

Petr V Nazarov

List of Publications by Year in descending order

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Version: 2024-02-01

60
papers

2,612
citations

331538

21
h-index

197736

49
g-index

66
all docs

66
docs citations

66
times ranked

7477
citing authors

#	ARTICLE	IF	CITATIONS
1	Stem cell-associated heterogeneity in Glioblastoma results from intrinsic tumor plasticity shaped by the microenvironment. <i>Nature Communications</i> , 2019, 10, 1787.	5.8	379
2	Use of Circulating MicroRNAs to Diagnose Acute Myocardial Infarction. <i>Clinical Chemistry</i> , 2012, 58, 559-567.	1.5	239
3	Signatures of MicroRNAs and Selected MicroRNA Target Genes in Human Melanoma. <i>Cancer Research</i> , 2010, 70, 4163-4173.	0.4	204
4	MicroRNA as biomarkers and regulators in B-cell chronic lymphocytic leukemia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 6573-6578.	3.3	159
5	Interplay of microRNAs, transcription factors and target genes: linking dynamic expression changes to function. <i>Nucleic Acids Research</i> , 2013, 41, 2817-2831.	6.5	130
6	Self-association of Transmembrane α -Helices in Model Membranes. <i>Journal of Biological Chemistry</i> , 2005, 280, 39324-39331.	1.6	123
7	Hypoxia-induced autophagy drives colorectal cancer initiation and progression by activating the PRKC/PKC-EZR (ezrin) pathway. <i>Autophagy</i> , 2020, 16, 1436-1452.	4.3	114
8	Altered metabolic landscape in IDH mutant gliomas affects phospholipid, energy, and oxidative stress pathways. <i>EMBO Molecular Medicine</i> , 2017, 9, 1681-1695.	3.3	111
9	The acquisition of resistance to TNF α in breast cancer cells is associated with constitutive activation of autophagy as revealed by a transcriptome analysis using a custom microarray. <i>Autophagy</i> , 2011, 7, 760-770.	4.3	99
10	RNAi/CRISPR Screens: from a Pool to a Valid Hit. <i>Trends in Biotechnology</i> , 2019, 37, 38-55.	4.9	90
11	RNA sequencing and transcriptome arrays analyses show opposing results for alternative splicing in patient derived samples. <i>BMC Genomics</i> , 2017, 18, 443.	1.2	74
12	Patient-derived organoids and orthotopic xenografts of primary and recurrent gliomas represent relevant patient avatars for precision oncology. <i>Acta Neuropathologica</i> , 2020, 140, 919-949.	3.9	72
13	Viruses: incredible nanomachines. New advances with filamentous phages. <i>European Biophysics Journal</i> , 2010, 39, 541-550.	1.2	67
14	Independent Component Analysis for Unraveling the Complexity of Cancer Omics Datasets. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4414.	1.8	62
15	Identification of SOCS2 and SOCS6 as biomarkers in human colorectal cancer. <i>British Journal of Cancer</i> , 2014, 111, 726-735.	2.9	54
16	Tumor suppressor miR-215 counteracts hypoxia-induced colon cancer stem cell activity. <i>Cancer Letters</i> , 2019, 450, 32-41.	3.2	49
17	What Do We Learn from Spheroid Culture Systems? Insights from Tumorspheres Derived from Primary Colon Cancer Tissue. <i>PLoS ONE</i> , 2016, 11, e0146052.	1.1	48
18	Dynamic regulation of microRNA expression following Interferon- β -induced gene transcription. <i>RNA Biology</i> , 2012, 9, 978-989.	1.5	40

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19	Analysis of the dynamic co-expression network of heart regeneration in the zebrafish. <i>Scientific Reports</i> , 2016, 6, 26822.	1.6	32
20	Constitutive activation of oncogenic PDGFR \pm -mutant proteins occurring in GIST patients induces receptor mislocalisation and alters PDGFR \pm signalling characteristics. <i>Cell Communication and Signaling</i> , 2015, 13, 21.	2.7	27
21	A DNA Repair and Cell-Cycle Gene Expression Signature in Primary and Recurrent Glioblastoma: Prognostic Value and Clinical Implications. <i>Cancer Research</i> , 2019, 79, 1226-1238.	0.4	26
22	AN1-type zinc finger protein 3 (ZFAND3) is a transcriptional regulator that drives Glioblastoma invasion. <i>Nature Communications</i> , 2020, 11, 6366.	5.8	24
23	FRET Study of Membrane Proteins: Determination of the Tilt and Orientation of the N-Terminal Domain of M13 Major Coat Protein. <i>Biophysical Journal</i> , 2007, 92, 1296-1305.	0.2	22
24	Deconvolution of transcriptomes and miRNomes by independent component analysis provides insights into biological processes and clinical outcomes of melanoma patients. <i>BMC Medical Genomics</i> , 2019, 12, 132.	0.7	22
25	FRET Study of Membrane Proteins: Simulation-Based Fitting for Analysis of Membrane Protein Embedment and Association. <i>Biophysical Journal</i> , 2006, 91, 454-466.	0.2	21
26	Integrative approaches for analysis of mRNA and microRNA high-throughput data. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 1154-1162.	1.9	20
27	Reference-free deconvolution, visualization and interpretation of complex DNA methylation data using DecompPipeline, MeDeCom and FactorViz. <i>Nature Protocols</i> , 2020, 15, 3240-3263.	5.5	19
28	From α -L α ™ to α -L α ™ and back again: the odyssey of membrane-bound M13 protein. <i>Trends in Biochemical Sciences</i> , 2009, 34, 249-255.	3.7	17
29	Crosstalk between different family members: IL27 recapitulates IFN γ responses in HCC cells, but is inhibited by IL6-type cytokines. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2017, 1864, 516-526.	1.9	17
30	Cytokine-mediated modulation of the hepatic miRNome: miR-146b-5p is an IL-6-inducible miRNA with multiple targets. <i>Journal of Leukocyte Biology</i> , 2018, 104, 987-1002.	1.5	17
31	Artificial Neural Network Modification of Simulation-Based Fitting: Application to a Protein-Lipid System. <i>Journal of Chemical Information and Computer Sciences</i> , 2004, 44, 568-574.	2.8	16
32	PRISMA and BioID disclose a motifs-based interactome of the intrinsically disordered transcription factor C/EBP β . <i>IScience</i> , 2021, 24, 102686.	1.9	16
33	Membrane-bound peptides mimicking transmembrane Vph1p helix 7 of yeast V-ATPase: A spectroscopic and polarity mismatch study. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2005, 1716, 137-145.	1.4	15
34	A mathematical model of actin filament turnover for fitting FRAP data. <i>European Biophysics Journal</i> , 2010, 39, 669-677.	1.2	15
35	Identification of beta-arrestin-1 as a diagnostic biomarker in lung cancer. <i>British Journal of Cancer</i> , 2018, 119, 580-590.	2.9	13
36	Predicting clinical outcome of neuroblastoma patients using an integrative network-based approach. <i>Biology Direct</i> , 2018, 13, 12.	1.9	13

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37	Prognostic transcriptional association networks: a new supervised approach based on regression trees. <i>Bioinformatics</i> , 2011, 27, 252-258.	1.8	12
38	Bronchial airway gene expression in smokers with lung or head and neck cancer. <i>Cancer Medicine</i> , 2014, 3, 322-336.	1.3	12
39	The PD-L1- and IL6-mediated dampening of the IL27/STAT1 anticancer responses are prevented by $\hat{\pm}$ -PD-L1 or $\hat{\pm}$ -IL6 antibodies. <i>Journal of Leukocyte Biology</i> , 2018, 104, 969-985.	1.5	12
40	Transcriptional variations in the wider peritumoral tissue environment of pancreatic cancer. <i>International Journal of Cancer</i> , 2018, 142, 1010-1021.	2.3	11
41	Structure of Membrane-Embedded M13 Major Coat Protein Is Insensitive to Hydrophobic Stress. <i>Biophysical Journal</i> , 2007, 93, 3541-3547.	0.2	10
42	An integrative simulation model linking major biochemical reactions of actin-polymerization to structural properties of actin filaments. <i>Biophysical Chemistry</i> , 2009, 140, 24-34.	1.5	10
43	Transcriptional response to cardiac injury in the zebrafish: systematic identification of genes with highly concordant activity across in vivo models. <i>BMC Genomics</i> , 2014, 15, 852.	1.2	10
44	XAB2 promotes Ku eviction from single-ended DNA double-strand breaks independently of the ATM kinase. <i>Nucleic Acids Research</i> , 2021, 49, 9906-9925.	6.5	8
45	In silico Approach for Validating and Unveiling New Applications for Prognostic Biomarkers of Endometrial Cancer. <i>Cancers</i> , 2021, 13, 5052.	1.7	8
46	Whole transcriptome microarrays identify long non-coding RNAs associated with cardiac hypertrophy. <i>Genomics Data</i> , 2015, 5, 68-71.	1.3	6
47	Decoding of exon splicing patterns in the human RUNX1 $\hat{\pm}$ RUNX1T1 fusion gene. <i>International Journal of Biochemistry and Cell Biology</i> , 2015, 68, 48-58.	1.2	6
48	Oncolytic H-1 Parvovirus Hijacks Galectin-1 to Enter Cancer Cells. <i>Viruses</i> , 2022, 14, 1018.	1.5	6
49	The oncogenic FIP1L1-PDGFR $\hat{\pm}$ fusion protein displays skewed signaling properties compared to its wild-type PDGFR $\hat{\pm}$ counterpart. <i>Jak-stat</i> , 2015, 4, e1062596.	2.2	5
50	Insights into ligand stimulation effects on gastro-intestinal stromal tumors signalling. <i>Cellular Signalling</i> , 2017, 29, 138-149.	1.7	4
51	Hub genes in a pan-cancer co-expression network show potential for predicting drug responses. <i>F1000Research</i> , 2018, 7, 1906.	0.8	4
52	BIODICA: a computational environment for Independent Component Analysis of omics data. <i>Bioinformatics</i> , 2022, 38, 2963-2964.	1.8	4
53	Systematic Transcriptional Profiling of Responses to STAT1- and STAT3-Activating Cytokines in Different Cancer Types. <i>Journal of Molecular Biology</i> , 2020, 432, 5902-5919.	2.0	3
54	Hub genes in a pan-cancer co-expression network show potential for predicting drug responses. <i>F1000Research</i> , 2018, 7, 1906.	0.8	3

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55	Data on quantification of signaling pathways activated by KIT and PDGFRA mutants. Data in Brief, 2016, 9, 828-838.	0.5	2
56	The soluble form of pan-RTK inhibitor and tumor suppressor LRIG1 mediates downregulation of AXL through direct protein-protein interaction in glioblastoma. Neuro-Oncology Advances, 2019, 1, vdz024.	0.4	2
57	A DNA Repair and Cell Cycle Gene Expression Signature in Pediatric High-Grade Gliomas: Prognostic and Therapeutic Value. Cancers, 2021, 13, 2252.	1.7	2
58	ORFhunter: An accurate approach to the automatic identification and annotation of open reading frames in human mRNA molecules. Software Impacts, 2022, 12, 100268.	0.8	2
59	Neural network data analysis for intracavity laser spectroscopy. , 2003, , .		0
60	Artificial Neural Network Modification of Simulation-Based Fitting: Application to a Protein-Lipid System.. ChemInform, 2004, 35, no.	0.1	0