

Filip Van Nieuwerburgh

List of Publications by Year in descending order

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Version: 2024-02-01

217
papers

8,679
citations

57758

44
h-index

60623

81
g-index

233
all docs

233
docs citations

233
times ranked

16328
citing authors

#	ARTICLE	IF	CITATIONS
1	Analysis of shared heritability in common disorders of the brain. <i>Science</i> , 2018, 360, .	12.6	1,085
2	Library construction for next-generation sequencing: Overviews and challenges. <i>BioTechniques</i> , 2014, 56, 61-77.	1.8	486
3	The Chara Genome: Secondary Complexity and Implications for Plant Terrestrialization. <i>Cell</i> , 2018, 174, 448-464.e24.	28.9	420
4	Genome-wide association study of obsessive-compulsive disorder. <i>Molecular Psychiatry</i> , 2013, 18, 788-798.	7.9	312
5	Partitioning the Heritability of Tourette Syndrome and Obsessive Compulsive Disorder Reveals Differences in Genetic Architecture. <i>PLoS Genetics</i> , 2013, 9, e1003864.	3.5	241
6	Dissection of the phytohormonal regulation of trichome formation and biosynthesis of the antimalarial compound artemisinin in <i>Artemisia annua</i> plants. <i>New Phytologist</i> , 2011, 189, 176-189.	7.3	192
7	Emended description of <i>Gardnerella vaginalis</i> and description of <i>Gardnerella leopoldii</i> sp. nov., <i>Gardnerella plotii</i> sp. nov. and <i>Gardnerella swidsinskii</i> sp. nov., with delineation of 13 genomic species within the genus <i>Gardnerella</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 679-687.	1.7	154
8	Directional RNA deep sequencing sheds new light on the transcriptional response of <i>Anabaena</i> sp. strain PCC 7120 to combined-nitrogen deprivation. <i>BMC Genomics</i> , 2011, 12, 332.	2.8	151
9	Development and evaluation of different normalization strategies for gene expression studies in <i>Candida albicans</i> biofilms by real-time PCR. <i>BMC Molecular Biology</i> , 2006, 7, 25.	3.0	139
10	Prevalence of Gender Nonconformity in Flanders, Belgium. <i>Archives of Sexual Behavior</i> , 2015, 44, 1281-1287.	1.9	138
11	The Quorum Sensing Inhibitor Hamamelitannin Increases Antibiotic Susceptibility of <i>Staphylococcus aureus</i> Biofilms by Affecting Peptidoglycan Biosynthesis and eDNA Release. <i>Scientific Reports</i> , 2016, 6, 20321.	3.3	138
12	Ancient Dispersal of the Human Fungal Pathogen <i>Cryptococcus gattii</i> from the Amazon Rainforest. <i>PLoS ONE</i> , 2013, 8, e71148.	2.5	122
13	Differential transcriptome analysis of glandular and filamentous trichomes in <i>Artemisia annua</i> . <i>BMC Plant Biology</i> , 2013, 13, 220.	3.6	106
14	Complete Nucleotide Sequence of CTX-M-15-Plasmids from Clinical <i>Escherichia coli</i> Isolates: Insertional Events of Transposons and Insertion Sequences. <i>PLoS ONE</i> , 2010, 5, e11202.	2.5	101
15	OSC2 and CYP716A14v2 Catalyze the Biosynthesis of Triterpenoids for the Cuticle of Aerial Organs of <i>Artemisia annua</i> . <i>Plant Cell</i> , 2015, 27, 286-301.	6.6	96
16	Forensic STR analysis using massive parallel sequencing. <i>Forensic Science International: Genetics</i> , 2012, 6, 810-818.	3.1	94
17	Chromosomal mosaicism in human blastocysts: the ultimate challenge of preimplantation genetic testing?. <i>Human Reproduction</i> , 2018, 33, 1342-1354.	0.9	94
18	TBX2 is a neuroblastoma core regulatory circuitry component enhancing MYCN/FOXM1 reactivation of DREAM targets. <i>Nature Communications</i> , 2018, 9, 4866.	12.8	91

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19	Strain Prioritization and Genome Mining for Eneidyne Natural Products. MBio, 2016, 7, .	4.1	89
20	The transcriptome of Mycobacterium tuberculosis in a lipid-rich dormancy model through RNAseq analysis. Scientific Reports, 2017, 7, 17665.	3.3	88
21	Discovery of the leinamycin family of natural products by mining actinobacterial genomes. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E11131-E11140.	7.1	84
22	My-Forensic-Loci-queries (MyFLq) framework for analysis of forensic STR data generated by massive parallel sequencing. Forensic Science International: Genetics, 2014, 9, 1-8.	3.1	75
23	Association between serotonergic candidate genes and specific phenotypes of obsessive compulsive disorder. Journal of Affective Disorders, 2006, 91, 39-44.	4.1	73
24	Presence and potential of cell free DNA in different types of forensic samples. Forensic Science International: Genetics, 2013, 7, 316-320.	3.1	72
25	Quantitation of artemisinin and its biosynthetic precursors in Artemisia annua L. by high performance liquid chromatographyâ€“electrospray quadrupole time-of-flight tandem mass spectrometry. Journal of Chromatography A, 2006, 1118, 180-187.	3.7	69
26	Transgenerational Inheritance of DNA Hypomethylation in <i>Daphnia magna</i> in Response to Salinity Stress. Environmental Science & Technology, 2018, 52, 10114-10123.	10.0	67
27	Association between the dopamine D2 receptor TaqI A2 allele and low activity COMT allele with obsessiveâ€“compulsive disorder in males. European Neuropsychopharmacology, 2006, 16, 446-450.	0.7	66
28	Assessment of Microbial Diversity in Biofilms Recovered from Endotracheal Tubes Using Culture Dependent and Independent Approaches. PLoS ONE, 2012, 7, e38401.	2.5	65
29	A Case of Phage Therapy against Pandrug-Resistant Achromobacter xylosoxidans in a 12-Year-Old Lung-Transplanted Cystic Fibrosis Patient. Viruses, 2021, 13, 60.	3.3	65
30	ADAR1 interaction with Z-RNA promotes editing of endogenous double-stranded RNA and prevents MDA5-dependent immune activation. Cell Reports, 2021, 36, 109500.	6.4	65
31	Transcriptome Analysis of Bombyx mori Larval Midgut during Persistent and Pathogenic Cytoplasmic Polyhedrosis Virus Infection. PLoS ONE, 2015, 10, e0121447.	2.5	63
32	Direct comparison of distinct naive pluripotent states in human embryonic stem cells. Nature Communications, 2017, 8, 15055.	12.8	60
33	Coumarin Reduces Virulence and Biofilm Formation in Pseudomonas aeruginosa by Affecting Quorum Sensing, Type III Secretion and C-di-GMP Levels. Frontiers in Microbiology, 2018, 9, 1952.	3.5	59
34	Prediction of Response to Paroxetine and Venlafaxine by Serotonin-Related Genes in Obsessive-Compulsive Disorder in a Randomized, Double-Blind Trial. Journal of Clinical Psychiatry, 2007, 68, 747-753.	2.2	59
35	Suboptimal culture conditions induce more deviations in gene expression in male than female bovine blastocysts. BMC Genomics, 2016, 17, 72.	2.8	58
36	Forensic SNP Genotyping using Nanopore MinION Sequencing. Scientific Reports, 2017, 7, 41759.	3.3	54

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37	Performance of four modern whole genome amplification methods for copy number variant detection in single cells. <i>Scientific Reports</i> , 2017, 7, 3422.	3.3	54
38	Comparative analysis of naive, primed and ground state pluripotency in mouse embryonic stem cells originating from the same genetic background. <i>Scientific Reports</i> , 2018, 8, 5884.	3.3	54
39	Illumina mate-paired DNA sequencing-library preparation using Cre-Lox recombination. <i>Nucleic Acids Research</i> , 2012, 40, e24-e24.	14.5	52
40	16S rRNA Amplicon Sequencing Demonstrates that Indoor-Reared Bumblebees (<i>Bombus terrestris</i>) Harbor a Core Subset of Bacteria Normally Associated with the Wild Host. <i>PLoS ONE</i> , 2015, 10, e0125152.	2.5	51
41	Quantitative Bias in Illumina TruSeq and a Novel Post Amplification Barcoding Strategy for Multiplexed DNA and Small RNA Deep Sequencing. <i>PLoS ONE</i> , 2011, 6, e26969.	2.5	51
42	In vivo study of Dicer-2-mediated immune response of the small interfering RNA pathway upon systemic infections of virulent and avirulent viruses in <i>Bombus terrestris</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2016, 70, 127-137.	2.7	50
43	Colony contact contributes to the diversity of gut bacteria in bumblebees (<i>Bombus terrestris</i>). <i>Insect Science</i> , 2017, 24, 270-277.	3.0	50
44	Automatic detection of spermatozoa for laser capture microdissection. <i>International Journal of Legal Medicine</i> , 2009, 123, 169-175.	2.2	49
45	Molecular diagnostics for congenital hearing loss including 15 deafness genes using a next generation sequencing platform. <i>BMC Medical Genomics</i> , 2012, 5, 17.	1.5	49
46	Viral Small-RNA Analysis of <i>Bombyx mori</i> Larval Midgut during Persistent and Pathogenic Cytoplasmic Polyhedrosis Virus Infection. <i>Journal of Virology</i> , 2015, 89, 11473-11486.	3.4	47
47	Statistical framework for detection of genetically modified organisms based on Next Generation Sequencing. <i>Food Chemistry</i> , 2016, 192, 788-798.	8.2	47
48	A multi-omics analysis of the grapevine pathogen <i>Lasiodiplodia theobromae</i> reveals that temperature affects the expression of virulence- and pathogenicity-related genes. <i>Scientific Reports</i> , 2019, 9, 13144.	3.3	47
49	Vapor nanobubble is the more reliable photothermal mechanism for inducing endosomal escape of siRNA without disturbing cell homeostasis. <i>Journal of Controlled Release</i> , 2020, 319, 262-275.	9.9	45
50	Safety assessment of the butyrate-producing <i>Butyricoccus pullicaecorum</i> strain 25-3T, a potential probiotic for patients with inflammatory bowel disease, based on oral toxicity tests and whole genome sequencing. <i>Food and Chemical Toxicology</i> , 2014, 72, 129-137.	3.6	43
51	Proteins involved in embryo-maternal interaction around the signalling of maternal recognition of pregnancy in the horse. <i>Scientific Reports</i> , 2018, 8, 5249.	3.3	43
52	Generation of Virus- and dsRNA-Derived siRNAs with Species-Dependent Length in Insects. <i>Viruses</i> , 2019, 11, 738.	3.3	43
53	Distinct and temporary-restricted epigenetic mechanisms regulate human $\hat{I}\pm\hat{I}^2$ and $\hat{I}^3\hat{I}$ T cell development. <i>Nature Immunology</i> , 2020, 21, 1280-1292.	14.5	43
54	A Doubling of Microphytobenthos Biomass Coincides with a Tenfold Increase in Denitrifier and Total Bacterial Abundances in Intertidal Sediments of a Temperate Estuary. <i>PLoS ONE</i> , 2015, 10, e0126583.	2.5	43

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55	Perfrin, a novel bacteriocin associated with netB positive <i>Clostridium perfringens</i> strains from broilers with necrotic enteritis. <i>Veterinary Research</i> , 2014, 45, 40.	3.0	42
56	Whole genome amplification with SurePlex results in better copy number alteration detection using sequencing data compared to the MALBAC method. <i>Scientific Reports</i> , 2015, 5, 11711.	3.3	42
57	Full Genome Sequences of All Nine <i>Chlamydia psittaci</i> Genotype Reference Strains. <i>Journal of Bacteriology</i> , 2012, 194, 6930-6931.	2.2	41
58	Shallow whole genome sequencing is well suited for the detection of chromosomal aberrations in human blastocysts. <i>Fertility and Sterility</i> , 2015, 104, 1276-1285.e1.	1.0	40
59	Practical Tools to Implement Massive Parallel Pyrosequencing of PCR Products in Next Generation Molecular Diagnostics. <i>PLoS ONE</i> , 2011, 6, e25531.	2.5	40
60	Gain of 20q11.21 in Human Pluripotent Stem Cells Impairs TGF- β -Dependent Neuroectodermal Commitment. <i>Stem Cell Reports</i> , 2019, 13, 163-176.	4.8	39
61	Microbial diversity and metabolite composition of Belgian red-brown acidic ales. <i>International Journal of Food Microbiology</i> , 2016, 221, 1-11.	4.7	38
62	Shorter CAG repeats in the androgen receptor gene may enhance hyperandrogenicity in polycystic ovary syndrome. <i>Gynecological Endocrinology</i> , 2008, 24, 669-673.	1.7	37
63	Quantification of Integrated HIV DNA by Repetitive-Sampling Alu-HIV PCR on the Basis of Poisson Statistics. <i>Clinical Chemistry</i> , 2014, 60, 886-895.	3.2	37
64	Divergence between the Highly Virulent Zoonotic Pathogen <i>Helicobacter heilmannii</i> and Its Closest Relative, the Low-Virulence <i>Helicobacter ailurogastricus</i> sp. nov. <i>Infection and Immunity</i> , 2016, 84, 293-306.	2.2	37
65	Caspase-14-Deficient Mice Are More Prone to the Development of Parakeratosis. <i>Journal of Investigative Dermatology</i> , 2013, 133, 742-750.	0.7	35
66	Impact of sugar syrup and pollen diet on the bacterial diversity in the gut of indoor-reared bumblebees (<i>Bombus terrestris</i>). <i>Apidologie</i> , 2016, 47, 548-560.	2.0	35
67	Forensic tri-allelic SNP genotyping using nanopore sequencing. <i>Forensic Science International: Genetics</i> , 2019, 38, 204-210.	3.1	35
68	Modification of citrulline residues with 2,3-butanedione facilitates their detection by liquid chromatography/mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2011, 25, 1536-1542.	1.5	34
69	The Equine Embryo Influences Immune-Related Gene Expression in the Oviduct1. <i>Biology of Reproduction</i> , 2016, 94, 36.	2.7	34
70	First draft genome assembly of the desert locust, <i>Schistocerca gregaria</i> . <i>F1000Research</i> , 2020, 9, 775.	1.6	34
71	Suspension fluorescence in situ hybridization (S-FISH) combined with automatic detection and laser microdissection for STR profiling of male cells in male/female mixtures. <i>International Journal of Legal Medicine</i> , 2009, 123, 441-447.	2.2	33
72	Fetal Microchimeric Cells in Blood of Women with an Autoimmune Thyroid Disease. <i>PLoS ONE</i> , 2011, 6, e29646.	2.5	33

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73	Genome-wide transcription start site profiling in biofilm-grown <i>Burkholderia cenocepacia</i> J2315. <i>BMC Genomics</i> , 2015, 16, 775.	2.8	33
74	The transcription factor ETS1 is an important regulator of human NK cell development and terminal differentiation. <i>Blood</i> , 2020, 136, 288-298.	1.4	33
75	Nanopore Sequencing of a Forensic STR Multiplex Reveals Loci Suitable for Single-Contributor STR Profiling. <i>Genes</i> , 2020, 11, 381.	2.4	33
76	Presence and Analysis of Plasmids in Human and Animal Associated <i>Arcobacter</i> Species. <i>PLoS ONE</i> , 2014, 9, e85487.	2.5	33
77	Improved canine exome designs, featuring ncRNAs and increased coverage of protein coding genes. <i>Scientific Reports</i> , 2015, 5, 12810.	3.3	31
78	Validation of a sensitive DNA walking strategy to characterise unauthorised GMOs using model food matrices mimicking common rice products. <i>Food Chemistry</i> , 2015, 173, 1259-1265.	8.2	31
79	Unique long non-coding RNA expression signature in ETV6/RUNX1-driven B-cell precursor acute lymphoblastic leukemia. <i>Oncotarget</i> , 2016, 7, 73769-73780.	1.8	30
80	Bovine Embryo-Secreted microRNA-30c Is a Potential Non-invasive Biomarker for Hampered Preimplantation Developmental Competence. <i>Frontiers in Genetics</i> , 2019, 10, 315.	2.3	29
81	The transcriptome of the marine calanoid copepod <i>Temora longicornis</i> under heat stress and recovery. <i>Marine Environmental Research</i> , 2019, 143, 10-23.	2.5	29
82	Dual RNA Sequencing of <i>Vitis vinifera</i> during <i>Lasiodiplodia theobromae</i> Infection Unveils Host-Pathogen Interactions. <i>International Journal of Molecular Sciences</i> , 2019, 20, 6083.	4.1	28
83	Forensic massively parallel sequencing data analysis tool: Implementation of MyFLq as a standalone web- and Illumina BaseSpace®-application. <i>Forensic Science International: Genetics</i> , 2015, 15, 2-7.	3.1	27
84	Decreased susceptibility of <i>Streptococcus anginosus</i> to vancomycin in a multispecies biofilm is due to increased thickness of the cell wall. <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 2323-2330.	3.0	27
85	Efficiency of Exome Sequencing for the Molecular Diagnosis of <i>Pseudoxanthoma Elasticum</i> . <i>Journal of Investigative Dermatology</i> , 2015, 135, 992-998.	0.7	25
86	Challenges and opportunities in the investigation of unexplained intellectual disability using family-based whole-exome sequencing. <i>Clinical Genetics</i> , 2015, 88, 140-148.	2.0	25
87	Ecological divergence of wild strawberry DNA methylation patterns at distinct spatial scales. <i>Molecular Ecology</i> , 2020, 29, 4871-4881.	3.9	25
88	Evaluation of three DNA extraction protocols for forensic STR typing after laser capture microdissection. <i>Forensic Science International: Genetics</i> , 2012, 6, 258-262.	3.1	24
89	First draft genome assembly of the desert locust, <i>Schistocerca gregaria</i> . <i>F1000Research</i> , 2020, 9, 775.	1.6	24
90	T-BET and EOMES Accelerate and Enhance Functional Differentiation of Human Natural Killer Cells. <i>Frontiers in Immunology</i> , 2021, 12, 732511.	4.8	24

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91	Development and performance of a targeted whole exome sequencing enrichment kit for the dog (<i>Canis Familiaris</i> Build 3.1). <i>Scientific Reports</i> , 2014, 4, 5597.	3.3	23
92	A different gut microbial community between larvae and adults of a wild bumblebee nest (<i>Bombus</i> Tj ETQq0 0 0 rgBT /Overlock 10 T	3.6	23
93	Hatching is modulated by microRNA-378a-3p derived from extracellular vesicles secreted by blastocysts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2122708119.	7.1	23
94	Characterization of the emerging zoonotic pathogen <i>Arcobacter</i> thereius by whole genome sequencing and comparative genomics. <i>PLoS ONE</i> , 2017, 12, e0180493.	2.5	21
95	Changes in DNA Methylation in <i>Arabidopsis thaliana</i> Plants Exposed Over Multiple Generations to Gamma Radiation. <i>Frontiers in Plant Science</i> , 2021, 12, 611783.	3.6	21
96	Aging of Preleukemic Thymocytes Drives CpG Island Hypermethylation in T-cell Acute Lymphoblastic Leukemia. <i>Blood Cancer Discovery</i> , 2020, 1, 274-289.	5.0	21
97	Response to serotonin reuptake inhibitors in OCD is not influenced by common CYP2D6 polymorphisms. <i>International Journal of Psychiatry in Clinical Practice</i> , 2009, 13, 345-348.	2.4	20
98	The role of the COMT Val ¹⁵⁸ /Met polymorphism in the phenotypic expression of obsessive-compulsive disorder. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2010, 153B, 167-176.	1.7	20
99	Metabolic activity, urease production, antibiotic resistance and virulence in dual species biofilms of <i>Staphylococcus epidermidis</i> and <i>Staphylococcus aureus</i> . <i>PLoS ONE</i> , 2017, 12, e0172700.	2.5	20
100	HES1 and HES4 have non-redundant roles downstream of Notch during early human T-cell development. <i>Haematologica</i> , 2020, 106, 130-141.	3.5	20
101	RUNX2 regulates leukemic cell metabolism and chemotaxis in high-risk T cell acute lymphoblastic leukemia. <i>Journal of Clinical Investigation</i> , 2021, 131, .	8.2	20
102	The genome of the extremophile <i>Artemia</i> provides insight into strategies to cope with extreme environments. <i>BMC Genomics</i> , 2021, 22, 635.	2.8	20
103	Variations in the exome of the LNCaP prostate cancer cell line. <i>Prostate</i> , 2012, 72, 1317-1327.	2.3	19
104	Genome Sequence of <i>Helicobacter heilmannii</i> Sensu Stricto ASB1 Isolated from the Gastric Mucosa of a Kitten with Severe Gastritis. <i>Genome Announcements</i> , 2013, 1, .	0.8	19
105	Myeloid-specific IRE1alpha deletion reduces tumour development in a diabetic, non-alcoholic steatohepatitis-induced hepatocellular carcinoma mouse model. <i>Metabolism: Clinical and Experimental</i> , 2020, 107, 154220.	3.4	19
106	Elucidation of the mechanism behind the potentiating activity of baicalin against <i>Burkholderia cenocepacia</i> biofilms. <i>PLoS ONE</i> , 2018, 13, e0190533.	2.5	19
107	Impact of allelic dropout on evidential value of forensic DNA profiles using RMNE. <i>Bioinformatics</i> , 2009, 25, 225-229.	4.1	18
108	Microbial community profiling of fresh basil and pitfalls in taxonomic assignment of enterobacterial pathogenic species based upon 16S rRNA amplicon sequencing. <i>International Journal of Food Microbiology</i> , 2017, 257, 148-156.	4.7	18

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109	Photothermally Triggered Endosomal Escape and Its Influence on Transfection Efficiency of Gold-Functionalized JetPEI/pDNA Nanoparticles. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2400.	4.1	18
110	Pre-clinical evaluation of second generation PIM inhibitors for the treatment of T-cell acute lymphoblastic leukemia and lymphoma. <i>Haematologica</i> , 2019, 104, e17-e20.	3.5	18
111	Honey bee predisposition of resistance to ubiquitous mite infestations. <i>Scientific Reports</i> , 2019, 9, 7794.	3.3	18
112	Catechol-O-methyltransferase gene expression is associated with response to citalopram in obsessive-compulsive disorder. <i>International Journal of Psychiatry in Clinical Practice</i> , 2012, 16, 277-283.	2.4	17
113	Oncogenic ZEB2 activation drives sensitivity toward KDM1A inhibition in T-cell acute lymphoblastic leukemia. <i>Blood</i> , 2017, 129, 981-990.	1.4	17
114	The presence of extracellular microRNAs in the media of cultured <i>Drosophila</i> cells. <i>Scientific Reports</i> , 2018, 8, 17312.	3.3	17
115	The effects of positioning, reason for screening and the referring veterinarian on prevalence estimates of canine hip dysplasia. <i>Veterinary Journal</i> , 2014, 201, 378-384.	1.7	16
116	Preimplantation genetic diagnosis for chromosomal rearrangements with the use of array comparative genomic hybridization at the blastocyst stage. <i>Fertility and Sterility</i> , 2017, 107, 212-219.e3.	1.0	16
117	The Small RNA ncS35 Regulates Growth in <i>Burkholderia cenocepacia</i> J2315. <i>MSphere</i> , 2018, 3, .	2.9	16
118	Influence of microbiota in the susceptibility of parasitic wasps to abamectin insecticide: deep sequencing, esterase and toxicity tests. <i>Pest Management Science</i> , 2019, 75, 79-86.	3.4	16
119	Analysing 454 amplicon resequencing experiments using the modular and database oriented Variant Identification Pipeline. <i>BMC Bioinformatics</i> , 2010, 11, 269.	2.6	15
120	Phospho-iTRAQ: Assessing Isobaric Labels for the Large-Scale Study Of Phosphopeptide Stoichiometry. <i>Journal of Proteome Research</i> , 2015, 14, 839-849.	3.7	15
121	Differential transcriptome analysis of the common shrimp <i>Crangon crangon</i> : Special focus on the nuclear receptors and RNAi-related genes. <i>General and Comparative Endocrinology</i> , 2015, 212, 163-177.	1.8	15
122	Performance of a TthPrimPol-based whole genome amplification kit for copy number alteration detection using massively parallel sequencing. <i>Scientific Reports</i> , 2016, 6, 31825.	3.3	15
123	Large expert-curated database for benchmarking document similarity detection in biomedical literature search. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	3.0	15
124	RRM2 enhances MYCN-driven neuroblastoma formation and acts as a synergistic target with CHK1 inhibition. <i>Science Advances</i> , 2022, 8, .	10.3	15
125	Short Tandem Repeat analysis after Whole Genome Amplification of single B-lymphoblastoid cells. <i>Scientific Reports</i> , 2018, 8, 1255.	3.3	14
126	Effect of β -adrenergic receptor agents on cardiac structure and function and whole-body gene expression in <i>Daphnia magna</i> . <i>Environmental Pollution</i> , 2018, 241, 869-878.	7.5	14

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127	Various Evolutionary Trajectories Lead to Loss of the Tobramycin-Potentiating Activity of the Quorum-Sensing Inhibitor Baicalin Hydrate in <i>Burkholderia cenocepacia</i> Biofilms. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	14
128	Dynamic epigenetic changes to <i>VHL</i> occur with sunitinib in metastatic clear cell renal cancer. <i>Oncotarget</i> , 2016, 7, 25241-25250.	1.8	14
129	The Prevalence of Nine Genetic Disorders in a Dog Population from Belgium, the Netherlands and Germany. <i>PLoS ONE</i> , 2013, 8, e74811.	2.5	13
130	Contemporary pharmacogenetic assays in view of the PharmGKB database. <i>Pharmacogenomics</i> , 2019, 20, 261-272.	1.3	13
131	Retrospective study of the impact of miniSTRs on forensic DNA profiling of touch DNA samples. <i>Science and Justice - Journal of the Forensic Science Society</i> , 2014, 54, 369-372.	2.1	12
132	Uncovering low-level mosaicism in human embryonic stem cells using high throughput single cell shallow sequencing. <i>Scientific Reports</i> , 2019, 9, 14844.	3.3	12
133	Marine biogenics in sea spray aerosols interact with the mTOR signaling pathway. <i>Scientific Reports</i> , 2019, 9, 675.	3.3	12
134	Extracellular vesicles spread the RNA interference signal of <i>Tribolium castaneum</i> TcA cells. <i>Insect Biochemistry and Molecular Biology</i> , 2020, 122, 103377.	2.7	12
135	Comparative analysis of mouse and human preimplantation development following <i>POU5F1</i> CRISPR/Cas9 targeting reveals interspecies differences. <i>Human Reproduction</i> , 2021, 36, 1242-1252.	0.9	12
136	Nanopore sequencing of a forensic combined STR and SNP multiplex. <i>Forensic Science International: Genetics</i> , 2022, 56, 102621.	3.1	12
137	Quantitative Proteomics to Characterize Specific Histone H2A Proteolysis in Chronic Lymphocytic Leukemia and the Myeloid THP-1 Cell Line. <i>International Journal of Molecular Sciences</i> , 2014, 15, 9407-9421.	4.1	11
138	The BCESM genomic region contains a regulator involved in quorum sensing and persistence in <i>Burkholderia cenocepacia</i> J2315. <i>Future Microbiology</i> , 2014, 9, 845-860.	2.0	11
139	Flagging False Positives Following Untargeted LC-MS Characterization of Histone Post-Translational Modification Combinations. <i>Journal of Proteome Research</i> , 2017, 16, 655-664.	3.7	11
140	Comparative analysis of different nuclear transfer techniques to prevent the transmission of mitochondrial DNA variants. <i>Molecular Human Reproduction</i> , 2019, 25, 797-810.	2.8	11
141	Truncating <i>SLC12A6</i> variants cause different clinical phenotypes in humans and dogs. <i>European Journal of Human Genetics</i> , 2019, 27, 1561-1568.	2.8	11
142	Genome-Wide Stress Responses to Copper and Arsenic in a Field Population of <i>Daphnia</i> . <i>Environmental Science & Technology</i> , 2019, 53, 3850-3859.	10.0	11
143	Comparative study of preimplantation development following distinct assisted oocyte activation protocols in a PLC-zeta knockout mouse model. <i>Molecular Human Reproduction</i> , 2020, 26, 801-815.	2.8	11
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