

Vladimir B. Bajic

List of Publications by Year in descending order

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Version: 2024-02-01

299
papers

21,151
citations

21215

62
h-index

14012

133
g-index

317
all docs

317
docs citations

317
times ranked

35772
citing authors

#	ARTICLE	IF	CITATIONS
1	Genes and comorbidities of thyroid cancer. Informatics in Medicine Unlocked, 2021, 25, 100680.	1.9	2
2	KAUST Metagenomic Analysis Platform (KMAP), enabling access to massive analytics of re-annotated metagenomic data. Scientific Reports, 2021, 11, 11511.	1.6	4
3	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. Nature Communications, 2021, 12, 3297.	5.8	11
4	DES-Tcell is a knowledgebase for exploring immunology-related literature. Scientific Reports, 2021, 11, 14344.	1.6	1
5	DTi2Vec: Drug-target interaction prediction using network embedding and ensemble learning. Journal of Cheminformatics, 2021, 13, 71.	2.8	27
6	Proteome-level assessment of origin, prevalence and function of leucine-aspartic acid (LD) motifs. Bioinformatics, 2020, 36, 1121-1128.	1.8	10
7	Antioxidant enzymes expression in lymphocytes of patients undergoing carotid endarterectomy. Medical Hypotheses, 2020, 134, 109419.	0.8	1
8	Redox control of vascular biology. BioFactors, 2020, 46, 246-262.	2.6	15
9	HbA1C as a marker of retrograde glycaemic control in diabetes patient with co-existed beta-thalassaemia: A case report and a literature review. Journal of Clinical Pharmacy and Therapeutics, 2020, 45, 379-383.	0.7	5
10	PATH ⁸ : A Tool That Facilitates the Searching for Heterologous Biosynthetic Routes. ACS Synthetic Biology, 2020, 9, 3217-3227.	1.9	7
11	Next-Generation Sequencing at High Sequencing Depth as a Tool to Study the Evolution of Metastasis Driven by Genetic Change Events of Lung Squamous Cell Carcinoma. Frontiers in Oncology, 2020, 10, 1215.	1.3	7
12	Sequencing effort dictates gene discovery in marine microbial metagenomes. Environmental Microbiology, 2020, 22, 4589-4603.	1.8	13
13	Automated Counting of Colony Forming Units Using Deep Transfer Learning From a Model for Congested Scenes Analysis. IEEE Access, 2020, 8, 164340-164346.	2.6	6
14	Comorbidity network analysis and genetics of colorectal cancer. Informatics in Medicine Unlocked, 2020, 21, 100492.	1.9	9
15	Splice2Deep: An ensemble of deep convolutional neural networks for improved splice site prediction in genomic DNA. Gene: X, 2020, 763, 100035.	2.3	33
16	DTiGEMS+: drug-target interaction prediction using graph embedding, graph mining, and similarity-based techniques. Journal of Cheminformatics, 2020, 12, 44.	2.8	62
17	Regulation of nitric oxide production in hypothyroidism. Biomedicine and Pharmacotherapy, 2020, 124, 109881.	2.5	18
18	Genome Insights of the Plant-Growth Promoting Bacterium Cronobacter muytjensii JZ38 With Volatile-Mediated Antagonistic Activity Against Phytophthora infestans. Frontiers in Microbiology, 2020, 11, 369.	1.5	39

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19	Computational Drug-target Interaction Prediction based on Graph Embedding and Graph Mining. , 2020, , .		3
20	Marine Metagenomic Sequence Counts of Reads Assigned to Taxa Consistently Proportionate to Read Counts Obtained for per g of Seawater Sample. , 2019, , 183-188.		1
21	Mining biosynthetic gene clusters in <i>Virgibacillus</i> genomes. BMC Genomics, 2019, 20, 696.	1.2	7
22	Marine biofilms constitute a bank of hidden microbial diversity and functional potential. Nature Communications, 2019, 10, 517.	5.8	100
23	Uncoupled Quorum Sensing Modulates the Interplay of Virulence and Resistance in a Multidrug-Resistant Clinical <i>Pseudomonas aeruginosa</i> Isolate Belonging to the MLST550 Clonal Complex. Antimicrobial Agents and Chemotherapy, 2019, 63, .	1.4	17
24	CpG traffic lights are markers of regulatory regions in human genome. BMC Genomics, 2019, 20, 102.	1.2	43
25	Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen. Nature Communications, 2019, 10, 2674.	5.8	240
26	Mining the deep Red-Sea brine pool microbial community for anticancer therapeutics. BMC Complementary and Alternative Medicine, 2019, 19, 142.	3.7	6
27	Glutathione Redox Homeostasis and Its Relation to Cardiovascular Disease. Oxidative Medicine and Cellular Longevity, 2019, 2019, 1-14.	1.9	89
28	Literature-Based Enrichment Insights into Redox Control of Vascular Biology. Oxidative Medicine and Cellular Longevity, 2019, 2019, 1-16.	1.9	8
29	Hybrid model for efficient prediction of poly(A) signals in human genomic DNA. Methods, 2019, 166, 31-39.	1.9	18
30	Comparison Study of Computational Prediction Tools for Drug-Target Binding Affinities. Frontiers in Chemistry, 2019, 7, 782.	1.8	85
31	Comparative genomics study reveals Red Sea <i>Bacillus</i> with characteristics associated with potential microbial cell factories (MCFs). Scientific Reports, 2019, 9, 19254.	1.6	6
32	Bioprospecting desert plant <i>Bacillus</i> endophytic strains for their potential to enhance plant stress tolerance. Scientific Reports, 2019, 9, 18154.	1.6	69
33	DeepGSR: an optimized deep-learning structure for the recognition of genomic signals and regions. Bioinformatics, 2019, 35, 1125-1132.	1.8	51
34	Characterization and identification of long non-coding RNAs based on feature relationship. Bioinformatics, 2019, 35, 2949-2956.	1.8	64
35	LncBook: a curated knowledgebase of human long non-coding RNAs. Nucleic Acids Research, 2019, 47, D128-D134.	6.5	177
36	The X Files: The Mystery of X Chromosome Instability in Alzheimer's Disease. Frontiers in Genetics, 2019, 10, 1368.	1.1	25

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37	Metagenomic Methods: From Seawater to the Database. , 2019, , 3-16.		1
38	DDR: efficient computational method to predict drugâ€target interactions using graph mining and machine learning approaches. <i>Bioinformatics</i> , 2018, 34, 1164-1173.	1.8	158
39	Draft Genome Sequences of Four <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Enteritidis Strains Implicated in Infections of Avian and Human Hosts. <i>Genome Announcements</i> , 2018, 6, .	0.8	1
40	HOCOMOCO: towards a complete collection of transcription factor binding models for human and mouse via large-scale ChIP-Seq analysis. <i>Nucleic Acids Research</i> , 2018, 46, D252-D259.	6.5	660
41	In silico toxicology: comprehensive benchmarking of multi-label classification methods applied to chemical toxicity data. <i>Wiley Interdisciplinary Reviews: Computational Molecular Science</i> , 2018, 8, e1352.	6.2	31
42	Metagenome-based diversity analyses suggest a strong locality signal for bacterial communities associated with oyster aquaculture farms in Ofunato Bay. <i>Gene</i> , 2018, 665, 149-154.	1.0	14
43	Seasonal changes in the communities of photosynthetic picoeukaryotes in Ofunato Bay as revealed by shotgun metagenomic sequencing. <i>Gene</i> , 2018, 665, 127-132.	1.0	6
44	Seasonal changes in the abundance of bacterial genes related to dimethylsulfoniopropionate catabolism in seawater from Ofunato Bay revealed by metagenomic analysis. <i>Gene</i> , 2018, 665, 174-184.	1.0	17
45	Taxonomic profiles in metagenomic analyses of free-living microbial communities in the Ofunato Bay. <i>Gene</i> , 2018, 665, 192-200.	1.0	15
46	Basin-scale seasonal changes in marine free-living bacterioplankton community in the Ofunato Bay. <i>Gene</i> , 2018, 665, 185-191.	1.0	10
47	Transcriptional landscape of <i>Mycobacterium tuberculosis</i> infection in macrophages. <i>Scientific Reports</i> , 2018, 8, 6758.	1.6	92
48	TELS: A Novel Computational Framework for Identifying Motif Signatures of Transcribed Enhancers. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 332-341.	3.0	4
49	Genome sequence analysis of <i>Zooshikella ganghwensis</i> strain VG4 and its potential for the synthesis of antimicrobial metabolites. <i>Biotechnology Reports (Amsterdam, Netherlands)</i> , 2018, 19, e00278.	2.1	4
50	The Genome Sequence of the Wild Tomato <i>Solanum pimpinellifolium</i> Provides Insights Into Salinity Tolerance. <i>Frontiers in Plant Science</i> , 2018, 9, 1402.	1.7	69
51	DES-Mutation: System for Exploring Links of Mutations and Diseases. <i>Scientific Reports</i> , 2018, 8, 13359.	1.6	13
52	A novel method for improved accuracy of transcription factor binding site prediction. <i>Nucleic Acids Research</i> , 2018, 46, e72-e72.	6.5	35
53	Genome Reduction in <i>Psychromonas</i> Species within the Gut of an Amphipod from the Oceanâ€™s Deepest Point. <i>MSystems</i> , 2018, 3, .	1.7	21
54	BioPS: System for screening and assessment of biofuel-production potential of cyanobacteria. <i>PLoS ONE</i> , 2018, 13, e0202002.	1.1	4

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55	In silico exploration of Red Sea <i>Bacillus</i> genomes for natural product biosynthetic gene clusters. <i>BMC Genomics</i> , 2018, 19, 382.	1.2	17
56	DPubChem: a web tool for QSAR modeling and high-throughput virtual screening. <i>Scientific Reports</i> , 2018, 8, 9110.	1.6	40
57	Shared activity patterns arising at genetic susceptibility loci reveal underlying genomic and cellular architecture of human disease. <i>PLoS Computational Biology</i> , 2018, 14, e1005934.	1.5	17
58	bTSSfinder: a novel tool for the prediction of promoters in cyanobacteria and <i>Escherichia coli</i> . <i>Bioinformatics</i> , 2017, 33, 334-340.	1.8	80
59	FARNA: knowledgebase of inferred functions of non-coding RNA transcripts. <i>Nucleic Acids Research</i> , 2017, 45, gkw973.	6.5	30
60	Discriminative identification of transcriptional responses of promoters and enhancers after stimulus. <i>Nucleic Acids Research</i> , 2017, 45, gkw1015.	6.5	3
61	Draft Genome Sequence of the Plant Growth-Promoting <i>Rhizobacterium Acinetobacter radioresistens</i> Strain SA188 Isolated from the Desert Plant <i>Indigofera argentea</i> . <i>Genome Announcements</i> , 2017, 5, .	0.8	5
62	Draft Genome Sequence of the Plant Growth-Promoting <i>Pseudomonas punonensis</i> Strain D1-6 Isolated from the Desert Plant <i>Erodium hirtum</i> in Jordan. <i>Genome Announcements</i> , 2017, 5, .	0.8	9
63	Draft Genome Sequence of Plant Growth-Promoting <i>Micrococcus luteus</i> Strain K39 Isolated from <i>Cyperus conglomeratus</i> in Saudi Arabia. <i>Genome Announcements</i> , 2017, 5, .	0.8	11
64	In silico screening for candidate chassis strains of free fatty acid-producing cyanobacteria. <i>BMC Genomics</i> , 2017, 18, 33.	1.2	11
65	Genomic characterization of two novel SAR11 isolates from the Red Sea, including the first strain of the SAR11 Ib clade. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	1.3	15
66	Building a bio-based industry in the Middle East through harnessing the potential of the Red Sea biodiversity. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 4837-4851.	1.7	10
67	DES-ncRNA: A knowledgebase for exploring information about human micro and long noncoding RNAs based on literature-mining. <i>RNA Biology</i> , 2017, 14, 963-971.	1.5	21
68	Bioprospecting Archaea: Focus on Extreme Halophiles. <i>Topics in Biodiversity and Conservation</i> , 2017, , 81-112.	0.3	10
69	DES-TOMATO: A Knowledge Exploration System Focused On Tomato Species. <i>Scientific Reports</i> , 2017, 7, 5968.	1.6	8
70	OmniGA: Optimized Omnivariate Decision Trees for Generalizable Classification Models. <i>Scientific Reports</i> , 2017, 7, 3898.	1.6	24
71	Draft Genome Sequence of <i>Ochrobactrum intermedium</i> Strain SA148, a Plant Growth-Promoting Desert <i>Rhizobacterium</i> . <i>Genome Announcements</i> , 2017, 5, .	0.8	5
72	Draft Genome Sequence of <i>Enterobacter</i> sp. Sa187, an Endophytic Bacterium Isolated from the Desert Plant <i>Indigofera argentea</i> . <i>Genome Announcements</i> , 2017, 5, .	0.8	5

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73	Complete Genome Sequence Analysis of <i>Enterobacter</i> sp. SA187, a Plant Multi-Stress Tolerance Promoting Endophytic Bacterium. <i>Frontiers in Microbiology</i> , 2017, 8, 2023.	1.5	83
74	Omni-PolyA: a method and tool for accurate recognition of Poly(A) signals in human genomic DNA. <i>BMC Genomics</i> , 2017, 18, 620.	1.2	30
75	Semantic prioritization of novel causative genomic variants. <i>PLoS Computational Biology</i> , 2017, 13, e1005500.	1.5	28
76	HMCAN-diff: a method to detect changes in histone modifications in cells with different genetic characteristics. <i>Nucleic Acids Research</i> , 2017, 45, gkw1319.	6.5	8
77	TcoF-DB v2: update of the database of human and mouse transcription co-factors and transcription factor interactions. <i>Nucleic Acids Research</i> , 2017, 45, D145-D150.	6.5	63
78	Draft Genome Sequence of <i>Halomonas elongata</i> Strain K4, an Endophytic Growth-Promoting Bacterium Enhancing Salinity Tolerance <i>In Planta</i> . <i>Genome Announcements</i> , 2016, 4, .	0.8	13
79	Bioprospecting Red Sea Coastal Ecosystems for Culturable Microorganisms and Their Antimicrobial Potential. <i>Marine Drugs</i> , 2016, 14, 165.	2.2	30
80	Draft genome of an <i>Aerophobetes</i> bacterium reveals a facultative lifestyle in deep-sea anaerobic sediments. <i>Science Bulletin</i> , 2016, 61, 1176-1186.	4.3	16
81	Delta-proteobacterial SAR324 group in hydrothermal plumes on the South Mid-Atlantic Ridge. <i>Scientific Reports</i> , 2016, 6, 22842.	1.6	21
82	DRABAL: novel method to mine large high-throughput screening assays using Bayesian active learning. <i>Journal of Cheminformatics</i> , 2016, 8, 64.	2.8	20
83	Draft Genome Sequence of the Phosphate-Solubilizing Bacterium <i>Pseudomonas argentinensis</i> Strain SA190 Isolated from the Desert Plant <i>Indigofera argentea</i> . <i>Genome Announcements</i> , 2016, 4, .	0.8	9
84	Genomes of coral dinoflagellate symbionts highlight evolutionary adaptations conducive to a symbiotic lifestyle. <i>Scientific Reports</i> , 2016, 6, 39734.	1.6	303
85	Draft Genome Sequence of the Plant Growth-Promoting <i>Cupriavidus gilardii</i> Strain JZ4 Isolated from the Desert Plant <i>Tribulus terrestris</i> . <i>Genome Announcements</i> , 2016, 4, .	0.8	17
86	Progress and challenges in bioinformatics approaches for enhancer identification. <i>Briefings in Bioinformatics</i> , 2016, 17, 967-979.	3.2	81
87	Inside Cover Image, Volume 6, Issue 2. <i>Wiley Interdisciplinary Reviews: Computational Molecular Science</i> , 2016, 6, ii-ii.	6.2	0
88	Metagenomics as a preliminary screen for antimicrobial bioprospecting. <i>Gene</i> , 2016, 594, 248-258.	1.0	26
89	<i>In silico</i> toxicology: computational methods for the prediction of chemical toxicity. <i>Wiley Interdisciplinary Reviews: Computational Molecular Science</i> , 2016, 6, 147-172.	6.2	460
90	Metabolic traits of an uncultured archaeal lineage -MSBL1- from brine pools of the Red Sea. <i>Scientific Reports</i> , 2016, 6, 19181.	1.6	66

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91	Transcriptome Profiling Strategies. , 2016, , 69-104.		0
92	DASPFIND: new efficient method to predict drugâ€‘target interactions. Journal of Cheminformatics, 2016, 8, 15.	2.8	88
93	DESM: portal for microbial knowledge exploration systems. Nucleic Acids Research, 2016, 44, D624-D633.	6.5	12
94	Comprehensive Genomic Analyses of the OM43 Clade, Including a Novel Species from the Red Sea, Indicate Ecotype Differentiation among Marine Methylophages. Applied and Environmental Microbiology, 2016, 82, 1215-1226.	1.4	37
95	Rhizosphere microbiome metagenomics of gray mangroves (<i>Avicennia marina</i>) in the Red Sea. Gene, 2016, 576, 626-636.	1.0	116
96	HOCOMOCO: expansion and enhancement of the collection of transcription factor binding sites models. Nucleic Acids Research, 2016, 44, D116-D125.	6.5	215
97	Late phase cell cycle proteins in Alzheimerâ€™s disease: a possible target for therapy?. Journal of Systems and Integrative Neuroscience, 2016, 3, .	0.6	3
98	Insights into the Transcriptional Architecture of Behavioral Plasticity in the Honey Bee <i>Apis mellifera</i> . Scientific Reports, 2015, 5, 11136.	1.6	59
99	DENDB: database of integrated human enhancers. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav085.	1.4	51
100	Synchronized dynamics of bacterial nicheâ€‘specific functions during biofilm development in a cold seep brine pool. Environmental Microbiology, 2015, 17, 4089-4104.	1.8	24
101	DWFS: A Wrapper Feature Selection Tool Based on a Parallel Genetic Algorithm. PLoS ONE, 2015, 10, e0117988.	1.1	94
102	DDMGD: the database of text-mined associations between genes methylated in diseases from different species. Nucleic Acids Research, 2015, 43, D879-D886.	6.5	17
103	LncRNAWiki: harnessing community knowledge in collaborative curation of human long non-coding RNAs. Nucleic Acids Research, 2015, 43, D187-D192.	6.5	110
104	BEACON: automated tool for Bacterial GENome Annotation ComparisON. BMC Genomics, 2015, 16, 616.	1.2	26
105	First Insights into the Viral Communities of the Deep-sea Anoxic Brines of the Red Sea. Genomics, Proteomics and Bioinformatics, 2015, 13, 304-309.	3.0	33
106	Soil and Rhizosphere Associated Fungi in Gray Mangroves (<i>Avicennia marina</i>) from the Red Sea â€‘ A Metagenomic Approach. Genomics, Proteomics and Bioinformatics, 2015, 13, 310-320.	3.0	67
107	The Value and Significance of Metagenomics of Marine Environments. Genomics, Proteomics and Bioinformatics, 2015, 13, 271-274.	3.0	13
108	Hepatic Proteomic Responses in Marine Medaka (<i>Oryzias melastigma</i>) Chronically Exposed to Antifouling Compound Butenolide [5-octylfuran-2(5H)-one] or 4,5-Dichloro-2-(1-octyl-4-isothiazolin-3-one) (DCOIT). Environmental Science & Technology, 2015, 49, 1851-1859.	4.6	41

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109	Distinct profiling of antimicrobial peptide families. <i>Bioinformatics</i> , 2015, 31, 849-856.	1.8	25
110	DEEP: a general computational framework for predicting enhancers. <i>Nucleic Acids Research</i> , 2015, 43, e6-e6.	6.5	124
111	Redefining the transcriptional regulatory dynamics of classically and alternatively activated macrophages by deepCAGE transcriptomics. <i>Nucleic Acids Research</i> , 2015, 43, 6969-6982.	6.5	54
112	Comparative genomics reveals adaptations of a halotolerant thaumarchaeon in the interfaces of brine pools in the Red Sea. <i>ISME Journal</i> , 2015, 9, 396-411.	4.4	60
113	Mining Chemical Activity Status from High-Throughput Screening Assays. <i>PLoS ONE</i> , 2015, 10, e0144426.	1.1	15
114	Pyrosequencing revealed shifts of prokaryotic communities between healthy and disease-like tissues of the Red Sea sponge <i>Crella cyathophora</i> . <i>PeerJ</i> , 2015, 3, e890.	0.9	20
115	Autophagy Inhibition Enhances the Mitochondrial-Mediated Apoptosis Induced by Mangrove (<i>Avicennia</i>) Tj ETQq1 1 0.784314 rgBT /Qv	0.5	7
116	Core Microbial Functional Activities in Ocean Environments Revealed by Global Metagenomic Profiling Analyses. <i>PLoS ONE</i> , 2014, 9, e97338.	1.1	20
117	Cytotoxicity and Apoptosis Induced by a Plumbagin Derivative in Estrogen Positive MCF-7 Breast Cancer Cells. <i>Anti-Cancer Agents in Medicinal Chemistry</i> , 2014, 14, 170-180.	0.9	57
118	Mining a database of single amplified genomes from Red Sea brine pool extremophiles, improving reliability of gene function prediction using a profile and pattern matching algorithm (PPMA). <i>Frontiers in Microbiology</i> , 2014, 5, 134.	1.5	15
119	Genomic analysis reveals versatile heterotrophic capacity of a potentially symbiotic sulfur-oxidizing bacterium in sponge. <i>Environmental Microbiology</i> , 2014, 16, 3548-3561.	1.8	76
120	Symbiotic Adaptation Drives Genome Streamlining of the Cyanobacterial Sponge Symbiont <i>Candidatus</i> <i>Synechococcus spongiarum</i> . <i>MBio</i> , 2014, 5, e00079-14.	1.8	83
121	Aerobic methanotrophic communities at the Red Sea brine-seawater interface. <i>Frontiers in Microbiology</i> , 2014, 5, 487.	1.5	29
122	Effect of Copper Treatment on the Composition and Function of the Bacterial Community in the Sponge <i>Haliclona cymaeformis</i> . <i>MBio</i> , 2014, 5, e01980.	1.8	39
123	DEOP: a database on osmoprotectants and associated pathways. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, .	1.4	34
124	Chemical Compounds Toxic to Invertebrates Isolated from Marine Cyanobacteria of Potential Relevance to the Agricultural Industry. <i>Toxins</i> , 2014, 6, 3058-3076.	1.5	10
125	A promoter-level mammalian expression atlas. <i>Nature</i> , 2014, 507, 462-470.	13.7	1,838
126	A Novel Mercuric Reductase from the Unique Deep Brine Environment of Atlantis II in the Red Sea. <i>Journal of Biological Chemistry</i> , 2014, 289, 1675-1687.	1.6	36

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127	Proteomic changes in brain tissues of marine medaka (<i>Oryzias melastigma</i>) after chronic exposure to two antifouling compounds: Butenolide and 4,5-dichloro-2-n-octyl-4-isothiazolin-3-one (DCOIT). <i>Aquatic Toxicology</i> , 2014, 157, 47-56.	1.9	29
128	Pyrosequencing Reveals the Microbial Communities in the Red Sea Sponge <i>Carteriospongia foliascens</i> and Their Impressive Shifts in Abnormal Tissues. <i>Microbial Ecology</i> , 2014, 68, 621-632.	1.4	37
129	Genomic differentiation among two strains of the PS1 clade isolated from geographically separated marine habitats. <i>FEMS Microbiology Ecology</i> , 2014, 89, 181-197.	1.3	22
130	Effects of cytosine methylation on transcription factor binding sites. <i>BMC Genomics</i> , 2014, 15, 119.	1.2	214
131	Promoter Analysis Reveals Globally Differential Regulation of Human Long Non-Coding RNA and Protein-Coding Genes. <i>PLoS ONE</i> , 2014, 9, e109443.	1.1	72
132	In situ environment rather than substrate type dictates microbial community structure of biofilms in a cold seep system. <i>Scientific Reports</i> , 2014, 4, 3587.	1.6	49
133	Chapter 14: Automated Mining of Disease-Specific Protein Interaction Networks Based on Biomedical Literature. <i>Science, Engineering, and Biology Informatics</i> , 2014, , 393-415.	0.1	0
134	Maternal serum protein profile and immune response protein subunits as markers for non-invasive prenatal diagnosis of trisomy 21, 18, and 13. <i>Prenatal Diagnosis</i> , 2013, 33, 223-231.	1.1	15
135	Induction of apoptosis in cancer cell lines by the Red Sea brine pool bacterial extracts. <i>BMC Complementary and Alternative Medicine</i> , 2013, 13, 344.	3.7	49
136	Exploration of miRNA families for hypotheses generation. <i>Scientific Reports</i> , 2013, 3, 2940.	1.6	68
137	On the classification of long non-coding RNAs. <i>RNA Biology</i> , 2013, 10, 924-933.	1.5	1,040
138	Dragon exploration system on marine sponge compounds interactions. <i>Journal of Cheminformatics</i> , 2013, 5, 11.	2.8	16
139	Cytotoxic and apoptotic evaluations of marine bacteria isolated from brine-seawater interface of the Red Sea. <i>BMC Complementary and Alternative Medicine</i> , 2013, 13, 29.	3.7	30
140	PIMiner: a web tool for extraction of protein interactions from biomedical literature. <i>International Journal of Data Mining and Bioinformatics</i> , 2013, 7, 450.	0.1	13
141	Genome Sequence of <i>Pseudomonas</i> sp. Strain Chol1, a Model Organism for the Degradation of Bile Salts and Other Steroid Compounds. <i>Genome Announcements</i> , 2013, 1, .	0.8	17
142	HMCAn: a method for detecting chromatin modifications in cancer samples using ChIP-seq data. <i>Bioinformatics</i> , 2013, 29, 2979-2986.	1.8	39
143	Poly(A) motif prediction using spectral latent features from human DNA sequences. <i>Bioinformatics</i> , 2013, 29, i316-i325.	1.8	40
144	Dragon PolyA Spotter: predictor of poly(A) motifs within human genomic DNA sequences. <i>Bioinformatics</i> , 2013, 29, 1484-1484.	1.8	12

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145	HOCOMOCO: a comprehensive collection of human transcription factor binding sites models. <i>Nucleic Acids Research</i> , 2013, 41, D195-D202.	6.5	206
146	Dragon TIS Spotter: an Arabidopsis-derived predictor of translation initiation sites in plants. <i>Bioinformatics</i> , 2013, 29, 117-118.	1.8	43
147	Information Exploration System for Sickle Cell Disease and Repurposing of Hydroxyfasudil. <i>PLoS ONE</i> , 2013, 8, e65190.	1.1	14
148	Simplified Method for Predicting a Functional Class of Proteins in Transcription Factor Complexes. <i>PLoS ONE</i> , 2013, 8, e68857.	1.1	1
149	Combining Position Weight Matrices and Document-Term Matrix for Efficient Extraction of Associations of Methylated Genes and Diseases from Free Text. <i>PLoS ONE</i> , 2013, 8, e77848.	1.1	11
150	INDIGO – Integrated Data Warehouse of Microbial Genomes with Examples from the Red Sea Extremophiles. <i>PLoS ONE</i> , 2013, 8, e82210.	1.1	83
151	Comparing Memory-Efficient Genome Assemblers on Stand-Alone and Cloud Infrastructures. <i>PLoS ONE</i> , 2013, 8, e75505.	1.1	21
152	Human endometrial milk fat globule-epidermal growth factor 8 (MFGE8) is up regulated by estradiol at the transcriptional level, and its secretion via microvesicles is stimulated by human chorionic gonadotropin (hCG). <i>Cell Signalling and Trafficking</i> , 2013, 1, 1.	1.0	5
153	DAMPD: a manually curated antimicrobial peptide database. <i>Nucleic Acids Research</i> , 2012, 40, D1108-D1112.	6.5	93
154	Protein domain recurrence and order can enhance prediction of protein functions. <i>Bioinformatics</i> , 2012, 28, i444-i450.	1.8	24
155	Dragon PolyA Spotter: predictor of poly(A) motifs within human genomic DNA sequences. <i>Bioinformatics</i> , 2012, 28, 127-129.	1.8	95
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157	Identification of estrogen responsive genes using esophageal squamous cell carcinoma (ESCC) as a model. <i>BMC Systems Biology</i> , 2012, 6, 135.	3.0	2
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