Roland Eils

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/2410917/publications.pdf

Version: 2024-02-01

429 papers	59,531 citations	2427 97 h-index	1385 222 g-index
475 all docs	475 docs citations	475 times ranked	88227 citing authors

#	Article	IF	Citations
1	Differentially methylated regions within lung cancer risk loci are enriched in deregulated enhancers. Epigenetics, 2022, 17, 117-132.	2.7	2
2	Pre-activated antiviral innate immunity in the upper airways controls early SARS-CoV-2 infection in children. Nature Biotechnology, 2022, 40, 319-324.	17.5	229
3	Neural network-based integration of polygenic and clinical information: development and validation of a prediction model for 10-year risk of major adverse cardiac events in the UK Biobank cohort. The Lancet Digital Health, 2022, 4, e84-e94.	12.3	21
4	Complement activation induces excessive T cell cytotoxicity in severe COVID-19. Cell, 2022, 185, 493-512.e25.	28.9	122
5	Age-Related Differences in Structure and Function of Nasal Epithelial Cultures From Healthy Children and Elderly People. Frontiers in Immunology, 2022, 13, 822437.	4.8	5
6	SSAM-lite: A Light-Weight Web App for Rapid Analysis of Spatially Resolved Transcriptomics Data. Frontiers in Genetics, 2022, 13, 785877.	2.3	2
7	Temporal control of the integrated stress response by a stochastic molecular switch. Science Advances, 2022, 8, eabk2022.	10.3	13
8	A targetable â€˜rogueâ€™ neutrophil-subset, [CD11b+DEspR+] immunotype, is associated with severity and mortality in acute respiratory distress syndrome (ARDS) and COVID-19-ARDS. Scientific Reports, 2022, 12, 5583.	3.3	9
9	The genomic and transcriptional landscape of primary central nervous system lymphoma. Nature Communications, 2022, 13, 2558.	12.8	52
10	Analysis of mutational signatures with yet another package for signature analysis. Genes Chromosomes and Cancer, 2021, 60, 314-331.	2.8	40
11	Olfactory transmucosal SARS-CoV-2 invasion as a port of central nervous system entry in individuals with COVID-19. Nature Neuroscience, 2021, 24, 168-175.	14.8	991
12	Optogenetic control of Neisseria meningitidis Cas9 genome editing using an engineered, light-switchable anti-CRISPR protein. Nucleic Acids Research, 2021, 49, e29-e29.	14.5	25
13	Hypertension delays viral clearance and exacerbates airway hyperinflammation in patients with COVID-19. Nature Biotechnology, 2021, 39, 705-716.	17.5	129
14	Identifying multimodal signatures underlying the somatic comorbidity of psychosis: the COMMITMENT roadmap. Molecular Psychiatry, 2021, 26, 722-724.	7.9	7
15	Putative second hit rare genetic variants in families with seemingly GBA-associated Parkinsonâ€™s disease. Npj Genomic Medicine, 2021, 6, 2.	3.8	11
16	Memory-like HCV-specific CD8+ T cells retain a molecular scar after cure of chronic HCV infection. Nature Immunology, 2021, 22, 229-239.	14.5	95
17	Single-Nucleus and In Situ RNAâ€“Sequencing Reveal Cell Topographies in the Human Pancreas. Gastroenterology, 2021, 160, 1330-1344.e11.	1.3	112
18	Functional States in Tumor-Initiating Cell Differentiation in Human Colorectal Cancer. Cancers, 2021, 13, 1097.	3.7	11

#	Article	IF	Citations
19	Hyperinflammation as underlying mechanism predisposing patients with cardiovascular diseases for severe COVID-19. European Heart Journal, 2021, 42, 1720-1721.	2.2	8
20	Gene Expression in Solitary Fibrous Tumors (SFTs) Correlates with Anatomic Localization and NAB2-STAT6 Gene Fusion Variants. American Journal of Pathology, 2021, 191, 602-617.	3.8	30
21	Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes. Cell, 2021, 184, 2239-2254.e39.	28.9	260
22	Integrative Ranking of Enhancer Networks Facilitates the Discovery of Epigenetic Markers in Cancer. Frontiers in Genetics, 2021, 12, 664654.	2.3	0
23	A method for the rational selection of drug repurposing candidates from multimodal knowledge harmonization. Scientific Reports, 2021, 11, 11049.	3.3	12
24	Knowledge bases and software support for variant interpretation in precision oncology. Briefings in Bioinformatics, 2021, 22, .	6.5	9
25	Mutational mechanisms shaping the coding and noncoding genome of germinal center derived B-cell lymphomas. Leukemia, 2021, 35, 2002-2016.	7.2	34
26	Cell segmentation-free inference of cell types from in situ transcriptomics data. Nature Communications, 2021, 12, 3545.	12.8	52
27	SARS-CoV-2-mediated dysregulation of metabolism and autophagy uncovers host-targeting antivirals. Nature Communications, 2021, 12, 3818.	12.8	172
28	Lipomatous Solitary Fibrous Tumors Harbor Rare NAB2-STAT6 Fusion Variants and Show Up-Regulation of the Gene PPARG, Encoding for a Regulator of Adipocyte Differentiation. American Journal of Pathology, 2021, 191, 1314-1324.	3.8	5
29	The DNA methylation landscape of multiple myeloma shows extensive inter- and intrapatient heterogeneity that fuels transcriptomic variability. Genome Medicine, 2021, 13, 127.	8.2	9
30	Virus-induced senescence is a driver and therapeutic target in COVID-19. Nature, 2021, 599, 283-289.	27.8	195
31	Single-cell analysis of patient-derived PDAC organoids reveals cell state heterogeneity and a conserved developmental hierarchy. Nature Communications, 2021, 12, 5826.	12.8	59
32	SARS-CoV-2 infection triggers profibrotic macrophage responses and lung fibrosis. Cell, 2021, 184, 6243-6261.e27.	28.9	277
33	An Engineering Approach Towards Multi-site Virtual Molecular Tumor Board Software. Communications in Computer and Information Science, 2021, , 156-170.	0.5	1
34	Genetic Interactions and Tissue Specificity Modulate the Association of Mutations with Drug Response. Molecular Cancer Therapeutics, 2020, 19, 927-936.	4.1	5
35	Framework for quality assessment of whole genome cancer sequences. Nature Communications, 2020, 11, 5040.	12.8	5
36	Nuclear NR4A2 (Nurr1) Immunostaining is a Novel Marker for Acinic Cell Carcinoma of the Salivary Glands Lacking the Classic NR4A3 (NOR-1) Upregulation. American Journal of Surgical Pathology, 2020, 44, 1290-1292.	3.7	22

#	Article	IF	Citations
37	Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. Nature Communications, 2020, 11, 4748.	12.8	27
38	Glioblastoma epigenome profiling identifies SOX10 as a master regulator of molecular tumour subtype. Nature Communications, 2020, 11, 6434.	12.8	48
39	Gene set inference from single-cell sequencing data using a hybrid of matrix factorization and variational autoencoders. Nature Machine Intelligence, 2020, 2, 800-809.	16.0	5
40	Automated 3D light-sheet screening with high spatiotemporal resolution reveals mitotic phenotypes. Journal of Cell Science, 2020, 133, .	2.0	21
41	Integrative Analysis of Multi-omics Data Identified EGFR and PTGS2 as Key Nodes in a Gene Regulatory Network Related to Immune Phenotypes in Head and Neck Cancer. Clinical Cancer Research, 2020, 26, 3616-3628.	7.0	31
42	COVID-19 severity correlates with airway epitheliumâ€“immune cell interactions identified by single-cell analysis. Nature Biotechnology, 2020, 38, 970-979.	17.5	887
43	NOTCH target gene HES5 mediates oncogenic and tumor suppressive functions in hepatocarcinogenesis. Oncogene, 2020, 39, 3128-3144.	5.9	28
44	Genomic footprints of activated telomere maintenance mechanisms in cancer. Nature Communications, 2020, 11, 733.	12.8	87
45	The landscape of viral associations in human cancers. Nature Genetics, 2020, 52, 320-330.	21.4	261
46	Coupling Cas9 to artificial inhibitory domains enhances CRISPR-Cas9 target specificity. Science Advances, 2020, 6, eaay0187.	10.3	45
47	Computational design of anti-CRISPR proteins with improved inhibition potency. Nature Chemical Biology, 2020, 16, 725-730.	8.0	14
48	Whole-genome fingerprint of the DNA methylome during chemically induced differentiation of the human AML cell line HL-60/S4. Biology Open, 2020, 9, .	1.2	3
49	<scp>SARS</scp> â€CoVâ€2 receptor <scp>ACE</scp> 2 and <scp>TMPRSS</scp> 2 are primarily expressed in bronchial transient secretory cells. EMBO Journal, 2020, 39, e105114.	7.8	812
50	Follicular T helper cells shape the HCV-specific CD4+ T cell repertoire after virus elimination. Journal of Clinical Investigation, 2020, 130, 998-1009.	8.2	39
51	Transcriptome profiling reveals Silibinin dose-dependent response network in non-small lung cancer cells. PeerJ, 2020, 8, e10373.	2.0	6
52	ShinyButchR: Interactive NMF-based decomposition workflow of genome-scale datasets. Biology Methods and Protocols, 2020, 5, bpaa022.	2.2	11
53	Membership Inference Against DNA Methylation Databases. , 2020, , .		4
54	NK cells switch from granzyme B to death receptorâ€“mediated cytotoxicity during serial killing. Journal of Experimental Medicine, 2019, 216, 2113-2127.	8.5	210

#	Article	IF	Citations
55	Pheno-seq â€“ linking visual features and gene expression in 3D cell culture systems. Scientific Reports, 2019, 9, 12367.	3.3	16
56	Segregation and potential functional impact of a rare stop-gain PABPC4L variant in familial atypical Parkinsonism. Scientific Reports, 2019, 9, 13576.	3.3	3
57	Enhancer hijacking activates oncogenic transcription factor NR4A3 in acinic cell carcinomas of the salivary glands. Nature Communications, 2019, 10, 368.	12.8	153
58	Deconvolution of single-cell multi-omics layers reveals regulatory heterogeneity. Nature Communications, 2019, 10, 470.	12.8	156
59	TGFÎ²-induced cytoskeletal remodeling mediates elevation of cell stiffness and invasiveness in NSCLC. Scientific Reports, 2019, 9, 7667.	3.3	25
60	Impact of cancer mutational signatures on transcription factor motifs in the human genome. BMC Medical Genomics, 2019, 12, 64.	1.5	11
61	Somatic mutations and promotor methylation of the ryanodine receptor 2 is a common event in the pathogenesis of head and neck cancer. International Journal of Cancer, 2019, 145, 3299-3310.	5.1	34
62	Mutational patterns and regulatory networks in epigenetic subgroups of meningioma. Acta Neuropathologica, 2019, 138, 295-308.	7.7	74
63	Leveraging implicit knowledge in neural networks for functional dissection and engineering of proteins. Nature Machine Intelligence, 2019, 1, 225-235.	16.0	18
64	Longitudinal trends of serum IgE and IL5RA expression throughout childhood are associated with asthma but not with persistent wheeze. Allergy: European Journal of Allergy and Clinical Immunology, 2019, 74, 2002-2006.	5.7	3
65	Cell-specific CRISPRâ€“Cas9 activation by microRNA-dependent expression of anti-CRISPR proteins. Nucleic Acids Research, 2019, 47, e75-e75.	14.5	79
66	Response to olaparib in a PALB2 germline mutated prostate cancer and genetic events associated with resistance. Journal of Physical Education and Sports Management, 2019, 5, a003657.	1.2	36
67	Defective homologous recombination DNA repair as therapeutic target in advanced chordoma. Nature Communications, 2019, 10, 1635.	12.8	64
68	Genomic and transcriptomic changes complement each other in the pathogenesis of sporadic Burkitt lymphoma. Nature Communications, 2019, 10, 1459.	12.8	99
69	Nuclear NR4A3 Immunostaining Is a Specific and Sensitive Novel Marker for Acinic Cell Carcinoma of the Salivary Glands. American Journal of Surgical Pathology, 2019, 43, 1264-1272.	3.7	94
70	Comprehensive Analysis of Chromatin States in Atypical Teratoid/Rhabdoid Tumor Identifies Diverging Roles for SWI/SNF and Polycomb in Gene Regulation. Cancer Cell, 2019, 35, 95-110.e8.	16.8	65
71	Abstract 2723: Defective homologous recombination DNA repair as therapeutic target in advanced chordoma. , 2019, , .		0
72	The landscape of genomic alterations across childhood cancers. Nature, 2018, 555, 321-327.	27.8	1,068

#	Article	IF	Citations
73	BioModels: expanding horizons to include more modelling approaches and formats. Nucleic Acids Research, 2018, 46, D1248-D1253.	14.5	80
74	Cutis laxa, exocrine pancreatic insufficiency and altered cellular metabolomics as additional symptoms in a new patient with ATP6AP1-CDG. Molecular Genetics and Metabolism, 2018, 123, 364-374.	1.1	23
75	Integrative genomic and transcriptomic analysis of leiomyosarcoma. Nature Communications, 2018, 9, 144.	12.8	197
76	MEST mediates the impact of prenatal bisphenol A exposure on long-term body weight development. Clinical Epigenetics, 2018, 10, 58.	4.1	72
77	Maternal phthalate exposure promotes allergic airway inflammation over 2 generations through epigenetic modifications. Journal of Allergy and Clinical Immunology, 2018, 141, 741-753.	2.9	92
78	Tagmentation-Based Library Preparation for Low DNA Input Whole Genome Bisulfite Sequencing. Methods in Molecular Biology, 2018, 1708, 105-122.	0.9	10
79	Early-onset childhood atopic dermatitis is related to NLRP2 repression. Journal of Allergy and Clinical Immunology, 2018, 141, 1482-1485.e16.	2.9	21
80	Pancreatic Ductal Adenocarcinoma Subtyping Using the Biomarkers Hepatocyte Nuclear Factor-1A and Cytokeratin-81 Correlates with Outcome and Treatment Response. Clinical Cancer Research, 2018, 24, 351-359.	7.0	81
81	Whole genome sequencing puts forward hypotheses on metastasis evolution and therapy in colorectal cancer. Nature Communications, 2018, 9, 4782.	12.8	103
82	Web-based design and analysis tools for CRISPR base editing. BMC Bioinformatics, 2018, 19, 542.	2.6	127
83	Molecular Evolution of Early-Onset Prostate Cancer Identifies Molecular Risk Markers and Clinical Trajectories. Cancer Cell, 2018, 34, 996-1011.e8.	16.8	190
84	Single-Fluorescent Protein Reporters Allow Parallel Quantification of Natural Killer Cell-Mediated Granzyme and Caspase Activities in Single Target Cells. Frontiers in Immunology, 2018, 9, 1840.	4.8	15
85	Engineered anti-CRISPR proteins for optogenetic control of CRISPRâ€“Cas9. Nature Methods, 2018, 15, 924-927.	19.0	161
86	Evaluating local features in high-resolution 3D-PLI data. , 2018, , .		0
87	Scale-bundle spline-based non-rigid registration for handling fissures. , 2018, , .		0
88	Controlling Cells with Light and LOV. Advanced Biology, 2018, 2, 1800098.	3.0	19
89	The transcriptomic and epigenetic map of vascular quiescence in the continuous lung endothelium. ELife, 2018, 7, .	6.0	43
90	HiGHmed â€“ An Open Platform Approach to Enhance Care and Research across Institutional Boundaries. Methods of Information in Medicine, 2018, 57, e66-e81.	1.2	64

#	Article	IF	Citations
91	Dissecting Privacy Risks in Biomedical Data. , 2018, , .		11
92	EnrichedHeatmap: an R/Bioconductor package for comprehensive visualization of genomic signal associations. BMC Genomics, 2018, 19, 234.	2.8	152
93	Genomic features of renal cell carcinoma with venous tumor thrombus. Scientific Reports, 2018, 8, 7477.	3.3	19
94	Spectrum and prevalence of genetic predisposition in medulloblastoma: a retrospective genetic study and prospective validation in a clinical trial cohort. Lancet Oncology, The, 2018, 19, 785-798.	10.7	268
95	Unraveling mitotic protein networks by 3D multiplexed epitope drug screening. Molecular Systems Biology, 2018, 14, e8238.	7.2	1
96	Rigid and non-rigid registration of polarized light imaging data for 3D reconstruction of the temporal lobe of the human brain at micrometer resolution. NeuroImage, 2018, 181, 235-251.	4.2	20
97	Familial Cancer Variant Prioritization Pipeline version 2 (FCVPPv2) applied to a papillary thyroid cancer family. Scientific Reports, 2018, 8, 11635.	3.3	30
98	Nucleosome repositioning during differentiation of a human myeloid leukemia cell line. Nucleus, 2017, 8, 188-204.	2.2	21
99	The benzene metabolite 1,4-benzoquinone reduces regulatory T-cell function: AÂpotential mechanism for tobacco smokeâ€“associated atopic dermatitis. Journal of Allergy and Clinical Immunology, 2017, 140, 603-605.	2.9	2
100	Diagnosis of CoPAN by whole exome sequencing: Waking up a sleeping tiger's eye. American Journal of Medical Genetics, Part A, 2017, 173, 1878-1886.	1.2	40
101	Meningiomas induced by low-dose radiation carry structural variants of NF2 and a distinct mutational signature. Acta Neuropathologica, 2017, 134, 155-158.	7.7	26
102	Quantitative diagnosis of breast tumors by morphometric classification of microenvironmental myoepithelial cells using a machine learning approach. Scientific Reports, 2017, 7, 46732.	3.3	34
103	Precision oncology based on omics data: The NCT Heidelberg experience. International Journal of Cancer, 2017, 141, 877-886.	5.1	133
104	Genetic subclone architecture of tumor clone-initiating cells in colorectal cancer. Journal of Experimental Medicine, 2017, 214, 2073-2088.	8.5	30
105	DDX3X mutations in two girls with a phenotype overlapping Torielloâ€“Carey syndrome. American Journal of Medical Genetics, Part A, 2017, 173, 1369-1373.	1.2	41
106	Quantification of substrate and cellular strains in stretchable 3D cell cultures: an experimental and computational framework. Journal of Microscopy, 2017, 266, 115-125.	1.8	2
107	The role of Vimentin in Regulating Cell Invasive Migration in Dense Cultures of Breast Carcinoma Cells. Nano Letters, 2017, 17, 6941-6948.	9.1	55
108	Quantitative Single-Molecule Localization Microscopy (qSMLM) of Membrane Proteins Based on Kinetic Analysis of Fluorophore Blinking Cycles. Methods in Molecular Biology, 2017, 1663, 115-126.	0.9	6

#	Article	IF	Citations
109	The whole-genome landscape of medulloblastoma subtypes. Nature, 2017, 547, 311-317.	27.8	787
110	Workflows for microscopy image analysis and cellular phenotyping. Journal of Biotechnology, 2017, 261, 70-75.	3.8	23
111	OTP: An automatized system for managing and processing NGS data. Journal of Biotechnology, 2017, 261, 53-62.	3.8	50
112	Screening drug effects in patientâ€derived cancer cells links organoid responses to genome alterations. Molecular Systems Biology, 2017, 13, 955.	7.2	163
113	Identifying Personal DNA Methylation Profiles by Genotype Inference. , 2017, , .		24
114	Impact of clinical exomes in neurodevelopmental and neurometabolic disorders. Molecular Genetics and Metabolism, 2017, 121, 297-307.	1.1	50
115	Mutant KIT as imatinib-sensitive target in metastatic sinonasal carcinoma. Annals of Oncology, 2017, 28, 142-148.	1.2	30
116	TALEN/CRISPR-mediated engineering of a promoterless anti-viral RNAi hairpin into an endogenous miRNA locus. Nucleic Acids Research, 2017, 45, e3-e3.	14.5	8
117	The Human Cell Atlas. ELife, 2017, 6, .	6.0	1,547
118	Transcription factors, coregulators, and epigenetic marks are linearly correlated and highly redundant. PLoS ONE, 2017, 12, e0186324.	2.5	13
119	Correlated receptor transport processes buffer single-cell heterogeneity. PLoS Computational Biology, 2017, 13, e1005779.	3.2	10
120	Environmentâ€induced epigenetic reprogramming in genomic regulatory elements in smoking mothers and their children. Molecular Systems Biology, 2016, 12, 861.	7.2	97
121	Alterations of microRNA and microRNA-regulated messenger RNA expression in germinal center B-cell lymphomas determined by integrative sequencing analysis. Haematologica, 2016, 101, 1380-1389.	3.5	43
122	Role of the ESCRT Complexes in Telomere Biology. MBio, 2016, 7, .	4.1	11
123	Copy Number Alterations in Enzyme-Coding and Cancer-Causing Genes Reprogram Tumor Metabolism. Cancer Research, 2016, 76, 4058-4067.	0.9	19
124	Complex heatmaps reveal patterns and correlations in multidimensional genomic data. Bioinformatics, 2016, 32, 2847-2849.	4.1	5,891
125	A comprehensive comparison of tools for differential ChIP-seq analysis. Briefings in Bioinformatics, 2016, 17, bbv110.	6.5	89
126	Optogenetic Control of Nuclear Protein Import in Living Cells Using Lightâ€Inducible Nuclear Localization Signals (LINuS). Current Protocols in Chemical Biology, 2016, 8, 131-145.	1.7	12

#	Article	IF	Citations
127	Identification of immunotherapeutic targets by genomic profiling of rectal NET metastases. OncoImmunology, 2016, 5, e1213931.	4.6	14
128	Recurrent MET fusion genes represent a drug target in pediatric glioblastoma. Nature Medicine, 2016, 22, 1314-1320.	30.7	183
129	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. Cell, 2016, 167, 1145-1149.	28.9	404
130	MYC/MIZ1-dependent gene repression inversely coordinates the circadian clock with cell cycle and proliferation. Nature Communications, 2016, 7, 11807.	12.8	103
131	Pedigree based DNA sequencing pipeline for germline genomes of cancer families. Hereditary Cancer in Clinical Practice, 2016, 14, 16.	1.5	7
132	Spatial niche formation but not malignant progression is a driving force for intratumoural heterogeneity. Nature Communications, 2016, 7, ncomms11845.	12.8	44
133	Prenatal maternal stress and wheeze in children: novel insights into epigenetic regulation. Scientific Reports, 2016, 6, 28616.	3.3	55
134	Death receptor-based enrichment of Cas9-expressing cells. BMC Biotechnology, 2016, 16, 17.	3.3	12
135	gtrellis: an R/Bioconductor package for making genome-level Trellis graphics. BMC Bioinformatics, 2016, 17, 169.	2.6	21
136	Active medulloblastoma enhancers reveal subgroup-specific cellular origins. Nature, 2016, 530, 57-62.	27.8	318
137	HilbertCurve: an R/Bioconductor package for high-resolution visualization of genomic data. Bioinformatics, 2016, 32, 2372-2374.	4.1	29
138	Optogenetic control of nuclear protein export. Nature Communications, 2016, 7, 10624.	12.8	183
139	CYP3A5 mediates basal and acquired therapy resistance in different subtypes of pancreatic ductal adenocarcinoma. Nature Medicine, 2016, 22, 278-287.	30.7	184
140	Increased vitamin D levels at birth and in early infancy increase offspring allergy riskâ€"evidence for involvement of epigenetic mechanisms. Journal of Allergy and Clinical Immunology, 2016, 137, 610-613.	2.9	43
141	Atypical Teratoid/Rhabdoid Tumors Are Comprised of Three Epigenetic Subgroups with Distinct Enhancer Landscapes. Cancer Cell, 2016, 29, 379-393.	16.8	438
142	New Brain Tumor Entities Emerge from Molecular Classification of CNS-PNETs. Cell, 2016, 164, 1060-1072.	28.9	702
143	Mixed Integer Linear Programming based machine learning approach identifiesregulatorsof telomerase in yeast. Nucleic Acids Research, 2016, 44, e93-e93.	14.5	10
144	Editorial: Synthetic biology â€“ ready for application. Biotechnology Journal, 2015, 10, 229-230.	3.5	4

#	Article	IF	Citations
145	Largeâ€scale tracking and classification for automatic analysis of cell migration and proliferation, and experimental optimization of highâ€throughput screens of neuroblastoma cells. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2015, 87, 524-540.	1.5	15
146	One, two or three? Probing the stoichiometry of membrane proteins by single-molecule localization microscopy. Scientific Reports, 2015, 5, 14072.	3.3	148
147	Quantitative analysis of chromatin interaction changes upon a 4.3 Mb deletion at mouse 4E2. BMC Genomics, 2015, 16, 982.	2.8	2
148	So rare we need to hunt for them: reframing the ethical debate on incidental findings. Genome Medicine, 2015, 7, 83.	8.2	19
149	On the role of spatial phase and phase correlation in vision, illusion, and cognition. Frontiers in Computational Neuroscience, 2015, 9, 45.	2.1	13
150	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. Nature Communications, 2015, 6, 10001.	12.8	266
151	Mechismo: predicting the mechanistic impact of mutations and modifications on molecular interactions. Nucleic Acids Research, 2015, 43, e10-e10.	14.5	95
152	Mutations in the SIX1/2 Pathway and the DROSHA/DGCR8 miRNA Microprocessor Complex Underlie High-Risk Blastemal Type Wilms Tumors. Cancer Cell, 2015, 27, 298-311.	16.8	248
153	The mutational pattern of primary lymphoma of the central nervous system determined by whole-exome sequencing. Leukemia, 2015, 29, 677-685.	7.2	139
154	Suppression of Early Hematogenous Dissemination of Human Breast Cancer Cells to Bone Marrow by Retinoic Acidâ€“Induced 2. Cancer Discovery, 2015, 5, 506-519.	9.4	45
155	Loss of function of PGAP1 as a cause of severe encephalopathy identified by Whole Exome Sequencing: Lessons of the bioinformatics pipeline. Molecular and Cellular Probes, 2015, 29, 323-329.	2.1	24
156	MapMyFlu: visualizing spatio-temporal relationships between related influenza sequences. Nucleic Acids Research, 2015, 43, W547-W551.	14.5	5
157	Hypermutation takes the driverâ€™s seat. Genome Medicine, 2015, 7, 31.	8.2	15
158	SIPA1L3 identified by linkage analysis and whole-exome sequencing as a novel gene for autosomal recessive congenital cataract. European Journal of Human Genetics, 2015, 23, 1627-1633.	2.8	15
159	DNA methylome analysis in Burkitt and follicular lymphomas identifies differentially methylated regions linked to somatic mutation and transcriptional control. Nature Genetics, 2015, 47, 1316-1325.	21.4	119
160	Tracking Virus Particles in Fluorescence Microscopy Images Using Multi-Scale Detection and Multi-Frame Association. IEEE Transactions on Image Processing, 2015, 24, 4122-4136.	9.8	23
161	Backbone circularization of Bacillus subtilis family 11 xylanase increases its thermostability and its resistance against aggregation. Molecular BioSystems, 2015, 11, 3231-3243.	2.9	21
162	Combinatorial treatment of CD95L and gemcitabine in pancreatic cancer cells induces apoptotic and RIP1-mediated necroptotic cell death network. Experimental Cell Research, 2015, 339, 1-9.	2.6	18

#	Article	IF	Citations
163	Automated Analysis of Single-Molecule Photobleaching Data by Statistical Modeling of Spot Populations. Biophysical Journal, 2015, 109, 2352-2362.	0.5	32
164	BAZ2A (TIP5) is involved in epigenetic alterations in prostate cancer and its overexpression predicts disease recurrence. Nature Genetics, 2015, 47, 22-30.	21.4	141
165	Revised Risk Estimation and Treatment Stratification of Low- and Intermediate-Risk Neuroblastoma Patients by Integrating Clinical and Molecular Prognostic Markers. Clinical Cancer Research, 2015, 21, 1904-1915.	7.0	80
166	Non-rigid multi-frame registration of cell nuclei in live cell fluorescence microscopy image data. Medical Image Analysis, 2015, 19, 1-14.	11.6	15
167	On the embryonic cell division beyond the contractile ring mechanism: experimental and computational investigation of effects of vitelline confinement, temperature and egg size. PeerJ, 2015, 3, e1490.	2.0	4
168	Databases, Standards, and Modeling Platforms for Systems Biology. , 2014, , 169-182.		0
169	Estimating the activity of transcription factors by the effect on their target genes. Bioinformatics, 2014, 30, i401-i407.	4.1	66
170	Characterizing Protein Interactions Employing a Genome-Wide siRNA Cellular Phenotyping Screen. PLoS Computational Biology, 2014, 10, e1003814.	3.2	10
171	Data-Derived Modeling Characterizes Plasticity of MAPK Signaling in Melanoma. PLoS Computational Biology, 2014, 10, e1003795.	3.2	20
172	RNAi screen identifies KIF15 as a novel regulator of integrin endocytic trafficking. Journal of Cell Science, 2014, 127, 2433-47.	2.0	25
173	Intra- and Interdimeric Caspase-8 Self-Cleavage Controls Strength and Timing of CD95-Induced Apoptosis. Science Signaling, 2014, 7, ra23.	3.6	63
174	Genetic variants in apoptosisâ€related genes associated with colorectal hyperplasia. Genes Chromosomes and Cancer, 2014, 53, 769-778.	2.8	2
175	Applications in Cancer Research: Mathematical Models of Apoptosis. , 2014, , 455-481.		0
176	A framework for modelling gene regulation which accommodates non-equilibrium mechanisms. BMC Biology, 2014, 12, 102.	3.8	53
177	Introducing Computational Systems Biology. , 2014, , 1-8.		4
178	Epigenomic alterations define lethal CIMP-positive ependymomas of infancy. Nature, 2014, 506, 445-450.	27.8	521
179	Genome Sequencing of SHH Medulloblastoma Predicts Genotype-Related Response to Smoothened Inhibition. Cancer Cell, 2014, 25, 393-405.	16.8	627
180	Decoding the regulatory landscape of medulloblastoma using DNA methylation sequencing. Nature, 2014, 510, 537-541.	27.8	378

#	Article	IF	Citations
181	Creating functional engineered variants of the single-module non-ribosomal peptide synthetase IndC by T domain exchange. Molecular BioSystems, 2014, 10, 1709-1718.	2.9	35
182	Recurrent RHOA mutations in pediatric <scp>B</scp>urkitt lymphoma treated according to the NHLâ€BFM protocols. Genes Chromosomes and Cancer, 2014, 53, 911-916.	2.8	51
183	Identification of DNA methylation changes atcis-regulatory elements during early steps of HSC differentiation using tagmentation-based whole genome bisulfite sequencing. Cell Cycle, 2014, 13, 3476-3487.	2.6	39
184	Efficient Keratinocyte Differentiation Strictly Depends on JNK-Induced Soluble Factors in Fibroblasts. Journal of Investigative Dermatology, 2014, 134, 1332-1341.	0.7	33
185	Engineering light-inducible nuclear localization signals for precise spatiotemporal control of protein dynamics in living cells. Nature Communications, 2014, 5, 4404.	12.8	203
186	Identification of Regulatory Networks in HSCs and Their Immediate Progeny via Integrated Proteome, Transcriptome, and DNA Methylome Analysis. Cell Stem Cell, 2014, 15, 507-522.	11.1	439
187	Network topology-based detection of differential gene regulation and regulatory switches in cell metabolism and signaling. BMC Systems Biology, 2014, 8, 56.	3.0	0
188	circlizeimplements and enhances circular visualization in R. Bioinformatics, 2014, 30, 2811-2812.	4.1	2,736
189	Enhancer hijacking activates GFI1 family oncogenes in medulloblastoma. Nature, 2014, 511, 428-434.	27.8	520
190	Dissecting the contribution of actin and vimentin intermediate filaments to mechanical phenotype of suspended cells using high-throughput deformability measurements and computational modeling. Journal of Biomechanics, 2014, 47, 2598-2605.	2.1	31
191	Recurrent somatic alterations of FGFR1 and NTRK2 in pilocytic astrocytoma. Nature Genetics, 2013, 45, 927-932.	21.4	674
192	Signatures of mutational processes in human cancer. Nature, 2013, 500, 415-421.	27.8	8,060
193	Secretory meningiomas are defined by combined KLF4 K409Q and TRAF7 mutations. Acta Neuropathologica, 2013, 125, 351-358.	7.7	208
194	Tagmentation-based whole-genome bisulfite sequencing. Nature Protocols, 2013, 8, 2022-2032.	12.0	161
195	Hypermutation of the Inactive X Chromosome Is a Frequent Event in Cancer. Cell, 2013, 155, 567-581.	28.9	67
196	SplicingCompass: differential splicing detection using RNA-Seq data. Bioinformatics, 2013, 29, 1141-1148.	4.1	61
197	Inflammation-mediated skin tumorigenesis induced by epidermal c-Fos. Genes and Development, 2013, 27, 1959-1973.	5.9	53
198	Genome sequencing: a systematic review of health economic evidence. Health Economics Review, 2013, 3, 29.	2.0	50

#	Article	IF	Citations
199	Integrative Genomic Analyses Reveal an Androgen-Driven Somatic Alteration Landscape in Early-Onset Prostate Cancer. Cancer Cell, 2013, 23, 159-170.	16.8	292
200	Caspase-8 cleaves its substrates from the plasma membrane upon CD95-induced apoptosis. Cell Death and Differentiation, 2013, 20, 599-610.	11.2	52
201	Mining Quasi-Bicliques from HIV-1-Human Protein Interaction Network: A Multiobjective Biclustering Approach. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 423-435.	3.0	29
202	Disease-gene discovery by integration of 3D gene expression and transcription factor binding affinities. Bioinformatics, 2013, 29, 468-475.	4.1	4
203	Modulation of Serines 17 and 24 in the LC3-interacting Region of Bnip3 Determines Pro-survival Mitophagy versus Apoptosis. Journal of Biological Chemistry, 2013, 288, 1099-1113.	3.4	374
204	Integrative DNA methylation and gene expression analysis in high-grade soft tissue sarcomas. Genome Biology, 2013, 14, r137.	9.6	78
205	Decision-Tree Based Model Analysis for Efficient Identification of Parameter Relations Leading to Different Signaling States. PLoS ONE, 2013, 8, e82593.	2.5	13
206	Coverage Bias and Sensitivity of Variant Calling for Four Whole-genome Sequencing Technologies. PLoS ONE, 2013, 8, e66621.	2.5	74
207	STK25 Protein Mediates TrkA and CCM2 Protein-dependent Death in Pediatric Tumor Cells of Neural Origin. Journal of Biological Chemistry, 2012, 287, 29285-29289.	3.4	21
208	Whole-genome analysis of gene expression associates the ubiquitin-proteasome system with the cardiomyopathy phenotype in disease-sensitized congenic mouse strains. Cardiovascular Research, 2012, 94, 87-95.	3.8	17
209	Multi-Parametric Analysis and Modeling of Relationships between Mitochondrial Morphology and Apoptosis. PLoS ONE, 2012, 7, e28694.	2.5	44
210	Identifying Virus-Cell Fusion in Two-Channel Fluorescence Microscopy Image Sequences Based on a Layered Probabilistic Approach. IEEE Transactions on Medical Imaging, 2012, 31, 1786-1808.	8.9	9
211	Tracking virus particles in fluorescence microscopy images using two-step multi-frame association. , 2012, , .		5
212	Genome Sequencing of Pediatric Medulloblastoma Links Catastrophic DNA Rearrangements with TP53 Mutations. Cell, 2012, 148, 59-71.	28.9	743
213	Recurrent mutation of the ID3 gene in Burkitt lymphoma identified by integrated genome, exome and transcriptome sequencing. Nature Genetics, 2012, 44, 1316-1320.	21.4	389
214	Time-Lapse Imaging of Neuroblastoma Cells to Determine Cell Fate upon Gene Knockdown. PLoS ONE, 2012, 7, e50988.	2.5	17
215	ICGC PedBrain - dissecting the genomic complexity underlying medulloblastoma using whole-genome sequencing. BMC Proceedings, 2012, 6, .	1.6	1
216	miR-17-5p Regulates Endocytic Trafficking through Targeting TBC1D2/Armus. PLoS ONE, 2012, 7, e52555.	2.5	34

#	Article	IF	Citations
217	Dissecting the genomic complexity underlying medulloblastoma. Nature, 2012, 488, 100-105.	27.8	765
218	MicroRNA profiling of primary highâ€grade soft tissue sarcomas. Genes Chromosomes and Cancer, 2012, 51, 982-996.	2.8	38
219	Liveâ€Cell Assays to Identify Regulators of <scp>ER</scp>â€toâ€<scp>G</scp>olgi Trafficking. Traffic, 2012, 13, 416-432.	2.7	13
220	Multiparametric image analysis reveals role of Caveolin1 in endosomal progression rather than internalization of EGFR. FEBS Letters, 2012, 586, 1179-1189.	2.8	14
221	Tracking Virus Particles in Microscopy Images Using Multi-Frame Association. Informatik Aktuell, 2012, , 231-236.	0.6	0
222	Cell Tracking for Automatic Migration and Proliferation Analysis in High-Throughput Screens. Informatik Aktuell, 2012, , 243-248.	0.6	0
223	Quantification of frap experiments in live cell image sequences by combining segmentation and registration. , 2011, , .		0
224	Caspase-8 activity has an essential role in CD95/Fas-mediated MAPK activation. Cell Death and Disease, 2011, 2, e212-e212.	6.3	38
225	Recruitment and Activation of a Lipid Kinase by Hepatitis C Virus NS5A Is Essential for Integrity of the Membranous Replication Compartment. Cell Host and Microbe, 2011, 9, 32-45.	11.0	435
226	Herpesviral replication compartments move and coalesce at nuclear speckles to enhance export of viral late mRNA. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, E136-44.	7.1	89
227	Probing compressibility of the nuclear interior in wild-type and lamin deficient cells using microscopic imaging and computational modeling. Journal of Biomechanics, 2011, 44, 2642-2648.	2.1	8
228	Bronchoalveolar lavage fluid of lung cancer patients: Mapping the uncharted waters using proteomics technology. Lung Cancer, 2011, 72, 136-138.	2.0	12
229	Negative feedback in the bone morphogenetic protein 4 (BMP4) synexpression group governs its dynamic signaling range and canalizes development. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 10202-10207.	7.1	67
230	Proteomic Bronchiolitis Obliterans Syndrome Risk Monitoring in Lung Transplant Recipients. Transplantation, 2011, 92, 477-485.	1.0	13
231	Nonrigid Registration of 2-D and 3-D Dynamic Cell Nuclei Images for Improved Classification of Subcellular Particle Motion. IEEE Transactions on Image Processing, 2011, 20, 1011-1022.	9.8	29
232	Understanding Life and Death at CD95. Advances in Experimental Medicine and Biology, 2011, 691, 151-161.	1.6	3
233	Integration of Activating and Inhibitory Receptor Signaling by Regulated Phosphorylation of Vav1 in Immune Cells. Science Signaling, 2011, 4, ra36.	3.6	56
234	Concurrent detection of autolysosome formation and lysosomal degradation by flow cytometry in a high-content screen for inducers of autophagy. BMC Biology, 2011, 9, 38.	3.8	119

#	Article	IF	Citations
235	Normalizing for individual cell population context in the analysis of high-content cellular screens. BMC Bioinformatics, 2011, 12, 485.	2.6	22
236	Comparative transcriptome profiling of amyloid precursor protein family members in the adult cortex. BMC Genomics, 2011, 12, 160.	2.8	39
237	Computational identification of signalling pathways in Plasmodium falciparum. Infection, Genetics and Evolution, 2011, 11, 755-764.	2.3	15
238	3D segmentation and quantification of mouse embryonic stem cells in fluorescence microscopy images. , 2011, , .		5
239	Enhancers regulate progression of development in mammalian cells. Nucleic Acids Research, 2011, 39, 8689-8702.	14.5	7
240	Tracking multiple particles in fluorescence microscopy images via probabilistic data association. , 2011, , .		14
241	Artesunate Activates Mitochondrial Apoptosis in Breast Cancer Cells via Iron-catalyzed Lysosomal Reactive Oxygen Species Production. Journal of Biological Chemistry, 2011, 286, 6587-6601.	3.4	201
242	RIP: the regulatory interaction predictorâ€"a machine learning-based approach for predicting target genes of transcription factors. Bioinformatics, 2011, 27, 2239-2247.	4.1	16
243	Statistical Shape Theory and Registration Methods for Analyzing the 3D Architecture of Chromatin in Interphase Cell Nuclei. , 2011, , 131-147.		0
244	Image- and model-based analysis of constitutive properties of cellular structures. Proceedings of SPIE, 2010, , .	0.8	0
245	BRCA1-associated breast and ovarian cancer risks in Poland: no association with commonly studied polymorphisms. Breast Cancer Research and Treatment, 2010, 119, 201-211.	2.5	70
246	Genetic polymorphisms in phase I and phase II enzymes and breast cancer risk associated with menopausal hormone therapy in postmenopausal women. Breast Cancer Research and Treatment, 2010, 119, 463-474.	2.5	69
247	Polymorphisms in the BRCA1 and ABCB1 genes modulate menopausal hormone therapy associated breast cancer risk in postmenopausal women. Breast Cancer Research and Treatment, 2010, 120, 727-736.	2.5	58
248	Postmenopausal estrogen monotherapyâ€"associated breast cancer risk is modified by CYP17A1_-34_T>C polymorphism. Breast Cancer Research and Treatment, 2010, 120, 737-744.	2.5	19
249	Bayesian statistical modelling of human protein interaction network incorporating protein disorder information. BMC Bioinformatics, 2010, 11, 46.	2.6	15
250	Comparison of normalization methods for Illumina BeadChip HumanHT-12 v3. BMC Genomics, 2010, 11, 349.	2.8	68
251	Identification of the Rage-dependent gene regulatory network in a mouse model of skin inflammation. BMC Genomics, 2010, 11, 537.	2.8	29
252	Identifying essential genes in bacterial metabolic networks with machine learning methods. BMC Systems Biology, 2010, 4, 56.	3.0	108

#	Article	IF	Citations
253	Analyzing the regulation of metabolic pathways in human breast cancer. BMC Medical Genomics, 2010, 3, 39.	1.5	44
254	Contactless determination of nuclear compressibility using 3D imageâ€•and modelâ€•based analysis of drugâ€•induced cellular deformation. Journal of Microscopy, 2010, 240, 216-226.	1.8	3
255	Integrated genomic profiling identifies two distinct molecular subtypes with divergent outcome in neuroblastoma with loss of chromosome 11q. Oncogene, 2010, 29, 865-875.	5.9	28
256	Phenotypic profiling of the human genome by time-lapse microscopy reveals cell division genes. Nature, 2010, 464, 721-727.	27.8	768
257	International network of cancer genome projects. Nature, 2010, 464, 993-998.	27.8	2,114
258	The MicroArray Quality Control (MAQC)-II study of common practices for the development and validation of microarray-based predictive models. Nature Biotechnology, 2010, 28, 827-838.	17.5	795
259	Large-scale in silico modeling of metabolic interactions between cell types in the human brain. Nature Biotechnology, 2010, 28, 1279-1285.	17.5	246
260	Comparison of performance of one-color and two-color gene-expression analyses in predicting clinical endpoints of neuroblastoma patients. Pharmacogenomics Journal, 2010, 10, 258-266.	2.0	62
261	An integrated genome research network for studying the genetics of alcohol addiction. Addiction Biology, 2010, 15, 369-379.	2.6	57
262	Model-based dissection of CD95 signaling dynamics reveals both a pro- and antiapoptotic role of c-FLIPL. Journal of Cell Biology, 2010, 190, 377-389.	5.2	135
263	Prognostic Impact of Gene Expressionâ€“Based Classification for Neuroblastoma. Journal of Clinical Oncology, 2010, 28, 3506-3515.	1.6	129
264	Autoantibodies Against the Exocrine Pancreas in Autoimmune Pancreatitis: Gene and Protein Expression Profiling and Immunoassays Identify Pancreatic Enzymes as a Major Target of the Inflammatory Process. American Journal of Gastroenterology, 2010, 105, 2060-2071.	0.4	126
265	PathWave: discovering patterns of differentially regulated enzymes in metabolic pathways. Bioinformatics, 2010, 26, 1225-1231.	4.1	26
266	Detecting host factors involved in virus infection by observing the clustering of infected cells in siRNA screening images. Bioinformatics, 2010, 26, i653-i658.	4.1	15
267	Dynamics within the CD95 deathâ€•inducing signaling complex decide life and death of cells. Molecular Systems Biology, 2010, 6, 352.	7.2	130
268	Omic data from evolved E. coli are consistent with computed optimal growth from genomeâ€•scale models. Molecular Systems Biology, 2010, 6, 390.	7.2	615
269	Tracking and Quantitative Analysis of Dynamic Movements of Cells and Particles. Cold Spring Harbor Protocols, 2010, 2010, pdb.top80-pdb.top80.	0.3	17
270	Tracking and Registration for Multidimensional Biomedical Image Analysis. Mathematics in Industry, 2010, , 229-234.	0.3	1

#	Article	IF	Citations
271	Quantification of fluorescent spots in time series of 3D confocal microscopy images of endoplasmic reticulum exit sites based on the HMAX transform. Proceedings of SPIE, 2010, , .	0.8	4
272	Phenocopy â€“ A Strategy to Qualify Chemical Compounds during Hit-to-Lead and/or Lead Optimization. PLoS ONE, 2010, 5, e14272.	2.5	13
273	Determination of Constitutive Properties of Single Cells and Intracellular Structures Using Image- and Model-Based Framework. IFMBE Proceedings, 2010, , 1121-1124.	0.3	0
274	Contactless Investigation of Nuclear Mechanics of Normal and Lamin Mutant Cells Using a 3D Image- and Model-Based Framework. , 2009, , .		0
275	Identifying fusion events in fluorescence microscopy images. , 2009, , .		3
276	Systems Biological Analysis of Epidermal Growth Factor Receptor Internalization Dynamics for Altered Receptor Levels. Journal of Biological Chemistry, 2009, 284, 17243-17252.	3.4	13
277	Automatic analysis of dividing cells in live cell movies to detect mitotic delays and correlate phenotypes in time. Genome Research, 2009, 19, 2113-2124.	5.5	58
278	RNAither, an automated pipeline for the statistical analysis of high-throughput RNAi screens. Bioinformatics, 2009, 25, 678-679.	4.1	48
279	Detection of non-uniform multi-body motion in image time-series using saccades-enhanced phase correlation. Proceedings of SPIE, 2009, , .	0.8	1
280	Non-rigid alignment of multi-channel fluorescence microscopy images of live cells for improved classification of subcellular particle motion. Proceedings of SPIE, 2009, , .	0.8	1
281	Optimal Experimental Design for Parameter Estimation of a Cell Signaling Model. PLoS Computational Biology, 2009, 5, e1000558.	3.2	114
282	Dynamics of HIV-1 Assembly and Release. PLoS Pathogens, 2009, 5, e1000652.	4.7	178
283	Discovery of transcriptional programs in cerebral ischemia by in silico promoter analysis. Brain Research, 2009, 1272, 3-13.	2.2	17
284	Singleâ€cellâ€based image analysis of highâ€throughput cell array screens for quantification of viral infection. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2009, 75A, 309-318.	1.5	35
285	Decision making in NK cells. Cell Communication and Signaling, 2009, 7, .	6.5	0
286	AP-1-Controlled Hepatocyte Growth Factor Activation Promotes Keratinocyte Migration via CEACAM1 and Urokinase Plasminogen Activator/Urokinase Plasminogen Receptor. Journal of Investigative Dermatology, 2009, 129, 1140-1148.	0.7	17
287	Deterministic and probabilistic approaches for tracking virus particles in time-lapse fluorescence microscopy image sequences. Medical Image Analysis, 2009, 13, 325-342.	11.6	98
288	Estimating novel potential drug targets of Plasmodium falciparum by analysing the metabolic network of knock-out strains in silico. Infection, Genetics and Evolution, 2009, 9, 351-358.	2.3	80

#	Article	IF	Citations
289	Prediction of small molecule binding property of protein domains with Bayesian classifiers based on Markov chains. Computational Biology and Chemistry, 2009, 33, 457-460.	2.3	5
290	CCM2 Mediates Death Signaling by the TrkA Receptor Tyrosine Kinase. Neuron, 2009, 63, 585-591.	8.1	58
291	Understanding apoptosis by systems biology approaches. Molecular BioSystems, 2009, 5, 1105.	2.9	45
292	An in silico Approach to Detect Efficient Malaria Drug Targets to Combat the Malaria Resistance Problem. , 2009, , .		3
293	Evaluation of Approaches for Tracking Virus Particles in Fluorescence Microscopy Images. Informatik Aktuell, 2009, , 207-211.	0.6	0
294	Determination of Material Properties of Cellular Structures Using Time Series of Microscopic Images and Numerical Model of Cell Mechanics. IFMBE Proceedings, 2009, , 1527-1530.	0.3	0
295	Etiology-dependent molecular mechanisms in human hepatocarcinogenesis. Hepatology, 2008, 47, 511-520.	7.3	173
296	Breast cancer: a candidate gene approach across the estrogen metabolic pathway. Breast Cancer Research and Treatment, 2008, 108, 137-149.	2.5	74
297	Using Bayesian multinomial classifier to predict whether a given protein sequence is intrinsically disordered. Journal of Theoretical Biology, 2008, 254, 799-803.	1.7	11
298	Shape normalization of 3D cell nuclei using elastic spherical mapping. Journal of Microscopy, 2008, 231, 105-114.	1.8	21
299	An ultrasensitive sorting mechanism for EGF Receptor Endocytosis. BMC Systems Biology, 2008, 2, 32.	3.0	12
300	Machine learning based analyses on metabolic networks supports high-throughput knockout screens. BMC Systems Biology, 2008, 2, 67.	3.0	42
301	Structural analysis of interphase X-chromatin based on statistical shape theory. Biochimica Et Biophysica Acta - Molecular Cell Research, 2008, 1783, 2089-2099.	4.1	5
302	Systemic Spread Is an Early Step in Breast Cancer. Cancer Cell, 2008, 13, 58-68.	16.8	1,076
303	Nonrigid Registration of 3-D Multichannel Microscopy Images of Cell Nuclei. IEEE Transactions on Image Processing, 2008, 17, 493-499.	9.8	40
304	Gene network dynamics controlling keratinocyte migration. Molecular Systems Biology, 2008, 4, 199.	7.2	52
305	Probabilistic tracking of virus particles in fluorescence microscopy images. , 2008, , .		5
306	Automated Classification of Mitotic Phenotypes of Human Cells Using Fluorescent Proteins. Methods in Cell Biology, 2008, 85, 539-554.	1.1	17

#	Article	IF	Citations
307	Subclassification and Individual Survival Time Prediction from Gene Expression Data of Neuroblastoma Patients by Using CASPAR. Clinical Cancer Research, 2008, 14, 6590-6601.	7.0	23
308	Systems Biology and Artificial Life: Towards Predictive Modeling of Biological Systems. Artificial Life, 2008, 14, 1-2.	1.3	7
309	Genome-wide transcriptional analysis of the human cell cycle identifies genes differentially regulated in normal and cancer cells. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 955-960.	7.1	145
310	Live Cell Dynamics of Promyelocytic Leukemia Nuclear Bodies upon Entry into and Exit from Mitosis. Molecular Biology of the Cell, 2008, 19, 3147-3162.	2.1	50
311	Nonlinear elastic model for image registration and soft tissue simulation based on piecewise St. Venant-Kirchhoff material approximation. Proceedings of SPIE, 2008, , .	0.8	2
312	Probabilistic Tracking of Virus Particles in Fluorescence Microscopy Image Sequences. Informatik Aktuell, 2008, , 448-452.	0.6	2
313	Automated Analysis of siRNA Screens of Virus Infected Cells Based on Immunofluorescence Microscopy. Informatik Aktuell, 2008, , 453-457.	0.6	0
314	TRACKING OF VIRUS PARTICLES IN TIME-LAPSE FLUORESCENCE MICROSCOPY IMAGE SEQUENCES. , 2007, , .		12
315	Translating Expression Profiling into a Clinically Feasible Test to Predict Neuroblastoma Outcome. Clinical Cancer Research, 2007, 13, 1459-1465.	7.0	28
316	Motion detection and pattern tracking in microscopical images using phase correlation approach. , 2007, , .		0
317	Geometrical probability approach for analysis of 3D chromatin structure in interphase cell nuclei. , 2007, , .		1
318	DETERMINATION OF MITOTIC DELAYS IN 3D FLUORESCENCE MICROSCOPY IMAGES OF HUMAN CELLS USING AN ERROR-CORRECTING FINITE STATE MACHINE. , 2007, , .		3
319	Analysis of CD95 Threshold Signaling. Journal of Biological Chemistry, 2007, 282, 13664-13671.	3.4	97
320	Human Resting CD4+ T Cells Are Constitutively Inhibited by TGFÎ² under Steady-State Conditions. Journal of Immunology, 2007, 178, 6931-6940.	0.8	37
321	New Insights into the Genetic Regulation of Plasmodium Falciparum Obtained by Bayesian Modeling. Gene Regulation and Systems Biology, 2007, 1, 117762500700100.	2.3	0
322	Model-based segmentation and quantification of fluorescent bacteria in 3D microscopy live cell images. , 2007, , .		0
323	Classification of neuroblastoma patients by published gene-expression markers reveals a low sensitivity for unfavorable courses of MYCN non-amplified disease. Cancer Letters, 2007, 250, 250-267.	7.2	22
324	Compensation of global movement for improved tracking of cells in time-lapse confocal microscopy image sequences. , 2007, , .		2

#	Article	IF	Citations
325	3D finite element analysis of uniaxial cell stretching: from image to insight. Physical Biology, 2007, 4, 104-113.	1.8	29
326	Quantitative comparison of DNA detection by GFP-lac repressor tagging, fluorescence in situ hybridization and immunostaining. BMC Biotechnology, 2007, 7, 92.	3.3	11
327	Cross-study analysis of gene expression data for intermediate neuroblastoma identifies two biological subtypes. BMC Cancer, 2007, 7, 89.	2.6	29
328	Using gene expression data and network topology to detect substantial pathways, clusters and switches during oxygen deprivation of Escherichia coli. BMC Bioinformatics, 2007, 8, 149.	2.6	11
329	Non-rigid Temporal Alignment of 2D and 3D Multi-channel Microscopy Image Sequences of Human Cells. Informatik Aktuell, 2007, , 16-20.	0.6	0
330	Stochastical Analysis of Finite Point Sampling of 3D Chromatin Fiber in Interphase Cell Nuclei. Lecture Notes in Computer Science, 2007, , 104-118.	1.3	0
331	Analyzing the Variability of the 3D Structure of Chromatin Fiber Using Statistical Shape Theory. Lecture Notes in Computer Science, 2007, , 497-506.	1.3	0
332	Variability Analysis of the Large-Scale Structure of Interphase Chromatin Fiber Based on Statistical Shape Theory. Lecture Notes in Computer Science, 2007, , 37-46.	1.3	2
333	Tracking of Virus Particles in Time-Lapse Fluorescence Microscopy Image Sequences. , 2007, , 6-10.		1
334	On Validation of Non-physical Techniques for Elastic Image Registration. , 2007, , 111-115.		0
335	New insights into the genetic regulation of Plasmodium falciparum obtained by Bayesian modeling. Gene Regulation and Systems Biology, 2007, 1, 137-49.	2.3	1
336	Introducing Computational Systems Biology. , 2006, , 1-14.		11
337	Databases for Systems Biology. , 2006, , 15-38.		5
338	Customized Oligonucleotide Microarray Gene Expressionâ€“Based Classification of Neuroblastoma Patients Outperforms Current Clinical Risk Stratification. Journal of Clinical Oncology, 2006, 24, 5070-5078.	1.6	243
339	Predicting protein subcellular locations using hierarchical ensemble of Bayesian classifiers based on Markov chains. BMC Bioinformatics, 2006, 7, 298.	2.6	72
340	Microarrays meet the Voltaire challenge: Drug discovery on a chip?. Drug Discovery Today: Technologies, 2006, 3, 153-161.	4.0	5
341	A highly standardized, robust, and cost-effective method for genome-wide transcriptome analysis of peripheral blood applicable to large-scale clinical trials. Genomics, 2006, 87, 653-664.	2.9	68
342	Topological analysis of 3D cell nuclei using finite element template-based spherical mapping. , 2006, , .		2

#	Article	IF	Citations
343	Transient colocalization of X-inactivation centres accompanies the initiation of X inactivation. Nature Cell Biology, 2006, 8, 293-299.	10.3	304
344	Discovering functional gene expression patterns in the metabolic network of Escherichia coli with wavelets transforms. BMC Bioinformatics, 2006, 7, 119.	2.6	17
345	GOPET: a tool for automated predictions of Gene Ontology terms. BMC Bioinformatics, 2006, 7, 161.	2.6	44
346	Group testing for pathway analysis improves comparability of different microarray datasets. Bioinformatics, 2006, 22, 2500-2506.	4.1	129
347	Tropical--parameter estimation and simulation of reaction-diffusion models based on spatio-temporal microscopy images. Bioinformatics, 2006, 22, 2709-2710.	4.1	11
348	Argonaute--a database for gene regulation by mammalian microRNAs. Nucleic Acids Research, 2006, 34, D115-D118.	14.5	72
349	Automated Analysis of the Mitotic Phases of Human Cells in 3D Fluorescence Microscopy Image Sequences. Lecture Notes in Computer Science, 2006, 9, 840-848.	1.3	24
350	High-Resolution Genomic Profiling Reveals Association of Chromosomal Aberrations on 1q and 16p with Histologic and Genetic Subgroups of Invasive Breast Cancer. Clinical Cancer Research, 2006, 12, 345-352.	7.0	85
351	Gene Expression Signature Predicting Pathologic Complete Response With Gemcitabine, Epirubicin, and Docetaxel in Primary Breast Cancer. Journal of Clinical Oncology, 2006, 24, 1839-1845.	1.6	146
352	Non-rigid Registration of 3D Multi-channel Microscopy Images of Cell Nuclei. Lecture Notes in Computer Science, 2006, 9, 907-914.	1.3	6
353	Non-rigid Registration of 3D Microscopy Images for the Normalization of Different Cell Nuclei. , 2006, , 364-368.		0
354	Automated Analysis of Mitotic Phenotypes in Fluorescence Microscopy Images of Human Cells. , 2006, , 374-378.		1
355	Spatial Modeling and Simulation of Diffusion in Nuclei of Living Cells. Lecture Notes in Computer Science, 2005, , 161-171.	1.3	0
356	Gene expression profiling of Philadelphia chromosome (Ph)-negative CD34+ hematopoietic stem and progenitor cells of patients with Ph-positive CML in major molecular remission during therapy with imatinib. Leukemia, 2005, 19, 458-460.	7.2	16
357	Microarray analysis reveals differential gene expression patterns and regulation of single target genes contributing to the opposing phenotype of TrkA- and TrkB-expressing neuroblastomas. Oncogene, 2005, 24, 165-177.	5.9	76
358	Distinct gene expression patterns associated with FLT3- and NRAS-activating mutations in acute myeloid leukemia with normal karyotype. Oncogene, 2005, 24, 1580-1588.	5.9	65
359	Distinct molecular phenotype of malignant CD34+ hematopoietic stem and progenitor cells in chronic myelogenous leukemia. Oncogene, 2005, 24, 5313-5324.	5.9	46
360	Prediction of clinical outcome and biological characterization of neuroblastoma by expression profiling. Oncogene, 2005, 24, 7902-7912.	5.9	113

#	Article	IF	Citations
361	A contractile nuclear actin network drives chromosome congression in oocytes. Nature, 2005, 436, 812-818.	27.8	220
362	Genomic analysis of single cytokeratin-positive cells from bone marrow reveals early mutational events in breast cancer. Cancer Cell, 2005, 8, 227-239.	16.8	239
363	CGH-Profiler: data mining based on genomic aberration profiles. BMC Bioinformatics, 2005, 6, 188.	2.6	1
364	Cross-platform analysis of cancer microarray data improves gene expression based classification of phenotypes. BMC Bioinformatics, 2005, 6, 265.	2.6	183
365	Inferring genetic regulatory logic from expression data. Bioinformatics, 2005, 21, 2706-2713.	4.1	53
366	Local gene density predicts the spatial position of genetic loci in the interphase nucleus. Experimental Cell Research, 2005, 311, 14-26.	2.6	55
367	General Stochastic Hybrid Method for the Simulation of Chemical Reaction Processes in Cells. Lecture Notes in Computer Science, 2005, , 248-251.	1.3	8
368	Global gene expression profiling and cluster analysis in Xenopus laevis. Mechanisms of Development, 2005, 122, 441-475.	1.7	59
369	Three-Dimensional Maps of All Chromosomes in Human Male Fibroblast Nuclei and Prometaphase Rosettes. PLoS Biology, 2005, 3, e157.	5.6	683
370	Inferring a System Model of Subcellular Topoisomerase IIÎ² Localization Dynamics. OMICS A Journal of Integrative Biology, 2004, 8, 167-175.	2.0	3
371	Mathematical modeling reveals threshold mechanism in CD95-induced apoptosis. Journal of Cell Biology, 2004, 166, 839-851.	5.2	301
372	Reliability of gene expression ratios for cDNA microarrays in multiconditional experiments with a reference design. Nucleic Acids Research, 2004, 32, 29e-29.	14.5	30
373	Automatic Identification of Subcellular Phenotypes on Human Cell Arrays. Genome Research, 2004, 14, 1130-1136.	5.5	190
374	Gene expression analysis on biochemical networks using the Potts spin model. Bioinformatics, 2004, 20, 1500-1505.	4.1	14
375	Applying Support Vector Machines for Gene Ontology based gene function prediction. BMC Bioinformatics, 2004, 5, 116.	2.6	60
376	Synergy between medical informatics and bioinformatics: facilitating genomic medicine for future health care. Journal of Biomedical Informatics, 2004, 37, 30-42.	4.3	129
377	4-D single particle tracking of synthetic and proteinaceous microspheres reveals preferential movement of nuclear particles along chromatin - poor tracks. BMC Cell Biology, 2004, 5, 45.	3.0	67
378	Pathways of urothelial cancer progression suggested by Bayesian network analysis of allelotyping data. International Journal of Cancer, 2004, 110, 850-856.	5.1	29

#	Article	IF	Citations
379	Topology of genes and nontranscribed sequences in human interphase nuclei. Experimental Cell Research, 2004, 301, 266-279.	2.6	88
380	Visualizing telomere dynamics in living mammalian cells using PNA probes. EMBO Journal, 2003, 22, 6631-6641.	7.8	176
381	Global Chromosome Positions Are Transmitted through Mitosis in Mammalian Cells. Cell, 2003, 112, 751-764.	28.9	268
382	Quantitative motion analysis and visualization of cellular structures. Methods, 2003, 29, 3-13.	3.8	51
383	Computational imaging in cell biology. Journal of Cell Biology, 2003, 161, 477-481.	5.2	129
384	From latent disseminated cells to overt metastasis: Genetic analysis of systemic breast cancer progression. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 7737-7742.	7.1	588
385	Genome-wide expression screens indicate a global role for protein kinase CK2 in chromatin remodeling. Journal of Cell Science, 2003, 116, 1563-1577.	2.0	69
386	Informatics United. Methods of Information in Medicine, 2003, 42, 126-133.	1.2	13
387	Acute myeloid leukemias with reciprocal rearrangements can be distinguished by specific gene expression profiles. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 10008-10013.	7.1	246
388	A cryptic t(5;11)(q35;p15.5) in 2 children with acute myeloid leukemia with apparently normal karyotypes, identified by a multiplex fluorescence in situ hybridization telomere assay. Blood, 2002, 99, 2526-2531.	1.4	72
389	Nuclear Envelope Breakdown Proceeds by Microtubule-Induced Tearing of the Lamina. Cell, 2002, 108, 83-96.	28.9	422
390	Analysis of Chromosome Territory Architecture in the Human Cell Nucleus. , 2002, , 133-140.		0
391	Metabolic-energy-dependent movement of PML bodies within the mammalian cell nucleus. Nature Cell Biology, 2002, 4, 106-110.	10.3	153
392	Microarray-based copy number and expression profiling in dedifferentiated and pleomorphic liposarcoma. Cancer Research, 2002, 62, 2993-8.	0.9	111
393	A new strategy for the detection of subtelomeric rearrangements. Human Genetics, 2001, 109, 576-583.	3.8	28
394	New concepts to improve resolution and sensitivity of molecular cytogenetic diagnostics by multicolor fluorescence in situ hybridization. Cytometry, 2001, 44, 7-15.	1.8	39
395	Subtelomeric chromosome rearrangements are detected using an innovative 12-color FISH assay (M-TEL). Nature Medicine, 2001, 7, 497-501.	30.7	72
396	Four-dimensional imaging and quantitative reconstruction to analyse complex spatiotemporal processes in live cells. Nature Cell Biology, 2001, 3, 852-855.	10.3	98

#	Article	IF	Citations
397	A database system for comparative genomic hybridization analysis. IEEE Engineering in Medicine and Biology Magazine, 2001, 20, 75-83.	0.8	10
398	An Active Contour Model for Segmentation Based on Cubic B-splines and Gradient Vector Flow. Lecture Notes in Computer Science, 2001, , 1373-1375.	1.3	3
399	New Tools for Visualization and Quantification in Dynamic Processes: Application to the Nuclear Envelope Dynamics During Mitosis. Lecture Notes in Computer Science, 2001, , 1323-1325.	1.3	4
400	Classification accuracy in multiple color fluorescence imaging microscopy. Cytometry, 2000, 41, 139-147.	1.8	71
401	Topology of double minutes (dmins) and homogeneously staining regions (HSRs) in nuclei of human neuroblastoma cell lines. Genes Chromosomes and Cancer, 2000, 29, 297-308.	2.8	31
402	Identification of a subtle t(16;19)(p13.3;p13.3) in an infant with multiple congenital abnormalities using a 12-colour multiplex FISH telomere assay, M-TEL. European Journal of Human Genetics, 2000, 8, 903-910.	2.8	35
403	Analysis of Chromosomal Alterations in Non-Small Cell Lung Cancer by Multiplex-FISH, Comparative Genomic Hybridization, and Multicolor Bar Coding. Laboratory Investigation, 2000, 80, 1031-1041.	3.7	41
404	Analysis of Fast Dynamic Processes in Living Cells: High-Resolution and High-Speed Dual-Color Imaging Combined with Automated Image Analysis. BioTechniques, 2000, 28, 722-730.	1.8	9
405	Quantitative Imaging of Pre-mRNA Splicing Factors in Living Cells. Molecular Biology of the Cell, 2000, 11, 413-418.	2.1	44
406	Time-resolved analysis and visualization of dynamic processes in living cells. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 7950-7955.	7.1	101
407	The 3D Positioning of ANT2 and ANT3 Genes within Female X Chromosome Territories Correlates with Gene Activity. Experimental Cell Research, 1999, 252, 363-375.	2.6	113
408	Compartmentalization of Interphase Chromosomes Observed in Simulation and Experiment. Journal of Molecular Biology, 1999, 285, 1053-1065.	4.2	190
409	Separate and variably shaped chromosome arm domains are disclosed by chromosome arm painting in human cell nuclei. Chromosome Research, 1998, 6, 25-33.	2.2	87
410	Highâ€precision distance measurements and volumeâ€conserving segmentation of objects near and below the resolution limit in threeâ€dimensional confocal fluorescence microscopy. Journal of Microscopy, 1998, 189, 118-136.	1.8	121
411	Evidence against a Looped Structure of the Inactive Human X-Chromosome Territory. Experimental Cell Research, 1998, 240, 187-196.	2.6	34
412	Spatial Distributions of Early and Late Replicating Chromatin in Interphase Chromosome Territories. Experimental Cell Research, 1998, 243, 398-407.	2.6	69
413	An optimized, fully automated system for fast and accurate identification of chromosomal rearrangements by multiplex-FISH (M-FISH). Cytogenetic and Genome Research, 1998, 82, 160-171.	1.1	104
414	Aspects of three-dimensional chromosome reorganization during the onset of human male meiotic prophase. Journal of Cell Science, 1998, 111, 2337-2351.	2.0	47

#	Article	IF	Citations
415	Resolution improvement by 3â€Ð reconstructions from tilted views in axial tomography and confocal theta microscopy. Bioimaging, 1997, 5, 171-182.	1.3	15
416	Core binding factor beta-smooth muscle myosin heavy chain chimeric protein involved in acute myeloid leukemia forms unusual nuclear rod-like structures in transformed NIH 3T3 cells.. Proceedings of the National Academy of Sciences of the United States of America, 1996, 93, 1630-1635.	7.1	30
417	Nuclear architecture and the induction of chromosomal aberrations. Mutation Research - Reviews in Genetic Toxicology, 1996, 366, 97-116.	2.9	115
418	Three-dimensional reconstruction of painted human interphase chromosomes: active and inactive X chromosome territories have similar volumes but differ in shape and surface structure.. Journal of Cell Biology, 1996, 135, 1427-1440.	5.2	215
419	3D Bildfolgen zur AuflÃ¶sungsverbesserung in der Fluoreszenzmikroskopie. Informatik Aktuell, 1996, , 92-105.	0.6	0
420	ModellgestÃ¼tzte Segmentierung von ReplikationsdomÃnen in dreidimensionalen konfokalen Mikroskopiebildern. Informatik Aktuell, 1996, , 408-419.	0.6	1
421	Simulation of the distribution of chromosome targets in cell nuclei under topological constraints. Bioimaging, 1995, 3, 108-120.	1.3	17
422	Three-dimensional distribution of centromeric or paracentromeric heterochromatin of chromosomes 1, 7, 15 and 17 in human lymphocyte nuclei studied with light microscopic axial tomography. Bioimaging, 1995, 3, 121-133.	1.3	10
423	Application of confocal laser microscopy and threeâ€dimensional Voronoi diagrams for volume and surface estimates of interphase chromosomes. Journal of Microscopy, 1995, 177, 150-161.	1.8	40
424	Threeâ€dimensional distribution of centromeric or paracentromeric heterochromatin of chromosomes 1, 7, 15 and 17 in human lymphocyte nuclei studied with light microscopic axial tomography. Bioimaging, 1995, 3, 121-133.	1.3	23
425	Assessing the similarity of spatial configurations using distance differences and bending energy: Application to chromosomal interphase arrangements in HeLa cell clones. , 0, , .		1
426	Systems biology of apoptosis. , 0, , 349-372.		2
427	Feature Selection for Evaluating Fluorescence Microscopy Images in Genome-Wide Cell Screens. , 0, , .		5
428	Automated Recognition of Mitotic Patterns in Fluorescence Microscopy Images of Human Cells. , 0, , .		8
429	SARS-CoV-2 receptor ACE2 and TMPRSS2 are primarily expressed in bronchial transient secretory cells. EMBO Journal, 0, , e105114.	7.8	340