Filip Van Nieuwerburgh

List of Publications by Year in descending order

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217 papers

8,679 citations

44 h-index

57758

81 g-index

233 all docs 233 docs citations

times ranked

233

16328 citing authors

#	Article	IF	CITATIONS
1	Systematic comparison of experimental and human obstructive cholestasis reveals conservation of canonical pathway activation and biomarkers relevant for cholestatic liver disease. Genes and Diseases, 2023, 10, 18-21.	3.4	1
2	Nanopore sequencing of a forensic combined STR and SNP multiplex. Forensic Science International: Genetics, 2022, 56, 102621.	3.1	12
3	Transcriptional dynamics of gametogenesis in the green seaweed Ulva mutabilis identifies an RWP-RK transcription factor linked to reproduction. BMC Plant Biology, 2022, 22, 19.	3.6	7
4	Metabolism and Health Effects of Rare Sugars in a CACO-2/HepG2 Coculture Model. Nutrients, 2022, 14, 611.	4.1	5
5	Lycopene Supplementation to Serum-Free Maturation Medium Improves In Vitro Bovine Embryo Development and Quality and Modulates Embryonic Transcriptomic Profile. Antioxidants, 2022, 11, 344.	5.1	7
6	Hatching is modulated by microRNA-378a-3p derived from extracellular vesicles secreted by blastocysts. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2122708119.	7.1	23
7	Profiling the Aerobic Window of Horses in Response to Training by Means of a Modified Lactate Minimum Speed Test: Flatten the Curve. Frontiers in Physiology, 2022, 13, 792052.	2.8	5
8	QueSTR probes: Quencher-labeled RNase H2-dependent probes for Short Tandem Repeat genotyping. Sensors and Actuators B: Chemical, 2022, 361, 131714.	7.8	2
9	Signatures of polygenic adaptation align with genomeâ€wide methylation patterns in wild strawberry plants. New Phytologist, 2022, 235, 1501-1514.	7.3	6
10	Identification and profiling of stable microRNAs in hemolymph of young and old Locusta migratoria fifth instars. Current Research in Insect Science, 2022, 2, 100041.	1.7	2
11	Microbial diversity and antimicrobial susceptibility in endotracheal tube biofilms recovered from mechanically ventilated COVID-19 patients. Biofilm, 2022, 4, 100079.	3.8	9
12	PIWI Proteins Play an Antiviral Role in Lepidopteran Cell Lines. Viruses, 2022, 14, 1442.	3.3	7
13	Enrichment of circulating trophoblasts from maternal blood using filtration-based Metacell® technology. PLoS ONE, 2022, 17, e0271226.	2.5	2
14	RRM2 enhances MYCN-driven neuroblastoma formation and acts as a synergistic target with CHK1 inhibition. Science Advances, 2022, 8, .	10.3	15
15	Recurrent chromosomal imbalances provide selective advantage to human embryonic stem cells under enhanced replicative stress conditions. Genes Chromosomes and Cancer, 2021, 60, 272-281.	2.8	3
16	Murine induced pluripotent stem cellâ€derived neuroimmune cell culture models emphasize opposite immuneâ€effector functions of interleukin 13â€primed microglia and macrophages in terms of neuroimmune toxicity. Glia, 2021, 69, 326-345.	4.9	4
17	Pharmacogenetics in clinical practice: current level of knowledge among Flemish physicians and pharmacists. Pharmacogenomics Journal, 2021, 21, 78-84.	2.0	9
18	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

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19	Activin A-derived human embryonic stem cells show increased competence to differentiate into primordial germ cell-like cells. Stem Cells, 2021, 39, 551-563.	3.2	11
20	Comparative genomics of Flavobacterium columnare unveils novel insights in virulence and antimicrobial resistance mechanisms. Veterinary Research, 2021, 52, 18.	3.0	5
21	Comparative analysis of mouse and human preimplantation development following <i>POU5F1</i> CRISPR/Cas9 targeting reveals interspecies differences. Human Reproduction, 2021, 36, 1242-1252.	0.9	12
22	Enrichment of circulating trophoblasts from maternal blood using laminar microscale vortices. Prenatal Diagnosis, 2021, 41, 1171-1178.	2.3	6
23	Long non-coding RNAs as novel therapeutic targets in juvenile myelomonocytic leukemia. Scientific Reports, 2021, 11, 2801.	3.3	8
24	RUNX2 regulates leukemic cell metabolism and chemotaxis in high-risk T cell acute lymphoblastic leukemia. Journal of Clinical Investigation, 2021, 131, .	8.2	20
25	Changes in DNA Methylation in Arabidopsis thaliana Plants Exposed Over Multiple Generations to Gamma Radiation. Frontiers in Plant Science, 2021, 12, 611783.	3.6	21
26	Endogenous suppression of WNT signalling in human embryonic stem cells leads to low differentiation propensity towards definitive endoderm. Scientific Reports, 2021, 11, 6137.	3.3	6
27	Detection of cytosine methylation in Burkholderia cenocepacia by single-molecule real-time sequencing and whole-genome bisulfite sequencing. Microbiology (United Kingdom), 2021, 167, .	1.8	4
28	Characterization of the inflammatory microenvironment and hepatic macrophage subsets in experimental hepatocellular carcinoma models. Oncotarget, 2021, 12, 562-577.	1.8	11
29	Metallothioneins alter macrophage phenotype and represent novel therapeutic targets for acetaminophen-induced liver injury. Journal of Leukocyte Biology, 2021, 111, 123-133.	3.3	8
30	Untangling the structural and molecular mechanisms underlying colour and rapid colour change in a lizard, <i>Agama atra</i> . Molecular Ecology, 2021, 30, 2262-2284.	3.9	8
31	Effects of Aleurone Supplementation on Glucose-Insulin Metabolism and Gut Microbiome in Untrained Healthy Horses. Frontiers in Veterinary Science, 2021, 8, 642809.	2.2	4
32	Digital Polymerase Chain Reaction for Assessment of Mutant Mitochondrial Carry-over after Nuclear Transfer for In Vitro Fertilization. Clinical Chemistry, 2021, 67, 968-976.	3.2	4
33	STRide probes: Single-labeled short tandem repeat identification probes. Biosensors and Bioelectronics, 2021, 180, 113135.	10.1	3
34	Rare Modifier Variants Alter the Severity of Cardiovascular Disease in Pseudoxanthoma Elasticum: Identification of Novel Candidate Modifier Genes and Disease Pathways Through Mixture of Effects Analysis. Frontiers in Cell and Developmental Biology, 2021, 9, 612581.	3.7	6
35	Veterinarians' Competence in Applying Basic Genetic Principles and Daily Implementation of Clinical Genetics: A Study in a University Environment. Journal of Veterinary Medical Education, 2021, , e20210029.	0.6	1
36	MYCN-induced nucleolar stress drives an early senescence-like transcriptional program in hTERT-immortalized RPE cells. Scientific Reports, 2021, 11, 14454.	3.3	6

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37	Genetic Responses of Metabolically Active Limnospira indica Strain PCC 8005 Exposed to Î ³ -Radiation during Its Lifecycle. Microorganisms, 2021, 9, 1626.	3.6	1
38	Effect of overconditioning on the hepatic global gene expression pattern of dairy cows at the end of pregnancy. Journal of Dairy Science, 2021, 104, 8152-8163.	3.4	5
39	The genome of the extremophile Artemia provides insight into strategies to cope with extreme environments. BMC Genomics, 2021, 22, 635.	2.8	20
40	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
41	Pre-Weaning Inulin Supplementation Alters the Ileal Transcriptome in Pigs Regarding Lipid Metabolism. Veterinary Sciences, 2021, 8, 207.	1.7	4
42	Annelid genomes: Enchytraeus crypticus, a soil model for the innate (and primed) immune system. Lab Animal, 2021, 50, 285-294.	0.4	11
43	The Impact of Maternal and Piglet Low Protein Diet and Their Interaction on the Porcine Liver Transcriptome around the Time of Weaning. Veterinary Sciences, 2021, 8, 233.	1.7	3
44	T-BET and EOMES Accelerate and Enhance Functional Differentiation of Human Natural Killer Cells. Frontiers in Immunology, 2021, 12, 732511.	4.8	0
45	T-BET and EOMES Accelerate and Enhance Functional Differentiation of Human Natural Killer Cells. Frontiers in Immunology, 2021, 12, 732511.	4.8	24
46	Vapor nanobubble is the more reliable photothermal mechanism for inducing endosomal escape of siRNA without disturbing cell homeostasis. Journal of Controlled Release, 2020, 319, 262-275.	9.9	45
47	Does the mode of dispersion determine the properties of dispersed Pseudomonas aeruginosa biofilm cells?. International Journal of Antimicrobial Agents, 2020, 56, 106194.	2.5	7
48	Ecological divergence of wild strawberry DNA methylation patterns at distinct spatial scales. Molecular Ecology, 2020, 29, 4871-4881.	3.9	25
49	Human Thymic CD10+ PD-1+ Intraepithelial Lymphocyte Precursors Acquire Interleukin-15 Responsiveness at the CD1a– CD95+ CD28– CCR7– Developmental Stage. International Journal of Molecular Sciences, 2020, 21, 8785.	4.1	7
50	Spatio-temporal patterns in the gene expression of the calanoid copepod Temora longicornis in the Belgian part of the North Sea. Marine Environmental Research, 2020, 160, 105037.	2.5	8
51	Distinct and temporary-restricted epigenetic mechanisms regulate human $\hat{l}\pm\hat{l}^2$ and $\hat{l}^3\hat{l}$ T cell development. Nature Immunology, 2020, 21, 1280-1292.	14.5	43
52	HES1 and HES4 have non-redundant roles downstream of Notch during early human T-cell development. Haematologica, 2020, 106, 130-141.	3.5	20
53	Pan-cancer pharmacogenetics: targeted sequencing panels or exome sequencing?. Pharmacogenomics, 2020, 21, 1073-1084.	1.3	3
54	Kinship analysis on single cells after whole genome amplification. Scientific Reports, 2020, 10, 14647.	3.3	6

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55	Comparative study of preimplantation development following distinct assisted oocyte activation protocols in a PLC-zeta knockout mouse model. Molecular Human Reproduction, 2020, 26, 801-815.	2.8	11
56	Distinct transcriptome signatures of Helicobacter suis and Helicobacter heilmannii strains upon adherence to human gastric epithelial cells. Veterinary Research, 2020, 51, 62.	3.0	3
57	The transcription factor ETS1 is an important regulator of human NK cell development and terminal differentiation. Blood, 2020, 136, 288-298.	1.4	33
58	Adjuvanting Allergen Extracts for Sublingual Immunotherapy: Calcitriol Downregulates CXCL8 Production in Primary Sublingual Epithelial Cells. Frontiers in Immunology, 2020, 11, 1033.	4.8	3
59	Maternal Recognition of Pregnancy in the Horse: Are MicroRNAs the Secret Messengers?. International Journal of Molecular Sciences, 2020, 21, 419.	4.1	10
60	Nanopore Sequencing of a Forensic STR Multiplex Reveals Loci Suitable for Single-Contributor STR Profiling. Genes, 2020, 11, 381.	2.4	33
61	Myeloid-specific IRE1alpha deletion reduces tumour development in a diabetic, non-alcoholic steatohepatitis-induced hepatocellular carcinoma mouse model. Metabolism: Clinical and Experimental, 2020, 107, 154220.	3.4	19
62	Extracellular vesicles spread the RNA interference signal of Tribolium castaneum TcA cells. Insect Biochemistry and Molecular Biology, 2020, 122, 103377.	2.7	12
63	First draft genome assembly of the desert locust, Schistocerca gregaria. F1000Research, 2020, 9, 775.	1.6	24
64	Aging of Preleukemic Thymocytes Drives CpG Island Hypermethylation in T-cell Acute Lymphoblastic Leukemia. Blood Cancer Discovery, 2020, 1, 274-289.	5.0	21
65	First draft genome assembly of the desert locust, Schistocerca gregaria. F1000Research, 2020, 9, 775.	1.6	34
66	Pre-clinical evaluation of second generation PIM inhibitors for the treatment of T-cell acute lymphoblastic leukemia and lymphoma. Haematologica, 2019, 104, e17-e20.	3.5	18
67	Genetic characterization and therapeutic targeting of <i>MYC</i> i>â€rearranged T cell acute lymphoblastic leukaemia. British Journal of Haematology, 2019, 185, 169-174.	2.5	9
68	Generation of Virus- and dsRNA-Derived siRNAs with Species-Dependent Length in Insects. Viruses, 2019, 11, 738.	3.3	43
69	Gain of $20q11.21$ in Human Pluripotent Stem Cells Impairs TGF- \hat{l}^2 -Dependent Neuroectodermal Commitment. Stem Cell Reports, 2019, 13, 163-176.	4.8	39
70	Uncovering low-level mosaicism in human embryonic stem cells using high throughput single cell shallow sequencing. Scientific Reports, 2019, 9, 14844.	3.3	12
71	Comparative analysis of different nuclear transfer techniques to prevent the transmission of mitochondrial DNA variants. Molecular Human Reproduction, 2019, 25, 797-810.	2.8	11
72	A multi-omics analysis of the grapevine pathogen Lasiodiplodia theobromae reveals that temperature affects the expression of virulence- and pathogenicity-related genes. Scientific Reports, 2019, 9, 13144.	3.3	47

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73	YtrASa, a GntR-Family Transcription Factor, Represses Two Genetic Loci Encoding Membrane Proteins in Sulfolobus acidocaldarius. Frontiers in Microbiology, 2019, 10, 2084.	3 . 5	9
74	Marine biogenics in sea spray aerosols interact with the mTOR signaling pathway. Scientific Reports, 2019, 9, 675.	3.3	12
75	Various Evolutionary Trajectories Lead to Loss of the Tobramycin-Potentiating Activity of the Quorum-Sensing Inhibitor Baicalin Hydrate in <i>Burkholderia cenocepacia</i> Biofilms. Antimicrobial Agents and Chemotherapy, 2019, 63, .	3.2	14
76	Honey bee predisposition of resistance to ubiquitous mite infestations. Scientific Reports, 2019, 9, 7794.	3.3	18
77	Rejections in an non-purpose bred assistance dog population: Reasons, consequences and methods for screening. PLoS ONE, 2019, 14, e0218339.	2.5	5
78	Truncating SLC12A6 variants cause different clinical phenotypes in humans and dogs. European Journal of Human Genetics, 2019, 27, 1561-1568.	2.8	11
79	Silicon ÂμPCR Chip for Forensic STR Profiling with Hybeacon Probe Melting Curves. Scientific Reports, 2019, 9, 7341.	3.3	5
80	Bovine Embryo-Secreted microRNA-30c Is a Potential Non-invasive Biomarker for Hampered Preimplantation Developmental Competence. Frontiers in Genetics, 2019, 10, 315.	2.3	29
81	Contemporary pharmacogenetic assays in view of the PharmGKB database. Pharmacogenomics, 2019, 20, 261-272.	1.3	13
82	WNT Inhibition and Increased FGF Signaling Promotes Derivation of Less Heterogeneous Primed Human Embryonic Stem Cells, Compatible with Differentiation. Stem Cells and Development, 2019, 28, 579-592.	2.1	9
83	Feasibility of single-cell analysis of model cancer and foetal cells in blood after isolation by cell picking. Tumor Biology, 2019, 41, 101042831882336.	1.8	1
84	Genome-Wide Stress Responses to Copper and Arsenic in a Field Population of <i>Daphnia</i> Environmental Science & Technology, 2019, 53, 3850-3859.	10.0	11
85	Large expert-curated database for benchmarking document similarity detection in biomedical literature search. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	15
86	Dual RNA Sequencing of Vitis vinifera during Lasiodiplodia theobromae Infection Unveils Host–Pathogen Interactions. International Journal of Molecular Sciences, 2019, 20, 6083.	4.1	28
87	Influence of microbiota in the susceptibility of parasitic wasps to abamectin insecticide: deep sequencing, esterase and toxicity tests. Pest Management Science, 2019, 75, 79-86.	3.4	16
88	Forensic tri-allelic SNP genotyping using nanopore sequencing. Forensic Science International: Genetics, 2019, 38, 204-210.	3.1	35
89	The transcriptome of the marine calanoid copepod Temora longicornis under heat stress and recovery. Marine Environmental Research, 2019, 143, 10-23.	2.5	29
90	Emended description of Gardnerella vaginalis and description of Gardnerella leopoldii sp. nov., Gardnerella piotii sp. nov. and Gardnerella swidsinskii sp. nov., with delineation of 13 genomic species within the genus Gardnerella. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 679-687.	1.7	154

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91	Small RNA NcS27 co-regulates utilization of carbon sources in Burkholderia cenocepacia J2315. Microbiology (United Kingdom), 2019, 165, 1135-1150.	1.8	4
92	Intraobserver and interobserver agreement on the radiographical diagnosis of canine cranial cruciate ligament rupture. Veterinary Record, 2018, 182, 484-484.	0.3	7
93	Comparative analysis of naive, primed and ground state pluripotency in mouse embryonic stem cells originating from the same genetic background. Scientific Reports, 2018, 8, 5884.	3.3	54
94	Short Tandem Repeat analysis after Whole Genome Amplification of single B-lymphoblastoid cells. Scientific Reports, 2018, 8, 1255.	3.3	14
95	The Small RNA ncS35 Regulates Growth in Burkholderia cenocepacia J2315. MSphere, 2018, 3, .	2.9	16
96	Proteins involved in embryo-maternal interaction around the signalling of maternal recognition of pregnancy in the horse. Scientific Reports, 2018, 8, 5249.	3.3	43
97	A different gut microbial community between larvae and adults of a wild bumblebee nest (<i>Bombus) Tj ETQq1 1</i>	1 0.78431 3.0	4 rgBT /Ov <mark>er</mark>
98	Genome-Wide Copy Number Alteration Detection in Preimplantation Genetic Diagnosis. Methods in Molecular Biology, 2018, 1712, 27-42.	0.9	1
99	The presence of extracellular microRNAs in the media of cultured Drosophila cells. Scientific Reports, 2018, 8, 17312.	3.3	17
100	TBX2 is a neuroblastoma core regulatory circuitry component enhancing MYCN/FOXM1 reactivation of DREAM targets. Nature Communications, 2018, 9, 4866.	12.8	91
101	Photothermally Triggered Endosomal Escape and Its Influence on Transfection Efficiency of Gold-Functionalized JetPEI/pDNA Nanoparticles. International Journal of Molecular Sciences, 2018, 19, 2400.	4.1	18
102	Transcriptional landscape changes during human embryonic stem cell derivation. Molecular Human Reproduction, 2018, 24, 543-555.	2.8	5
103	Chromosomal mosaicism in human blastocysts: the ultimate challenge of preimplantation genetic testing?. Human Reproduction, 2018, 33, 1342-1354.	0.9	94
104	Multiplex STR amplification sensitivity in a silicon microchip. Scientific Reports, 2018, 8, 9853.	3.3	8
105	A prokaryotic–eukaryotic relation in the fat body of <i>Bombus terrestris</i> . Environmental Microbiology Reports, 2018, 10, 644-650.	2.4	6
106	Analysis of shared heritability in common disorders of the brain. Science, 2018, 360, .	12.6	1,085
107	The Chara Genome: Secondary Complexity and Implications for Plant Terrestrialization. Cell, 2018, 174, 448-464.e24.	28.9	420
108	Transgenerational Inheritance of DNA Hypomethylation in <i>Daphnia magna</i> in Response to Salinity Stress. Environmental Science & Environmental Sci	10.0	67

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109	Massively parallel sequencing of micro-manipulated cells targeting a comprehensive panel of disease-causing genes: A comparative evaluation of upstream whole-genome amplification methods. PLoS ONE, 2018, 13, e0196334.	2.5	10
110	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
111	Decreased susceptibility of Streptococcus anginosus to vancomycin in a multispecies biofilm is due to increased thickness of the cell wall. Journal of Antimicrobial Chemotherapy, 2018, 73, 2323-2330.	3.0	27
112	Effect of \hat{l}^2 -adrenergic receptor agents on cardiac structure and function and whole-body gene expression in Daphnia magna. Environmental Pollution, 2018, 241, 869-878.	7.5	14
113	Elucidation of the mechanism behind the potentiating activity of baicalin against Burkholderia cenocepacia biofilms. PLoS ONE, 2018, 13, e0190533.	2.5	19
114	Colony contact contributes to the diversity of gut bacteria in bumblebees (<i>Bombus terrestris</i> lnsect Science, 2017, 24, 270-277.	3.0	50
115	Epigenetic sampling effects: nephrectomy modifies the clear cell renal cell cancer methylome. Cellular Oncology (Dordrecht), 2017, 40, 293-297.	4.4	2
116	Forensic SNP Genotyping using Nanopore MinION Sequencing. Scientific Reports, 2017, 7, 41759.	3.3	54
117	Oncogenic ZEB2 activation drives sensitivity toward KDM1A inhibition in T-cell acute lymphoblastic leukemia. Blood, 2017, 129, 981-990.	1.4	17
118	Direct comparison of distinct naive pluripotent states in human embryonic stem cells. Nature Communications, 2017, 8, 15055.	12.8	60
119	STR profiling and Copy Number Variation analysis on single, preserved cells using current Whole Genome Amplification methods. Scientific Reports, 2017, 7, 17189.	3.3	8
120	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
121	Microbial community profiling of fresh basil and pitfalls in taxonomic assignment of enterobacterial pathogenic species based upon 16S rRNA amplicon sequencing. International Journal of Food Microbiology, 2017, 257, 148-156.	4.7	18
122	Performance of four modern whole genome amplification methods for copy number variant detection in single cells. Scientific Reports, 2017, 7, 3422.	3.3	54
123	RMNE calculation in forensic profiles with a high number of loci and allelic drop-outs using polynomial expansion. Forensic Science International: Genetics, 2017, 26, e14-e16.	3.1	1
124	Flagging False Positives Following Untargeted LC–MS Characterization of Histone Post-Translational Modification Combinations. Journal of Proteome Research, 2017, 16, 655-664.	3.7	11
125	Preimplantation genetic diagnosis for chromosomal rearrangements with the use of array comparative genomic hybridization at the blastocyst stage. Fertility and Sterility, 2017, 107, 212-219.e3.	1.0	16
126	The transcriptome of Mycobacterium tuberculosis in a lipid-rich dormancy model through RNAseq analysis. Scientific Reports, 2017, 7, 17665.	3.3	88

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127	Metabolic activity, urease production, antibiotic resistance and virulence in dual species biofilms of Staphylococcus epidermidis and Staphylococcus aureus. PLoS ONE, 2017, 12, e0172700.	2.5	20
128	Characterization of the emerging zoonotic pathogen Arcobacter thereius by whole genome sequencing and comparative genomics. PLoS ONE, 2017, 12, e0180493.	2.5	21
129	Toward the most ideal case–control design with related and unrelated dogs in wholeâ€exome sequencing studies. Animal Genetics, 2016, 47, 200-207.	1.7	5
130	Strain Prioritization and Genome Mining for Enediyne Natural Products. MBio, 2016, 7, .	4.1	89
131	Assessing the impact of minimizing arginine conversion in fully defined SILAC culture medium in human embryonic stem cells. Proteomics, 2016, 16, 2605-2614.	2.2	2
132	The Quorum Sensing Inhibitor Hamamelitannin Increases Antibiotic Susceptibility of Staphylococcus aureus Biofilms by Affecting Peptidoglycan Biosynthesis and eDNA Release. Scientific Reports, 2016, 6, 20321.	3.3	138
133	Performance of a TthPrimPol-based whole genome amplification kit for copy number alteration detection using massively parallel sequencing. Scientific Reports, 2016, 6, 31825.	3.3	15
134	Suboptimal culture conditions induce more deviations in gene expression in male than female bovine blastocysts. BMC Genomics, 2016, 17, 72.	2.8	58
135	The Equine Embryo Influences Immune-Related Gene Expression in the Oviduct1. Biology of Reproduction, 2016, 94, 36.	2.7	34
136	InÂvivo study of Dicer-2-mediated immune response of the small interfering RNA pathway upon systemic infections of virulent and avirulent viruses in Bombus terrestris. Insect Biochemistry and Molecular Biology, 2016, 70, 127-137.	2.7	50
137	Microbial diversity and metabolite composition of Belgian red-brown acidic ales. International Journal of Food Microbiology, 2016, 221, 1-11.	4.7	38
138	Divergence between the Highly Virulent Zoonotic Pathogen Helicobacter heilmannii and Its Closest Relative, the Low-Virulence "Helicobacter ailurogastricus―sp. nov. Infection and Immunity, 2016, 84, 293-306.	2.2	37
139	Impact of sugar syrup and pollen diet on the bacterial diversity in the gut of indoor-reared bumblebees (Bombus terrestris). Apidologie, 2016, 47, 548-560.	2.0	35
140	Forensic Loci Allele Database (FLAD): Automatically generated, permanent identifiers for sequenced forensic alleles. Forensic Science International: Genetics, 2016, 20, e1-e3.	3.1	7
141	Statistical framework for detection of genetically modified organisms based on Next Generation Sequencing. Food Chemistry, 2016, 192, 788-798.	8.2	47
142	Unique long non-coding RNA expression signature in ETV6/RUNX1-driven B-cell precursor acute lymphoblastic leukemia. Oncotarget, 2016, 7, 73769-73780.	1.8	30
143	Dynamic epigenetic changes to <i>VHL</i> occur with sunitinib in metastatic clear cell renal cancer. Oncotarget, 2016, 7, 25241-25250.	1.8	14
144	Unique Long Non-Coding RNA Expression Signature in ETV6/RUNX1-Driven B-Cell Precursor Acute Lymphoblastic Leukemia. Blood, 2016, 128, 3920-3920.	1.4	1

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145	Whole genome amplification with SurePlex results in better copy number alteration detection using sequencing data compared to the MALBAC method. Scientific Reports, 2015, 5, 11711.	3.3	42
146	Improved canine exome designs, featuring ncRNAs and increased coverage of protein coding genes. Scientific Reports, 2015, 5, 12810.	3.3	31
147	An heuristic filtering tool to identify phenotype-associated genetic variants applied to human intellectual disability and canine coat colors. BMC Bioinformatics, 2015, 16, 391.	2.6	3
148	Genome-wide transcription start site profiling in biofilm-grown Burkholderia cenocepacia J2315. BMC Genomics, 2015, 16, 775.	2.8	33
149	16S rRNA Amplicon Sequencing Demonstrates that Indoor-Reared Bumblebees (Bombus terrestris) Harbor a Core Subset of Bacteria Normally Associated with the Wild Host. PLoS ONE, 2015, 10, e0125152.	2.5	51
150	Genome Sequence of Devriesea agamarum, Isolated from Agamid Lizards with Dermatitis. Genome Announcements, 2015, 3, .	0.8	3
151	Effect of multiple allelic drop-outs in forensic RMNE calculations. Forensic Science International: Genetics, 2015, 19, 243-249.	3.1	4
152	Phospho-iTRAQ: Assessing Isobaric Labels for the Large-Scale Study Of Phosphopeptide Stoichiometry. Journal of Proteome Research, 2015, 14, 839-849.	3.7	15
153	Forensic massively parallel sequencing data analysis tool: Implementation of MyFLq as a standalone web- and Illumina BaseSpace®-application. Forensic Science International: Genetics, 2015, 15, 2-7.	3.1	27
154	OSC2 and CYP716A14v2 Catalyze the Biosynthesis of Triterpenoids for the Cuticle of Aerial Organs of <i>Artemisia annua</i> . Plant Cell, 2015, 27, 286-301.	6.6	96
155	Prevalence of Gender Nonconformity in Flanders, Belgium. Archives of Sexual Behavior, 2015, 44, 1281-1287.	1.9	138
156	Efficiency of Exome Sequencing for the Molecular Diagnosis of Pseudoxanthoma Elasticum. Journal of Investigative Dermatology, 2015, 135, 992-998.	0.7	25
157	Validation of a sensitive DNA walking strategy to characterise unauthorised GMOs using model food matrices mimicking common rice products. Food Chemistry, 2015, 173, 1259-1265.	8.2	31
158	Shallow whole genome sequencing is well suited for the detection of chromosomal aberrations in human blastocysts. Fertility and Sterility, 2015, 104, 1276-1285.e1.	1.0	40
159	Viral Small-RNA Analysis of Bombyx mori Larval Midgut during Persistent and Pathogenic Cytoplasmic Polyhedrosis Virus Infection. Journal of Virology, 2015, 89, 11473-11486.	3.4	47
160	Differential transcriptome analysis of the common shrimp Crangon crangon: Special focus on the nuclear receptors and RNAi-related genes. General and Comparative Endocrinology, 2015, 212, 163-177.	1.8	15
161	Challenges and opportunities in the investigation of unexplained intellectual disability using familyâ€based wholeâ€exome sequencing. Clinical Genetics, 2015, 88, 140-148.	2.0	25
162	Transcriptome Analysis of Bombyx mori Larval Midgut during Persistent and Pathogenic Cytoplasmic Polyhedrosis Virus Infection. PLoS ONE, 2015, 10, e0121447.	2.5	63

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163	A Doubling of Microphytobenthos Biomass Coincides with a Tenfold Increase in Denitrifier and Total Bacterial Abundances in Intertidal Sediments of a Temperate Estuary. PLoS ONE, 2015, 10, e0126583.	2.5	43
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