

# Mikhail G Dozmorov

## List of Publications by Year in descending order

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125  
papers

4,917  
citations

109321

35  
h-index

118850

62  
g-index

144  
all docs

144  
docs citations

144  
times ranked

9228  
citing authors

#	ARTICLE	IF	CITATIONS
1	Dissecting the Balance Between Metabolic and Oncogenic Functions of Astrocyte- <i>Elevated Gene-1/Metadherin</i> . <i>Hepatology Communications</i> , 2022, 6, 561-575.	4.3	4
2	preciseTAD: a transfer learning framework for 3D domain boundary prediction at base-pair resolution. <i>Bioinformatics</i> , 2022, 38, 621-630.	4.1	4
3	Exploitation of Sulfated Glycosaminoglycan Status for Precision Medicine of Triplatin in Triple-Negative Breast Cancer. <i>Molecular Cancer Therapeutics</i> , 2022, 21, 271-281.	4.1	9
4	MYCN upregulates the transsulfuration pathway to suppress the ferroptotic vulnerability in MYCN-amplified neuroblastoma. <i>Cell Stress</i> , 2022, 6, 21-29.	3.2	5
5	Distinct hepatic immunological patterns are associated with the progression or inhibition of hepatocellular carcinoma. <i>Cell Reports</i> , 2022, 38, 110454.	6.4	19
6	<i>MYCN</i> -Amplified Neuroblastoma Is Addicted to Iron and Vulnerable to Inhibition of the System Xc-/Glutathione Axis. <i>Cancer Research</i> , 2021, 81, 1896-1908.	0.9	73
7	Adolescent stress sensitizes the adult neuroimmune transcriptome and leads to sex-specific microglial and behavioral phenotypes. <i>Neuropsychopharmacology</i> , 2021, 46, 949-958.	5.4	22
8	Targeting transcription of MCL-1 sensitizes HER2-amplified breast cancers to HER2 inhibitors. <i>Cell Death and Disease</i> , 2021, 12, 179.	6.3	11
9	Catastrophic ATP loss underlies a metabolic combination therapy tailored for <i>MYCN</i> -amplified neuroblastoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	10
10	Oncogenic B-Myb Is Associated With Deregulation of the DREAM-Mediated Cell Cycle Gene Expression Program in High Grade Serous Ovarian Carcinoma Clinical Tumor Samples. <i>Frontiers in Oncology</i> , 2021, 11, 637193.	2.8	6
11	Chromatin conformation capture (Hi-C) sequencing of patient-derived xenografts: analysis guidelines. <i>GigaScience</i> , 2021, 10, .	6.4	6
12	Review of multi-omics data resources and integrative analysis for human brain disorders. <i>Briefings in Functional Genomics</i> , 2021, 20, 223-234.	2.7	19
13	DNA Methylation in Babies Born to Nonsmoking Mothers Exposed to Secondhand Smoke during Pregnancy: An Epigenome-Wide Association Study. <i>Environmental Health Perspectives</i> , 2021, 129, 57010.	6.0	15
14	Unmasking BCL-2 Addiction in Synovial Sarcoma by Overcoming Low NOXA. <i>Cancers</i> , 2021, 13, 2310.	3.7	6
15	Venetoclax-based Rational Combinations are Effective in Models of <i>MYCN</i> -amplified Neuroblastoma. <i>Molecular Cancer Therapeutics</i> , 2021, 20, 1400-1411.	4.1	10
16	Histone acetylation at the sulfotransferase 1a1 gene is associated with its hepatic expression in normal aging. <i>Pharmacogenetics and Genomics</i> , 2021, 31, 207-214.	1.5	5
17	Pharmaceutical Interference of the EWS-FLI1-driven Transcriptome By Cotargeting H3K27ac and RNA Polymerase Activity in Ewing Sarcoma. <i>Molecular Cancer Therapeutics</i> , 2021, 20, 1868-1879.	4.1	8
18	Overexpression of ERAP2N in Human Trophoblast Cells Promotes Cell Death. <i>International Journal of Molecular Sciences</i> , 2021, 22, 8585.	4.1	5

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19	Restoring the DREAM Complex Inhibits the Proliferation of High-Risk HPV Positive Human Cells. <i>Cancers</i> , 2021, 13, 489.	3.7	5
20	Identification of nuclear export inhibitor-based combination therapies in preclinical models of triple-negative breast cancer. <i>Translational Oncology</i> , 2021, 14, 101235.	3.7	7
21	Longitudinal studies can identify distinct inflammatory cytokines associated with the inhibition or progression of liver cancer. <i>Liver International</i> , 2020, 40, 468-472.	3.9	13
22	Sjögren's Syndrome Minor Salivary Gland CD4+ Memory T Cells Associate with Glandular Disease Features and Have a Germinal Center T Follicular Helper Transcriptional Profile. <i>Journal of Clinical Medicine</i> , 2020, 9, 2164.	2.4	23
23	Anthrax Edema and Lethal Toxins Differentially Target Human Lung and Blood Phagocytes. <i>Toxins</i> , 2020, 12, 464.	3.4	5
24	SpectralTAD: an R package for defining a hierarchy of topologically associated domains using spectral clustering. <i>BMC Bioinformatics</i> , 2020, 21, 319.	2.6	24
25	Assessing the Role of Long Noncoding RNA in Nucleus Accumbens in Subjects With Alcohol Dependence. <i>Alcoholism: Clinical and Experimental Research</i> , 2020, 44, 2468-2480.	2.4	12
26	Gloomy Prospects and Roller Coasters: Finding Coherence in Genome-Wide Association Studies. <i>Philosophy of Science</i> , 2020, 87, 1084-1095.	1.0	3
27	Regulatory T Cells Support Breast Cancer Progression by Opposing IFN- $\beta$ -Dependent Functional Reprogramming of Myeloid Cells. <i>Cell Reports</i> , 2020, 33, 108482.	6.4	28
28	A method for estimating coherence of molecular mechanisms in major human disease and traits. <i>BMC Bioinformatics</i> , 2020, 21, 473.	2.6	1
29	Gut microbiota manipulation during the prepubertal period shapes behavioral abnormalities in a mouse neurodevelopmental disorder model. <i>Scientific Reports</i> , 2020, 10, 4697.	3.3	29
30	TADCompare: An R Package for Differential and Temporal Analysis of Topologically Associated Domains. <i>Frontiers in Genetics</i> , 2020, 11, 158.	2.3	37
31	DNA methylation and histone acetylation changes to cytochrome P450 2E1 regulation in normal aging and impact on rates of drug metabolism in the liver. <i>GeroScience</i> , 2020, 42, 819-832.	4.6	26
32	Evaluation of combined BCL-2/MCL-1 inhibition as a therapeutic approach for synovial sarcoma. <i>Journal of Clinical Oncology</i> , 2020, 38, e23561-e23561.	1.6	2
33	IGFBP-3/IGFBP-3 Receptor System as an Anti-Tumor and Anti-Metastatic Signaling in Cancer. <i>Cells</i> , 2020, 9, 1261.	4.1	68
34	Disease classification: from phenotypic similarity to integrative genomics and beyond. <i>Briefings in Bioinformatics</i> , 2019, 20, 1769-1780.	6.5	19
35	Syndecan-1 facilitates breast cancer metastasis to the brain. <i>Breast Cancer Research and Treatment</i> , 2019, 178, 35-49.	2.5	57
36	multiHiCcompare: joint normalization and comparative analysis of complex Hi-C experiments. <i>Bioinformatics</i> , 2019, 35, 2916-2923.	4.1	70

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37	R Tutorial: Detection of Differentially Interacting Chromatin Regions From Multiple Hi-C Datasets. <i>Current Protocols in Bioinformatics</i> , 2019, 66, e76.	25.8	6
38	Preexisting Commensal Dysbiosis Is a Host-Intrinsic Regulator of Tissue Inflammation and Tumor Cell Dissemination in Hormone Receptor-Positive Breast Cancer. <i>Cancer Research</i> , 2019, 79, 3662-3675.	0.9	118
39	Disruption of the MBD2-NuRD complex but not MBD3-NuRD induces high level HbF expression in human adult erythroid cells. <i>Haematologica</i> , 2019, 104, 2361-2371.	3.5	41
40	Separation of breast cancer and organ microenvironment transcriptomes in metastases. <i>Breast Cancer Research</i> , 2019, 21, 36.	5.0	36
41	DYRK1A regulates the recruitment of 53BP1 to the sites of DNA damage in part through interaction with RNF169. <i>Cell Cycle</i> , 2019, 18, 531-551.	2.6	32
42	PATH-61. IMMUNOHISTOCHEMICAL PHENOTYPING AND SURVIVAL ANALYSIS OF WHO GRADE II-IV GLIOMAS. <i>Neuro-Oncology</i> , 2019, 21, vi157-vi157.	1.2	0
43	Concomitant PPAR $\alpha$ and FXR Activation as a Putative Mechanism of NASH Improvement after Gastric Bypass Surgery: a GEO Datasets Analysis. <i>Journal of Gastrointestinal Surgery</i> , 2019, 23, 51-57.	1.7	18
44	The cell cycle regulatory DREAM complex is disrupted by high expression of oncogenic B-Myb. <i>Oncogene</i> , 2019, 38, 1080-1092.	5.9	54
45	The Coherence Problem: Finding Meaning in GWAS Complexity. <i>Behavior Genetics</i> , 2019, 49, 187-195.	2.1	8
46	OKN-007 Increases temozolomide (TMZ) Sensitivity and Suppresses TMZ-Resistant Glioblastoma (GBM) Tumor Growth. <i>Translational Oncology</i> , 2019, 12, 320-335.	3.7	33
47	Coamplification of <i>miR-4728</i> protects <i>HER2</i> -amplified breast cancers from targeted therapy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E2594-E2603.	7.1	23
48	Associations between maternal cytokine levels during gestation and measures of child cognitive abilities and executive functioning. <i>Brain, Behavior, and Immunity</i> , 2018, 70, 390-397.	4.1	30
49	Gene expression profiling of primary human type I alveolar epithelial cells exposed to <i>Bacillus anthracis</i> spores reveals induction of neutrophil and monocyte chemokines. <i>Microbial Pathogenesis</i> , 2018, 121, 9-21.	2.9	2
50	Characterizing the efficacy of cancer therapeutics in patient-derived xenograft models of metastatic breast cancer. <i>Breast Cancer Research and Treatment</i> , 2018, 170, 221-234.	2.5	28
51	Epithelial-to-Mesenchymal Transition Antagonizes Response to Targeted Therapies in Lung Cancer by Suppressing BIM. <i>Clinical Cancer Research</i> , 2018, 24, 197-208.	7.0	74
52	GitHub Statistics as a Measure of the Impact of Open-Source Bioinformatics Software. <i>Frontiers in Bioengineering and Biotechnology</i> , 2018, 6, 198.	4.1	16
53	RIG-I Signaling via MAVS Is Dispensable for Survival in Lethal Influenza Infection <i>In Vivo</i> . <i>Mediators of Inflammation</i> , 2018, 2018, 1-14.	3.0	10
54	Astrocyte Elevated Gene-1 Regulates Macrophage Activation in Hepatocellular Carcinogenesis. <i>Cancer Research</i> , 2018, 78, 6436-6446.	0.9	22

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55	Targeted inhibition of histone H3K27 demethylation is effective in high-risk neuroblastoma. <i>Science Translational Medicine</i> , 2018, 10, .	12.4	70
56	HiCcompare: an R-package for joint normalization and comparison of HI-C datasets. <i>BMC Bioinformatics</i> , 2018, 19, 279.	2.6	110
57	HDAC2-dependent Antipsychotic-like Effects of Chronic Treatment with the HDAC Inhibitor SAHA in Mice. <i>Neuroscience</i> , 2018, 388, 102-117.	2.3	31
58	Trans-Ethnic Mapping of BANK1 Identifies Two Independent SLE-Risk Linkage Groups Enriched for Co-Transcriptional Splicing Marks. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2331.	4.1	12
59	Risk stratification of gastrointestinal stromal tumors by CtBP2 and CD44 analysis.. <i>Journal of Clinical Oncology</i> , 2018, 36, 48-48.	1.6	0
60	Reforming disease classification system—are we there yet?. <i>Annals of Translational Medicine</i> , 2018, 6, S30-S30.	1.7	1
61	Angiopoietin pathway gene expression associated with poor breast cancer survival. <i>Breast Cancer Research and Treatment</i> , 2017, 162, 191-198.	2.5	51
62	The role of epigenomics in personalized medicine. <i>Expert Review of Precision Medicine and Drug Development</i> , 2017, 2, 33-45.	0.7	61
63	A novel role of astrocyte elevated gene-1 (AEG-1) in regulating nonalcoholic steatohepatitis (NASH). <i>Hepatology</i> , 2017, 66, 466-480.	7.3	35
64	Bile acids as global regulators of hepatic nutrient metabolism. <i>Liver Research</i> , 2017, 1, 10-16.	1.4	23
65	Effects of DNA Methylation on Progression to Interstitial Fibrosis and Tubular Atrophy in Renal Allograft Biopsies: A Multi-Omics Approach. <i>American Journal of Transplantation</i> , 2017, 17, 3060-3075.	4.7	28
66	Age-associated DNA methylation changes in naive CD4 <sup>+</sup> T cells suggest an evolving autoimmune epigenotype in aging T cells. <i>Epigenomics</i> , 2017, 9, 429-445.	2.1	47
67	Transcriptional Classification and Functional Characterization of Human Airway Macrophage and Dendritic Cell Subsets. <i>Journal of Immunology</i> , 2017, 198, 1183-1201.	0.8	53
68	Sexually divergent DNA methylation patterns with hippocampal aging. <i>Aging Cell</i> , 2017, 16, 1342-1352.	6.7	67
69	Epigenomic annotation-based interpretation of genomic data: from enrichment analysis to machine learning. <i>Bioinformatics</i> , 2017, 33, 3323-3330.	4.1	32
70	Identification of breast cancer associated variants that modulate transcription factor binding. <i>PLoS Genetics</i> , 2017, 13, e1006761.	3.5	37
71	Analysis of The Cancer Genome Atlas sequencing data reveals novel properties of the human papillomavirus 16 genome in head and neck squamous cell carcinoma. <i>Oncotarget</i> , 2017, 8, 17684-17699.	1.8	113
72	Current Developments in Machine Learning Techniques in Biological Data Mining. <i>Bioinformatics and Biology Insights</i> , 2017, 11, 117793221668754.	2.0	6

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73	Improving sensitivity of linear regression-based cell type-specific differential expression deconvolution with per-gene vs. global significance threshold. <i>BMC Bioinformatics</i> , 2016, 17, 334.	2.6	11
74	GenomeRunner web server: regulatory similarity and differences define the functional impact of SNP sets. <i>Bioinformatics</i> , 2016, 32, 2256-2263.	4.1	46
75	Hypomethylation coordinates antagonistically with hypermethylation in cancer development: a case study of leukemia. <i>Human Genomics</i> , 2016, 10, 18.	2.9	40
76	Expression and methylation data from SLE patient and healthy control blood samples subdivided with respect to ARID3a levels. <i>Data in Brief</i> , 2016, 9, 213-219.	1.0	9
77	Human effector B lymphocytes express ARID3a and secrete interferon alpha. <i>Journal of Autoimmunity</i> , 2016, 75, 130-140.	6.5	30
78	Epigenetic Reprogramming in Naive CD4+ T Cells Favoring T Cell Activation and Non- $\text{Th1}$ Effector T Cell Immune Response as an Early Event in Lupus Flares. <i>Arthritis and Rheumatology</i> , 2016, 68, 2200-2209.	5.6	88
79	Establishing an analytic pipeline for genome-wide DNA methylation. <i>Clinical Epigenetics</i> , 2016, 8, 45.	4.1	36
80	High-density genotyping of immune-related loci identifies new SLE risk variants in individuals with Asian ancestry. <i>Nature Genetics</i> , 2016, 48, 323-330.	21.4	219
81	Staphylococcal Nuclease and Tudor Domain Containing 1 (SND1 Protein) Promotes Hepatocarcinogenesis by Inhibiting Monoglyceride Lipase (MGLL). <i>Journal of Biological Chemistry</i> , 2016, 291, 10736-10746.	3.4	33
82	Exploitation of the Apoptosis-Primed State of MYCN-Amplified Neuroblastoma to Develop a Potent and Specific Targeted Therapy Combination. <i>Cancer Cell</i> , 2016, 29, 159-172.	16.8	104
83	A Whole Methylome CpG-SNP Association Study of Psychosis in Blood and Brain Tissue. <i>Schizophrenia Bulletin</i> , 2016, 42, 1018-1026.	4.3	41
84	Epigenomic functional characterization of genetic susceptibility variants in systemic vasculitis. <i>Journal of Autoimmunity</i> , 2016, 67, 76-81.	6.5	12
85	Detrimental effects of duplicate reads and low complexity regions on RNA- and ChIP-seq data. <i>BMC Bioinformatics</i> , 2015, 16, S10.	2.6	19
86	B-Cell and Monocyte Contribution to Systemic Lupus Erythematosus Identified by Cell-Type-Specific Differential Expression Analysis in RNA-Seq Data. <i>Bioinformatics and Biology Insights</i> , 2015, 9s3, BBI.S29470.	2.0	30
87	Activation of the JAK/STAT pathway in Behcet's disease. <i>Genes and Immunity</i> , 2015, 16, 170-175.	4.1	59
88	PDGFR $\beta$ signaling drives adipose tissue fibrosis by targeting progenitor cell plasticity. <i>Genes and Development</i> , 2015, 29, 1106-1119.	5.9	131
89	High density methylation QTL analysis in human blood via next-generation sequencing of the methylated genomic DNA fraction. <i>Genome Biology</i> , 2015, 16, 291.	8.8	112
90	Polycomb repressive complex 2 epigenomic signature defines age-associated hypermethylation and gene expression changes. <i>Epigenetics</i> , 2015, 10, 484-495.	2.7	60

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91	Abstract 1473: Are the genomic gene expression profiles maintained between the original donor and patient-derived xenograft tumors. , 2015, , .		0
92	Epigenomic elements enriched in the promoters of autoimmunity susceptibility genes. <i>Epigenetics</i> , 2014, 9, 276-285.	2.7	42
93	Differential effects of selective frankincense (Ru Xiang) essential oil versus non-selective sandalwood (Tan Xiang) essential oil on cultured bladder cancer cells: a microarray and bioinformatics study. <i>Chinese Medicine</i> , 2014, 9, 18.	4.0	27
94	Functional characterization of the MECP2/IRAK1 lupus risk haplotype in human T cells and a human MECP2 transgenic mouse. <i>Journal of Autoimmunity</i> , 2013, 41, 168-174.	6.5	55
95	Variants at multiple loci implicated in both innate and adaptive immune responses are associated with Sjögren's syndrome. <i>Nature Genetics</i> , 2013, 45, 1284-1292.	21.4	427
96	mirCoX: a database of miRNA-mRNA expression correlations derived from RNA-seq meta-analysis. <i>BMC Bioinformatics</i> , 2013, 14, S17.	2.6	18
97	Systematic classification of non-coding RNAs by epigenomic similarity. <i>BMC Bioinformatics</i> , 2013, 14, S2.	2.6	73
98	Genome-wide DNA methylation study suggests epigenetic accessibility and transcriptional poising of interferon-regulated genes in naïve CD4+ T cells from lupus patients. <i>Journal of Autoimmunity</i> , 2013, 43, 78-84.	6.5	294
99	Fucosyltransferase VII improves the function of selectin ligands on cord blood hematopoietic stem cells. <i>Glycobiology</i> , 2013, 23, 1184-1191.	2.5	18
100	Suppression and Activation of the Malignant Phenotype by Extracellular Matrix in Xenograft Models of Bladder Cancer: A Model for Tumor Cell "Dormancy". <i>PLoS ONE</i> , 2013, 8, e64181.	2.5	15
101	GenomeRunner: automating genome exploration. <i>Bioinformatics</i> , 2012, 28, 419-420.	4.1	41
102	Fine mapping and conditional analysis identify a new mutation in the autoimmunity susceptibility gene BLK that leads to reduced half-life of the BLK protein. <i>Annals of the Rheumatic Diseases</i> , 2012, 71, 1219-1226.	0.9	33
103	The curcuminoid CLEFMA selectively induces cell death in H441 lung adenocarcinoma cells via oxidative stress. <i>Investigational New Drugs</i> , 2012, 30, 558-567.	2.6	24
104	System Level Changes in Gene Expression in Maturing Bladder Mucosa. <i>Journal of Urology</i> , 2011, 185, 1952-1958.	0.4	5
105	Predicting gene ontology from a global meta-analysis of 1-color microarray experiments. <i>BMC Bioinformatics</i> , 2011, 12, S14.	2.6	26
106	High-throughput processing and normalization of one-color microarrays for transcriptional meta-analyses. <i>BMC Bioinformatics</i> , 2011, 12, S2.	2.6	13
107	Genome-wide DNA methylation patterns in CD4+ T cells from patients with systemic lupus erythematosus. <i>Epigenetics</i> , 2011, 6, 593-601.	2.7	224
108	Elevated AKR1C3 expression promotes prostate cancer cell survival and prostate cell-mediated endothelial cell tube formation: implications for prostate cancer progression. <i>BMC Cancer</i> , 2010, 10, 672.	2.6	52

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109	A Comprehensive and Universal Method for Assessing the Performance of Differential Gene Expression Analyses. PLoS ONE, 2010, 5, e12657.	2.5	15
110	From Microarray to Biology. Systems Biology, 2010, , 85-107.	0.1	0
111	Unique patterns of molecular profiling between human prostate cancer LNCaP and PCa cells. Prostate, 2009, 69, 1077-1090.	2.3	82
112	Gene expression profiling of human alveolar macrophages infected by B. anthracis spores demonstrates TNF- $\alpha$ and NF- $\kappa$ B are key components of the innate immune response to the pathogen. BMC Infectious Diseases, 2009, 9, 152.	2.9	27
113	Persistent LTP without triggered protein synthesis. Neuroscience Research, 2009, 63, 59-65.	1.9	33
114	From microarray to biology: an integrated experimental, statistical and in silico analysis of how the extracellular matrix modulates the phenotype of cancer cells. BMC Bioinformatics, 2008, 9, S4.	2.6	15
115	Abnormal Expression of Differentiation Related Proteins and Proteoglycan Core Proteins in the Urothelium of Patients With Interstitial Cystitis. Journal of Urology, 2008, 179, 764-769.	0.4	106
116	Differentially expressed gene networks in cultured smooth muscle cells from normal and neuropathic bladder. Journal of Smooth Muscle Research, 2007, 43, 55-72.	1.2	45
117	Systems biology approach for mapping the response of human urothelial cells to infection by Enterococcus faecalis. BMC Bioinformatics, 2007, 8, S2.	2.6	9
118	5 $\alpha$ -androstane-3 $\beta$ ,17 $\beta$ -diol selectively activates the canonical PI3K/AKT pathway: a bioinformatics-based evidence for androgen-activated cytoplasmic signaling. Genomic Medicine, 2007, 1, 139-146.	0.3	3
119	Proteome-level display by 2-dimensional chromatography of extracellular matrix-dependent modulation of the phenotype of bladder cancer cells. Proteome Science, 2006, 4, 13.	1.7	8
120	Contribution of AMPA and NMDA receptors to early and late phases of LTP in hippocampal slices. Neuroscience Research, 2006, 55, 182-188.	1.9	17
121	Analysis of the interaction of extracellular matrix and phenotype of bladder cancer cells. BMC Cancer, 2006, 6, 12.	2.6	25
122	Slowly developing depression of N-methyl-D-aspartate receptor mediated responses in young rat hippocampi. BMC Neuroscience, 2004, 5, 26.	1.9	4
123	Characterization of NMDA induced depression in rat hippocampus: involvement of AMPA and NMDA receptors. Neuroscience Letters, 2004, 357, 87-90.	2.1	20
124	Active decay of composite excitatory postsynaptic potentials in hippocampal slices from young rats. Brain Research, 2003, 973, 44-55.	2.2	8
125	Comparing fluctuations of synaptic responses mediated via AMPA and NMDA receptor channels—implications for synaptic plasticity. BioSystems, 2001, 62, 45-56.	2.0	2