

Glen M Borchert

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

38
papers

1,962
citations

16
h-index

44
g-index

50
ext. papers

2,240
ext. citations

5.1
avg. IF

4.67
L-index

#	Paper	IF	Citations
38	Utilizing Machine Learning Techniques to Predict the Efficacy of Aerobic Exercise Intervention on Young Hypertensive Patients Based on Cardiopulmonary Exercise Testing. <i>Journal of Healthcare Engineering</i> , 2021 , 2021, 6633832	3.7	
37	A long noncoding RNA antisense to ICAM-1 is involved in allergic asthma associated hyperreactive response of airway epithelial cells. <i>Mucosal Immunology</i> , 2021 , 14, 630-639	9.2	4
36	Characterization of long G4-rich enhancer-associated genomic regions engaging in a novel loop:loop G4 kissing interaction. <i>Nucleic Acids Research</i> , 2020 , 48, 5907-5925	20.1	10
35	Development of a support vector machine learning and smart phone Internet of Things-based architecture for real-time sleep apnea diagnosis. <i>BMC Medical Informatics and Decision Making</i> , 2020 , 20, 298	3.6	5
34	A partial encryption algorithm for medical images based on quick response code and reversible data hiding technology. <i>BMC Medical Informatics and Decision Making</i> , 2020 , 20, 297	3.6	7
33	Exploring Observability of Attractor Cycles in Boolean Networks for Biomarker Detection. <i>IEEE Access</i> , 2019 , 7, 127745-127753	3.5	1
32	Long Noncoding Transcriptome in Chronic Obstructive Pulmonary Disease. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2019 , 61, 678-688	5.7	17
31	Characterization of novel small RNAs (sRNAs) contributing to the desiccation response of serovar Typhimurium. <i>RNA Biology</i> , 2019 , 16, 1643-1657	4.8	4
30	Using an artificial neural network to map cancer common data elements to the biomedical research integrated domain group model in a semi-automated manner. <i>BMC Medical Informatics and Decision Making</i> , 2019 , 19, 276	3.6	1
29	Muscle fatigue detection and treatment system driven by internet of things. <i>BMC Medical Informatics and Decision Making</i> , 2019 , 19, 275	3.6	3
28	A semantics-oriented computational approach to investigate microRNA regulation on glucocorticoid resistance in pediatric acute lymphoblastic leukemia. <i>BMC Medical Informatics and Decision Making</i> , 2018 , 18, 57	3.6	5
27	ADAR Mediated RNA Editing Modulates MicroRNA Targeting in Human Breast Cancer. <i>Processes</i> , 2018 , 6,	2.9	8
26	A PWM-Based Muscle Fatigue Detection and Recovery System 2018 ,		5
25	Viral MicroRNAs, Host MicroRNAs Regulating Viruses, and Bacterial MicroRNA-Like RNAs. <i>Methods in Molecular Biology</i> , 2017 , 1617, 39-56	1.4	16
24	MicroRNA Expression: Protein Participants in MicroRNA Regulation. <i>Methods in Molecular Biology</i> , 2017 , 1617, 27-37	1.4	19
23	Computational Prediction of MicroRNA Target Genes, Target Prediction Databases, and Web Resources. <i>Methods in Molecular Biology</i> , 2017 , 1617, 109-122	1.4	23
22	Human snoRNA-93 is processed into a microRNA-like RNA that promotes breast cancer cell invasion. <i>Npj Breast Cancer</i> , 2017 , 3, 25	7.8	31

21	MeSH term-based semantic analysis of microRNA regulation on glucocorticoid resistance in pediatric acute lymphoblastic leukemia 2017 ,		1
20	Genome-Wide Analysis of MicroRNA-Regulated Transcripts. <i>Methods in Molecular Biology</i> , 2017 , 1617, 93-107	1.4	2
19	The development of non-coding RNA ontology. <i>International Journal of Data Mining and Bioinformatics</i> , 2016 , 15, 214-232	0.5	7
18	OmniSearch: a semantic search system based on the Ontology for MicroRNA Target (OMIT) for microRNA-target gene interaction data. <i>Journal of Biomedical Semantics</i> , 2016 , 7, 25	2.2	16
17	Novel small RNA (sRNA) landscape of the starvation-stress response transcriptome of <i>Salmonella enterica</i> serovar typhimurium. <i>RNA Biology</i> , 2016 , 13, 331-42	4.8	14
16	The Non-Coding RNA Ontology (NCRO): a comprehensive resource for the unification of non-coding RNA biology. <i>Journal of Biomedical Semantics</i> , 2016 , 7, 24	2.2	5
15	Bone-remodeling transcript levels are independent of perching in end-of-lay white leghorn chickens. <i>International Journal of Molecular Sciences</i> , 2015 , 16, 2663-77	6.3	8
14	"On the job" learning: A bioinformatics course incorporating undergraduates in actual research projects and manuscript submissions. <i>Biochemistry and Molecular Biology Education</i> , 2015 , 43, 154-61	1.3	8
13	An oxidative DNA "damage" and repair mechanism localized in the VEGF promoter is important for hypoxia-induced VEGF mRNA expression. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2015 , 309, L1367-75	5.8	94
12	OMIT: dynamic, semi-automated ontology development for the microRNA domain. <i>PLoS ONE</i> , 2014 , 9, e100855	3.7	14
11	Burgeoning evidence indicates that microRNAs were initially formed from transposable element sequences. <i>Mobile Genetic Elements</i> , 2014 , 4, e29255		62
10	The western painted turtle genome, a model for the evolution of extreme physiological adaptations in a slowly evolving lineage. <i>Genome Biology</i> , 2013 , 14, R28	18.3	227
9	Continuing analysis of microRNA origins: Formation from transposable element insertions and noncoding RNA mutations. <i>Mobile Genetic Elements</i> , 2013 , 3, e27755		31
8	G-quadruplex recognition activities of <i>E. Coli</i> MutS. <i>BMC Molecular Biology</i> , 2012 , 13, 23	4.5	18
7	OrbId: Origin-based identification of microRNA targets. <i>Mobile Genetic Elements</i> , 2012 , 2, 184-192		19
6	Repression of human activation induced cytidine deaminase by miR-93 and miR-155. <i>BMC Cancer</i> , 2011 , 11, 347	4.8	38
5	Comprehensive analysis of microRNA genomic loci identifies pervasive repetitive-element origins. <i>Mobile Genetic Elements</i> , 2011 , 1, 8-17		60
4	Histone H2A and H2B are monoubiquitinated at AID-targeted loci. <i>PLoS ONE</i> , 2010 , 5, e11641	3.7	11

- 3 Adenosine deamination in human transcripts generates novel microRNA binding sites. *Human Molecular Genetics*, **2009**, 18, 4801-7 5.6 111
- 2 RNA polymerase III transcribes human microRNAs. *Nature Structural and Molecular Biology*, **2006**, 13, 1097-101 17.6 1056
- 1 Evolutionary Origin of MicroRNAs1-8