Vladimir Benes

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.

217
papers

29,998
citations

65
h-index

173
g-index

234
ext. papers

35,386
ext. citations

11.2
avg, IF

6.47
L-index

#	Paper	IF	Citations
217	Enrichment of gut microbiome strains for cultivation-free genome sequencing using droplet microfluidics.. *Cell Reports Methods*, **2022**, 2, None		2
216	gga-miRNOME, a microRNA-sequencing dataset from chick embryonic tissues.. *Scientific Data*, **2022** , 9, 29	8.2	0
215	Impact of high platelet turnover on the platelet transcriptome: Results from platelet RNA-sequencing in patients with sepsis.. *PLoS ONE*, **2022**, 17, e0260222	3.7	0
214	Chemical genetics in Silene latifolia elucidate regulatory pathways involved in gynoecium development.. *Journal of Experimental Botany*, **2022**,	7	1
213	Co-translational assembly orchestrates competing biogenesis pathways.. *Nature Communications*, **2022**, 13, 1224	17.4	2
212	A faecal microbiota signature with high specificity for pancreatic cancer.. *Gut*, **2022**,	19.2	5
211	Rewired glycosylation activity promotes scarless regeneration and functional recovery in spiny mice after complete spinal cord transection.. *Developmental Cell*, **2021**,	10.2	3
210	Single-cell proteo-genomic reference maps of the hematopoietic system enable the purification and massive profiling of precisely defined cell states. *Nature Immunology*, **2021**, 22, 1577-1589	19.1	14
209	Trophectoderm cell failure leads to peri-implantation lethality in Trpm7-deficient mouse embryos. *Cell Reports*, **2021**, 37, 109851	10.6	0
208	The expansion of human T-betCD21 B cells is T cell dependent. *Science Immunology*, **2021**, 6, eabh0891	28	11
207	FoxO1-GAB1 axis regulates homing capacity and tonic AKT activity in chronic lymphocytic leukemia. *Blood*, **2021**, 138, 758-772	2.2	3
206	Versatile workflow for cell type-resolved transcriptional and epigenetic profiles from cryopreserved human lung. *JCI Insight*, **2021**, 6,	9.9	2
205	Comprehensive microRNA and transcriptomic profiling of rheumatoid arthritis monocytes: role of microRNA-146b in pro-inflammatory progression. *Rheumatology*, **2021**, 60, 5424-5435	3.9	3
204	Genomic insights into the pathogenesis of Epstein-Barr virus-associated diffuse large B-cell lymphoma by whole-genome and targeted amplicon sequencing. *Blood Cancer Journal*, **2021**, 11, 102	7	6
203	AXL Inhibition in Macrophages Stimulates Host-versus-Leukemia Immunity and Eradicates Na�ve and Treatment-Resistant Leukemia. *Cancer Discovery*, **2021**, 11, 2924-2943	24.4	5
202	A novel method to identify Post-Aire stages of medullary thymic epithelial cell differentiation. *European Journal of Immunology*, **2021**, 51, 311-318	6.1	2
201	Single-cell transcriptomics reveals immune response of intestinal cell types to viral infection. *Molecular Systems Biology*, **2021**, 17, e9833	12.2	4

200	Web-based LinRegPCR: application for the visualization and analysis of (RT)-qPCR amplification and melting data. *BMC Bioinformatics*, **2021**, 22, 398	3.6	3
199	Metabolic cooperation and spatiotemporal niche partitioning in a kefir microbial community. *Nature Microbiology*, **2021**, 6, 196-208	26.6	44
198	Patient-derived gene and protein expression signatures of NGLY1 deficiency. *Journal of Biochemistry*, **2021**,	3.1	1
197	VISOR: a versatile haplotype-aware structural variant simulator for short- and long-read sequencing. *Bioinformatics*, **2020**, 36, 1267-1269	7.2	8
196	Toll-like receptor signaling in thymic epithelium controls monocyte-derived dendritic cell recruitment and Treg generation. *Nature Communications*, **2020**, 11, 2361	17.4	18
195	Tracy: basecalling, alignment, assembly and deconvolution of sanger chromatogram trace files. *BMC Genomics*, **2020**, 21, 230	4.5	19
194	Complex Evolution of Insect Insulin Receptors and Homologous Decoy Receptors, and Functional Significance of Their Multiplicity. *Molecular Biology and Evolution*, **2020**, 37, 1775-1789	8.3	30
193	Deciphering Patterns of Adaptation and Acclimation in the Transcriptome of Phaeocystis antarctica to Changing Iron Conditions. *Journal of Phycology*, **2020**, 56, 747-760	3	4
192	Global miRNA and mRNA expression profiles identify miRNA-26a-2-3p-dependent repression of IFN signature in systemic sclerosis human monocytes. *European Journal of Immunology*, **2020**, 50, 1057-1066	6.1	5
191	Heme oxygenase-1 deficiency triggers exhaustion of hematopoietic stem cells. *EMBO Reports*, **2020** , 21, e47895	6.5	14
190	A Mutation Upstream of the Ribosomal Operon Downregulates Bordetella pertussis Virulence Factor Production without Compromising Bacterial Survival within Human Macrophages. *MSystems*, **2020**, 5,	7.6	3
189	THU0053 CONTRIBUTION OF DEFECTIVE NON-APOPTOTIC FAS SIGNALING TO IMMUNE DYSREGULATION IN AUTOIMMUNE LYMPHOPROLIFERATIVE SYNDROME (ALPS). *Annals of the Rheumatic Diseases*, **2020**, 79, 238.3-238	2.4	
188	Single-cell transcriptomics identifies CD44 as a marker and regulator of endothelial to haematopoietic transition. *Nature Communications*, **2020**, 11, 586	17.4	33
187	gen. nov., sp. nov., an acidophilic actinobacterium, and proposal of the new actinobacterial family fam. nov. *International Journal of Systematic and Evolutionary Microbiology*, **2020**, 70, 5106-5114	2.2	1
186	Apoptotic Cell Exclusion and Bias-Free Single-Cell Selection Are Important Quality Control Requirements for Successful Single-Cell Sequencing Applications. *Cytometry Part A: the Journal of the International Society for Analytical Cytology*, **2020**, 97, 156-167	4.6	9
185	Single-cell analysis of structural variations and complex rearrangements with tri-channel processing. *Nature Biotechnology*, **2020**, 38, 343-354	44.5	17
184	Positive selection and convergent evolution shape molecular phenotypic traits of innate immunity receptors in tits (Paridae). *Molecular Ecology*, **2020**, 29, 3056-3070	5.7	1
183	Glycogen accumulation, central carbon metabolism, and aging of hematopoietic stem and progenitor cells. *Scientific Reports*, **2020**, 10, 11597	4.9	3

182	The Digital MIQE Guidelines Update: Minimum Information for Publication of Quantitative Digital PCR Experiments for 2020. *Clinical Chemistry*, **2020**, 66, 1012-1029	5.5	85
181	Long-read only assembly of Drechmeria coniospora genomes reveals widespread chromosome plasticity and illustrates the limitations of current nanopore methods. *GigaScience*, **2020**, 9,	7.6	4
180	Extensive 5Qsurveillance guards against non-canonical NAD-caps of nuclear mRNAs in yeast. *Nature Communications*, **2020**, 11, 5508	17.4	9
179	MorphoSeq: Full Single-Cell Transcriptome Dynamics Up to Gastrulation in a Chordate. *Cell*, **2020**, 181, 922-935.e21	56.2	24
178	Loss of N-Glycanase 1 Alters Transcriptional and Translational Regulation in K562 Cell Lines. *G3: Genes, Genomes, Genetics*, **2020**, 10, 1585-1597	3.2	5
177	Antibiotics-induced monodominance of a novel gut bacterial order. *Gut*, **2019**, 68, 1781-1790	19.2	33
176	Fluctuating Light Interacts with Time of Day and Leaf Development Stage to Reprogram Gene Expression. *Plant Physiology*, **2019**, 179, 1632-1657	6.6	36
175	Small-molecule-mediated chemical knock-down of MuRF1/MuRF2 and attenuation of diaphragm dysfunction in chronic heart failure. *Journal of Cachexia, Sarcopenia and Muscle*, **2019**, 10, 1102-1115	10.3	17
174	Aspirin impairs acetyl-coenzyme A metabolism in redox-compromised yeast cells. *Scientific Reports*, **2019**, 9, 6152	4.9	4
173	Mitochondrial protein-induced stress triggers a global adaptive transcriptional programme. *Nature Cell Biology*, **2019**, 21, 442-451	23.4	84
172	Aire-expressing ILC3-like cells in the lymph node display potent APC features. *Journal of Experimental Medicine*, **2019**, 216, 1027-1037	16.6	21
171	MicroRNA miR-34a downregulates FOXP1 during DNA damage response to limit BCR signalling in chronic lymphocytic leukaemia B cells. *Leukemia*, **2019**, 33, 403-414	10.7	30
170	MicroRNAs from saliva of anopheline mosquitoes mimic human endogenous miRNAs and may contribute to vector-host-pathogen interactions. *Scientific Reports*, **2019**, 9, 2955	4.9	13
169	Isolation of Open Chromatin Identifies Regulators of Systemic Acquired Resistance. *Plant Physiology*, **2019**, 181, 817-833	6.6	13
168	Alfred: interactive multi-sample BAM alignment statistics, feature counting and feature annotation for long- and short-read sequencing. *Bioinformatics*, **2019**, 35, 2489-2491	7.2	29
167	The molecular signature of AML with increased ALDH activity suggests a stem cell origin. *Leukemia and Lymphoma*, **2018**, 59, 2201-2210	1.9	9
166	Whole-Body Single-Cell Sequencing Reveals Transcriptional Domains in the Annelid Larval Body. *Molecular Biology and Evolution*, **2018**, 35, 1047-1062	8.3	29
165	RNA-Sequencing from Low-Input Material in Multiple Myeloma for Application in Clinical Routine. *Methods in Molecular Biology*, **2018**, 1792, 97-115	1.4	2

164	Unbiased classification of mosquito blood cells by single-cell genomics and high-content imaging. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, E7568-E7577	11.5	28
163	ToTem: a tool for variant calling pipeline optimization. *BMC Bioinformatics*, **2018**, 19, 243	3.6	1
162	Coordinated expression and genetic polymorphisms in Grainyhead-like genes in human non-melanoma skin cancers. *BMC Cancer*, **2018**, 18, 23	4.8	6
161	Signal transduction-dependent small regulatory RNA is involved in glutamate metabolism of the human pathogen. *Rna*, **2018**, 24, 1530-1541	5.8	9
160	The Response of Three Southern Ocean Phytoplankton Species to Ocean Acidification and Light Availability: A Transcriptomic Study. *Protist*, **2018**, 169, 958-975	2.5	13
159	Virome Analysis Reveals No Association of Head and Neck Vascular Anomalies with an Active Viral Infection. *In Vivo*, **2018**, 32, 1323-1331	2.3	
158	Domestic Fowl Breed Variation in Egg White Protein Expression: Application of Proteomics and Transcriptomics. *Journal of Agricultural and Food Chemistry*, **2018**, 66, 11854-11863	5.7	9
157	Single-cell transcriptomics reveals a new dynamical function of transcription factors during embryonic hematopoiesis. *ELife*, **2018**, 7,	8.9	21
156	Identification of a genetically defined ultra-high-risk group in relapsed pediatric T-lymphoblastic leukemia. *Blood Cancer Journal*, **2017**, 7, e523	7	54
155	Vitamin A-Retinoic Acid Signaling Regulates Hematopoietic Stem Cell Dormancy. *Cell*, **2017**, 169, 807-823.e19	36.2	200
154	Single-Virus Droplet Microfluidics for High-Throughput Screening of Neutralizing Epitopes on HIV Particles. *Cell Chemical Biology*, **2017**, 24, 751-757.e3	8.2	23
153	Potential protective role of Grainyhead-like genes in the development of clear cell renal cell carcinoma. *Molecular Carcinogenesis*, **2017**, 56, 2414-2423	5	6
152	Thymic epithelial cells require p53 to support their long-term function in thymopoiesis in mice. *Blood*, **2017**, 130, 478-488	2.2	19
151	Genotypes of SLC22A4 and SLC22A5 regulatory loci are predictive of the response of chronic myeloid leukemia patients to imatinib treatment. *Journal of Experimental and Clinical Cancer Research*, **2017**, 36, 55	12.8	11
150	Distribution, Community Composition, and Potential Metabolic Activity of Bacterioplankton in an Urbanized Mediterranean Sea Coastal Zone. *Applied and Environmental Microbiology*, **2017**, 83,	4.8	24
149	Characterization of Two Historic Smallpox Specimens from a Czech Museum. *Viruses*, **2017**, 9,	6.2	18
148	Genetic code expansion for multiprotein complex engineering. *Nature Methods*, **2016**, 13, 997-1000	21.6	48
147	Highly recurrent mutations of SGK1, DUSP2 and JUNB in nodular lymphocyte predominant Hodgkin lymphoma. *Leukemia*, **2016**, 30, 844-53	10.7	48

146	The Slicer Activity of ARGONAUTE1 Is Required Specifically for the Phasing, Not Production, of Trans-Acting Short Interfering RNAs in Arabidopsis. *Plant Cell*, **2016**, 28, 1563-80	11.6	50
145	Asymptomatic Multiple Myeloma - Background of Progression, Evolution, and Prognosis. *Blood*, **2016**, 128, 235-235	2.2	3
144	Identification of an Ultra High-Risk and Targetable Molecular Signature in Relapsed Pediatric T-ALL. *Blood*, **2016**, 128, 1084-1084	2.2	
143	Transition out of HSC Dormancy By a Continuous Upregulation of Metabolism Is Controlled Via Dietary Vitamin A/ Retinoic Acid Signaling. *Blood*, **2016**, 128, LBA-4-LBA-4	2.2	1
142	Durable coexistence of donor and recipient strains after fecal microbiota transplantation. *Science*, **2016**, 352, 586-9	33.3	326
141	The differential expression of alternatively polyadenylated transcripts is a common stress-induced response mechanism that modulates mammalian mRNA expression in a quantitative and qualitative fashion. *Rna*, **2016**, 22, 1441-53	5.8	26
140	Identification of cytokine-induced modulation of microRNA expression and secretion as measured by a novel microRNA specific qPCR assay. *Scientific Reports*, **2015**, 5, 11590	4.9	42
139	Intracellular microRNA profiles form in the Xenopus laevis oocyte that may contribute to asymmetric cell division. *Scientific Reports*, **2015**, 5, 11157	4.9	6
138	Replicative senescence is associated with nuclear reorganization and with DNA methylation at specific transcription factor binding sites. *Clinical Epigenetics*, **2015**, 7, 19	7.7	42
137	RNA splicing regulated by RBFOX1 is essential for cardiac function in zebrafish. *Journal of Cell Science*, **2015**, 128, 3030-40	5.3	12
136	RDML-Ninja and RDMLdb for standardized exchange of qPCR data. *BMC Bioinformatics*, **2015**, 16, 197	3.6	9
135	Pediatric T-cell lymphoblastic leukemia evolves into relapse by clonal selection, acquisition of mutations and promoter hypomethylation. *Haematologica*, **2015**, 100, 1442-50	6.6	50
134	Lymphocyte gene expression signatures from patients and mouse models of hereditary hemochromatosis reveal a function of HFE as a negative regulator of CD8+ T-lymphocyte activation and differentiation in vivo. *PLoS ONE*, **2015**, 10, e0124246	3.7	17
133	Consequences of the loss of the Grainyhead-like 1 gene for renal gene expression, regulation of blood pressure and heart rate in a mouse model. *Acta Biochimica Polonica*, **2015**, 62, 287-96	2	5
132	Early transcriptional events linked to induction of diapause revealed by RNAseq in larvae of drosophilid fly, Chymomyza costata. *BMC Genomics*, **2015**, 16, 720	4.5	60
131	miRNAs in multiple myeloma--a survival relevant complex regulator of gene expression. *Oncotarget* , **2015**, 6, 39165-83	3.3	37
130	Identification of novel sequence variations in microRNAs in chronic lymphocytic leukemia. *Carcinogenesis*, **2014**, 35, 992-1002	4.6	15
129	Sequencing of a patient with balanced chromosome abnormalities and neurodevelopmental disease identifies disruption of multiple high risk loci by structural variation. *PLoS ONE*, **2014**, 9, e90894	3.7	17

128	Potential of fecal microbiota for early-stage detection of colorectal cancer. *Molecular Systems Biology*, **2014**, 10, 766	12.2	575
127	Dynamic DNA methylation orchestrates cardiomyocyte development, maturation and disease. *Nature Communications*, **2014**, 5, 5288	17.4	202
126	Alternative polyadenylation diversifies post-transcriptional regulation by selective RNA-protein interactions. *Molecular Systems Biology*, **2014**, 10, 719	12.2	64
125	SUMOylation regulates the chromatin occupancy and anti-proliferative gene programs of glucocorticoid receptor. *Nucleic Acids Research*, **2014**, 42, 1575-92	20.1	62
124	Disruption of EXOC6B in a patient with developmental delay, epilepsy, and a de novo balanced t(2;8) translocation. *European Journal of Human Genetics*, **2013**, 21, 1177-80	5.3	14
123	Primate genome architecture influences structural variation mechanisms and functional consequences. *Proceedings of the National Academy of Sciences of the United States of America*, **2013**, 110, 15764-9	11.5	69
122	The need for transparency and good practices in the qPCR literature. *Nature Methods*, **2013**, 10, 1063-7	21.6	197
121	Accounting for technical noise in single-cell RNA-seq experiments. *Nature Methods*, **2013**, 10, 1093-5	21.6	659
120	Integrative genomic analyses reveal an androgen-driven somatic alteration landscape in early-onset prostate cancer. *Cancer Cell*, **2013**, 23, 159-70	24.3	259
119	The digital MIQE guidelines: Minimum Information for Publication of Quantitative Digital PCR Experiments. *Clinical Chemistry*, **2013**, 59, 892-902	5.5	554
118	Multiple epigenetic mechanisms and the piRNA pathway enforce LINE1 silencing during adult spermatogenesis. *Molecular Cell*, **2013**, 50, 601-8	17.6	134
117	An efficient method for genome-wide polyadenylation site mapping and RNA quantification. *Nucleic Acids Research*, **2013**, 41, e65	20.1	81
116	Actin-binding protein regulation by microRNAs as a novel microbial strategy to modulate phagocytosis by host cells: the case of N-Wasp and miR-142-3p. *Frontiers in Cellular and Infection Microbiology*, **2013**, 3, 19	5.9	56
115	Expression Profiling of MicroRNAs by Quantitative Real-Time PCR **2013**, 307-322		3
114	CBF▯MYH11 Hypomethylation Signature In Patients With Acute Myeloid Leukaemia. *Blood*, **2013**, 122, 3774-3774	2.2	
113	Direct regulation of microRNA biogenesis and expression by estrogen receptor beta in hormone-responsive breast cancer. *Oncogene*, **2012**, 31, 4196-206	9.2	84
112	A role for Fkbp6 and the chaperone machinery in piRNA amplification and transposon silencing. *Molecular Cell*, **2012**, 47, 970-9	17.6	97
111	DELLY: structural variant discovery by integrated paired-end and split-read analysis. *Bioinformatics*, **2012**, 28, i333-i339	7.2	1069

110	Genomics of DNA cytosine methylation in Escherichia coli reveals its role in stationary phase transcription. *Nature Communications*, **2012**, 3, 886	17.4	87
109	Genome sequencing of pediatric medulloblastoma links catastrophic DNA rearrangements with TP53 mutations. *Cell*, **2012**, 148, 59-71	56.2	600
108	Df31 protein and snoRNAs maintain accessible higher-order structures of chromatin. *Molecular Cell*, **2012**, 48, 434-44	17.6	88
107	RNA-sequencing as useful screening tool in the combat against the misuse of anabolic agents. *Analytical Chemistry*, **2012**, 84, 6863-8	7.8	17
106	Hfe deficiency impairs pulmonary neutrophil recruitment in response to inflammation. *PLoS ONE*, **2012**, 7, e39363	3.7	13
105	Dissecting the genomic complexity underlying medulloblastoma. *Nature*, **2012**, 488, 100-5	50.4	623
104	Genome-wide RNAi screening identifies human proteins with a regulatory function in the early secretory pathway. *Nature Cell Biology*, **2012**, 14, 764-74	23.4	141
103	HnRNP L and L-like cooperate in multiple-exon regulation of CD45 alternative splicing. *Nucleic Acids Research*, **2012**, 40, 5666-78	20.1	36
102	Role of CXCL13 in asthma: novel therapeutic target. *Chest*, **2012**, 141, 886-894	5.3	19
101	Sequence Variations in miRNA Genes Are Common and May Affect Their Expression in Patients with Chronic Lymphocytic Leukemia. *Blood*, **2012**, 120, 3895-3895	2.2	
100	Iron regulatory protein-1 and -2: transcriptome-wide definition of binding mRNAs and shaping of the cellular proteome by iron regulatory proteins. *Blood*, **2011**, 118, e168-79	2.2	84
99	RNA-Seq analysis in mutant zebrafish reveals role of U1C protein in alternative splicing regulation. *EMBO Journal*, **2011**, 30, 1965-76	13	34
98	Global analysis of estrogen receptor beta binding to breast cancer cell genome reveals an extensive interplay with estrogen receptor alpha for target gene regulation. *BMC Genomics*, **2011**, 12, 36	4.5	127
97	Exome sequencing identifies MRPL3 mutation in mitochondrial cardiomyopathy. *Human Mutation*, **2011**, 32, 1225-31	4.7	110
96	Direct and indirect effects of H-NS and Fis on global gene expression control in Escherichia coli. *Nucleic Acids Research*, **2011**, 39, 2073-91	20.1	196
95	Primer sequence disclosure: a clarification of the MIQE guidelines. *Clinical Chemistry*, **2011**, 57, 919-21	5.5	52
94	Differentially expressed genes associated with human limbal epithelial phenotypes: new molecules that potentially facilitate selection of stem cell-enriched populations **2011**, 52, 1252-60		22
93	Nuclear hormone 1,25-dihydroxyvitamin D3 elicits a genome-wide shift in the locations of VDR chromatin occupancy. *Nucleic Acids Research*, **2011**, 39, 9181-93	20.1	172

92	Kaposi@ sarcoma herpesvirus microRNAs target caspase 3 and regulate apoptosis. *PLoS Pathogens*, **2011**, 7, e1002405	7.6	92
91	The liver-specific microRNA miR-122 controls systemic iron homeostasis in mice. *Journal of Clinical Investigation*, **2011**, 121, 1386-96	15.9	176
90	Prognostication by miRNome-Profiling in Multiple Myeloma. *Blood*, **2011**, 118, 1822-1822	2.2	
89	Mutational Analysis of Mir-29 Family Members in Chronic Lymphocytic Leukemia. *Blood*, **2011**, 118, 1770-1770	2.2	
88	Thyrotroph embryonic factor regulates light-induced transcription of repair genes in zebrafish embryonic cells. *PLoS ONE*, **2010**, 5, e12542	3.7	44
87	CRX ChIP-seq reveals the cis-regulatory architecture of mouse photoreceptors. *Genome Research*, **2010**, 20, 1512-25	9.7	145
86	Expression profiling of microRNA using real-time quantitative PCR, how to use it and what is available. *Methods*, **2010**, 50, 244-9	4.6	271
85	Widespread estrogen-dependent repression of micrornas involved in breast tumor cell growth. *Cancer Research*, **2009**, 69, 8332-40	10.1	200
84	RNA degradation compromises the reliability of microRNA expression profiling. *BMC Biotechnology*, **2009**, 9, 102	3.5	79
83	The MIQE guidelines: minimum information for publication of quantitative real-time PCR experiments. *Clinical Chemistry*, **2009**, 55, 611-22	5.5	9710
82	Unreliable real-time PCR analysis of human endogenous retrovirus-W (HERV-W) RNA expression and DNA copy number in multiple sclerosis. *AIDS Research and Human Retroviruses*, **2009**, 25, 377-8; author reply 379-81	1.6	29
81	Importin 8 is a gene silencing factor that targets argonaute proteins to distinct mRNAs. *Cell*, **2009**, 136, 496-507	56.2	262
80	Aging and replicative senescence have related effects on human stem and progenitor cells. *PLoS ONE*, **2009**, 4, e5846	3.7	347
79	MicroRNA signatures predict oestrogen receptor, progesterone receptor and HER2/neu receptor status in breast cancer. *Breast Cancer Research*, **2009**, 11, R27	8.3	332
78	Inhibition of aurora kinases for tailored risk-adapted treatment of multiple myeloma. *Blood*, **2009**, 113, 4331-40	2.2	85
77	Inhibition of HIF1A Signaling by a Novel Class of Sulfonanilides for Targeted Treatment of Multiple Myeloma.. *Blood*, **2009**, 114, 2856-2856	2.2	2
76	How to Assay microRNA Expression A Technology Guide **2009**, 215-240		1
75	An assessment of air as a source of DNA contamination encountered when performing PCR. *Journal of Biomolecular Techniques*, **2009**, 20, 236-40	1.1	21

74	Cyclical DNA methylation of a transcriptionally active promoter. *Nature*, **2008**, 452, 45-50	50.4	757
73	Transient cyclical methylation of promoter DNA. *Nature*, **2008**, 452, 112-5	50.4	540
72	miChip: an array-based method for microRNA expression profiling using locked nucleic acid capture probes. *Nature Protocols*, **2008**, 3, 321-9	18.8	110
71	Transcriptome profiling of estrogen-regulated genes in human primary osteoblasts reveals an osteoblast-specific regulation of the insulin-like growth factor binding protein 4 gene. *Molecular Endocrinology*, **2008**, 22, 361-79		20
70	Replicative senescence of mesenchymal stem cells: a continuous and organized process. *PLoS ONE*, **2008**, 3, e2213	3.7	795
69	Diverse roles of hnRNP L in mammalian mRNA processing: a combined microarray and RNAi analysis. *Rna*, **2008**, 14, 284-96	5.8	116
68	Inhibition of Aurora-Kinases for Tailored Risk-Adapted Treatment of Multiple Myeloma. *Blood*, **2008** , 112, 248-248	2.2	
67	Adhesion of hematopoietic progenitor cells to human mesenchymal stem cells as a model for cell-cell interaction. *Experimental Hematology*, **2007**, 35, 314-25	3.1	108
66	Pax-Six-Eya-Dach network during amphioxus development: conservation in vitro but context specificity in vivo. *Developmental Biology*, **2007**, 306, 143-59	3.1	137
65	miChip: a microarray platform for expression profiling of microRNAs based on locked nucleic acid (LNA) oligonucleotide capture probes. *Methods*, **2007**, 43, 146-52	4.6	60
64	Modular proteins from the Drosophila sallimus (sls) gene and their expression in muscles with different extensibility. *Journal of Molecular Biology*, **2007**, 367, 953-69	6.5	71
63	Life cycle transcriptome of the malaria mosquito Anopheles gambiae and comparison with the fruitfly Drosophila melanogaster. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 11304-9	11.5	59
62	The molecular elasticity of the insect flight muscle proteins projectin and kettin. *Proceedings of the National Academy of Sciences of the United States of America*, **2006**, 103, 4451-6	11.5	79
61	A sensitive array for microRNA expression profiling (miChip) based on locked nucleic acids (LNA). *Rna*, **2006**, 12, 913-20	5.8	343
60	Adhesion of Hematopoietic Progenitor Cells to Human Mesenchymal Stromal Cells as a Model for Interaction between Stem Cells and Their Niche.. *Blood*, **2006**, 108, 1399-1399	2.2	1
59	Vertebrate-type intron-rich genes in the marine annelid Platynereis dumerilii. *Science*, **2005**, 310, 1325-6	33.3	198
58	Quantitative real-time RT-PCR--a perspective. *Journal of Molecular Endocrinology*, **2005**, 34, 597-601	4.5	897
57	Multiple mechanisms induce transcriptional silencing of a subset of genes, including oestrogen receptor alpha, in response to deacetylase inhibition by valproic acid and trichostatin A. *Oncogene*, **2005**, 24, 4894-907	9.2	141

56	Alternative splicing microarrays reveal functional expression of neuron-specific regulators in Hodgkin lymphoma cells. *Journal of Biological Chemistry*, **2005**, 280, 4779-84	5.4	70
55	Targeted mutagenesis of the murine IRP1 and IRP2 genes reveals context-dependent RNA processing differences in vivo. *Rna*, **2004**, 10, 1019-25	5.8	41
54	Diversity of vertebrate splicing factor U2AF35: identification of alternatively spliced U2AF1 mRNAS. *Journal of Biological Chemistry*, **2004**, 279, 27039-49	5.4	42
53	Developmentally regulated switching of titin size alters myofibrillar stiffness in the perinatal heart. *Circulation Research*, **2004**, 94, 967-75	15.7	147
52	Transcriptional complexes engaged by apo-estrogen receptor-alpha isoforms have divergent outcomes. *EMBO Journal*, **2004**, 23, 3653-66	13	92
51	Microcontact printing of DNA molecules. *Analytical Chemistry*, **2004**, 76, 1641-7	7.8	192
50	Characterization of an Escherichia coli elaC deletion mutant. *Biochemical and Biophysical Research Communications*, **2004**, 320, 1365-73	3.4	26
49	Standardization of protocols in cDNA microarray analysis. *Drug Discovery Today*, **2004**, 9, S26-31	8.8	
48	Oculomotor nerve schwannoma. *British Journal of Neurosurgery*, **2003**, 17, 168-173	1	23
47	Standardization of protocols in cDNA microarray analysis. *Trends in Biochemical Sciences*, **2003**, 28, 244-9	10.3	46
46	Cloning and developmental expression of amphioxus Dachschund. *Gene Expression Patterns*, **2003**, 3, 65-9	1.5	16
45	Engineering the mouse genome with bacterial artificial chromosomes to create multipurpose alleles. *Nature Biotechnology*, **2003**, 21, 443-7	44.5	118
44	Surgical correction of symptomatic vertebral artery kinking. *British Journal of Neurosurgery*, **2003**, 17, 174-8	1	4
43	The genome sequence of the malaria mosquito Anopheles gambiae. *Science*, **2002**, 298, 129-49	33.3	1622
42	A genomic switch at the transition from cell proliferation to terminal differentiation in the Drosophila eye. *Developmental Cell*, **2002**, 3, 511-21	10.2	63
41	Functional equivalency of amphioxus and vertebrate Pax258 transcription factors suggests that the activation of mid-hindbrain specific genes in vertebrates occurs via the recruitment of Pax regulatory elements. *Gene*, **2002**, 282, 143-50	3.8	23
40	The genomic response of the Drosophila embryo to JNK signaling. *Developmental Cell*, **2001**, 1, 579-86	10.2	95
39	Sequence and analysis of chromosome 3 of the plant Arabidopsis thaliana. *Nature*, **2000**, 408, 820-2	50.4	153

38	An estimate of large-scale sequencing accuracy. *EMBO Reports*, **2000**, 1, 29-31	6.5	17
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11	Analysis of microribonucleic acid expression by quantitative real-time polymerase chain reaction80-87		
10	DNA damage independent inhibition of NF-B transcription by anthracyclines		1
9	Single-cell transcriptomics reveals immune response of intestinal cell types to viral infection		4
8	McQ An open-source multiplexed SARS-CoV-2 quantification platform		2
7	Local emergence and decline of a SARS-CoV-2 variant with mutations L452R and N501Y in the spike protein		6
6	Patient-derived gene and protein expression signatures of NGLY1 deficiency		1
5	Co-translational assembly counteracts promiscuous interactions		1
4	Identification of developmentally important genes inSilene latifoliathrough chemical genetics and transcriptome profiling		1
3	Identification of LINE retrotransposons and long non-coding RNAs expressed in the octopus brain		1

2	Single-cell proteo-genomic reference maps of the hematopoietic system enable the purification and massive profiling of precisely defined cell states	2
1	Expanded FLP toolbox for spatiotemporal protein degradation and transcriptomic profiling in C. elegans	2