizing mutation-expression network relationships in multiple cancers. <i>Computational Biology and Chemistry</i> , 2016, 63, 73-82.	2.3	22

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19	Why Chemotherapy Does Not Work: Cancer Genome Evolution and the Illusion of Oncogene Addiction. , 2016, , 177-190.		0
20	Global DNA methylation profiling reveals new insights into epigenetically deregulated protein coding and long noncoding RNAs in CLL. <i>Clinical Epigenetics</i> , 2016, 8, 106.	4.1	45
21	Systematic tracking of coordinated differential network motifs identifies novel disease-related genes by integrating multiple data. <i>Neurocomputing</i> , 2016, 206, 3-12.	5.9	4
22	Relationship between microRNA genes incidence and cancer-associated genomic regions in canine tumors: a comprehensive bioinformatics study. <i>Functional and Integrative Genomics</i> , 2016, 16, 143-152.	3.5	8
23	NCG 5.0: updates of a manually curated repository of cancer genes and associated properties from cancer mutational screenings. <i>Nucleic Acids Research</i> , 2016, 44, D992-D999.	14.5	95
24	HER2 Signaling Drives DNA Anabolism and Proliferation through SRC-3 Phosphorylation and E2F1-Regulated Genes. <i>Cancer Research</i> , 2016, 76, 1463-1475.	0.9	35
25	ccmGDB: a database for cancer cell metabolism genes. <i>Nucleic Acids Research</i> , 2016, 44, D959-D968.	14.5	41
26	Colorectal cancer atlas: An integrative resource for genomic and proteomic annotations from colorectal cancer cell lines and tissues. <i>Nucleic Acids Research</i> , 2016, 44, D969-D974.	14.5	55
27	A single-copy Sleeping Beauty transposon mutagenesis screen identifies new PTEN-cooperating tumor suppressor genes. <i>Nature Genetics</i> , 2017, 49, 730-741.	21.4	53
28	Discovering potential driver genes through an integrated model of somatic mutation profiles and gene functional information. <i>Molecular BioSystems</i> , 2017, 13, 2135-2144.	2.9	20
29	Identifying DNase I hypersensitive sites as driver distal regulatory elements in breast cancer. <i>Nature Communications</i> , 2017, 8, 436.	12.8	22
30	Perturbed human sub-networks by <i>Fusobacterium nucleatum</i> candidate virulence proteins. <i>Microbiome</i> , 2017, 5, 89.	11.1	27
31	Cancer drug target identification and node-level analysis of the network of MAPK pathways. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2018, 7, 1.	2.1	2
32	ConsensusDriver Improves upon Individual Algorithms for Predicting Driver Alterations in Different Cancer Types and Individual Patients. <i>Cancer Research</i> , 2018, 78, 290-301.	0.9	20
33	Protein Domain Level Cancer Drug Targets in the Network of MAPK pathways. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 16, 1-1.	3.0	0
34	The Network of Cancer Genes (NCG): a comprehensive catalogue of known and candidate cancer genes from cancer sequencing screens. <i>Genome Biology</i> , 2019, 20, 1.	8.8	938
35	A random walk-based method to identify driver genes by integrating the subcellular localization and variation frequency into bipartite graph. <i>BMC Bioinformatics</i> , 2019, 20, 238.	2.6	28
36	The prognostic signature of the somatic mutations in Ewing sarcoma: from a network view. <i>Japanese Journal of Clinical Oncology</i> , 2019, 49, 604-613.	1.3	2

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37	Identifying driver genes involving gene dysregulated expression, tissue-specific expression and gene-gene network. BMC Medical Genomics, 2019, 12, 168.	1.5	11
38	Nuclear localization of LDL receptor-related protein 1B in mammary gland carcinogenesis. Journal of Molecular Medicine, 2019, 97, 257-268.	3.9	22
39	Rapid preliminary purity evaluation of tumor biopsies using deep learning approach. Computational and Structural Biotechnology Journal, 2020, 18, 1746-1753.	4.1	2
40	Germline copy number variations in BRCA1/2 negative families: Role in the molecular etiology of hereditary breast cancer in Tunisia. PLoS ONE, 2021, 16, e0245362.	2.5	9
41	Pan-cancer detection of driver genes at the single-patient resolution. Genome Medicine, 2021, 13, 12.	8.2	17
42	Identification of the miRNA signature associated with survival in patients with ovarian cancer. Aging, 2021, 13, 12660-12690.	3.1	13
43	EARN: an ensemble machine learning algorithm to predict driver genes in metastatic breast cancer. BMC Medical Genomics, 2021, 14, 122.	1.5	12
45	DGPathinter: a novel model for identifying driver genes via knowledge-driven matrix factorization with prior knowledge from interactome and pathways. PeerJ Computer Science, 0, 3, e133.	4.5	4
49	Application of Bioinformatics Databases in the Study of Oxidative Stress Related Cancers. , 2022, , 1-12.		0
50	Application of Bioinformatics Databases in the Study of Oxidative Stress Related Cancers. , 2022, , 3229-3240.		0