Alexander E Pozhitkov

List of Publications by Year
in descending order

40 papers	893 citations	471509 17 h-index	477307 29 g-index
46 all docs	46 docs citations	46 times ranked	1327 citing authors

#	Article	IF	Citations
1	SUMOylation inhibition enhances dexamethasone sensitivity in multiple myeloma. Journal of Experimental and Clinical Cancer Research, 2022, 41, 8.	8.6	16
2	The City of Hope POSEIDON enterprise-wide platform for real-world data and evidence in cancer.. Journal of Clinical Oncology, 2021, 39, e18813-e18813.	1.6	2
3	A Non-genetic Mechanism Involving the Integrin Î²4/Paxillin Axis Contributes to Chemoresistance in Lung Cancer. IScience, 2020, 23, 101496.	4.1	27
4	Glucocorticoid receptor expression in multiple myeloma patients is a predictor of survival. Leukemia and Lymphoma, 2020, 61, 3493-3497.	1.3	4
5	Effects of selected deubiquitinating enzyme inhibitors on the proliferation and motility of lung cancer and mesothelioma cell lines. International Journal of Oncology, 2020, 57, 80-86.	3.3	1
6	Leflunomide regulates c-Myc expression in myeloma cells through PIM targeting. Blood Advances, 2019, 3, 1027-1032.	5.2	14
7	MiR-16 regulates crosstalk in NF-Î²B tolerogenic inflammatory signaling between myeloma cells and bone marrow macrophages. JCI Insight, 2019, 4, .	5.0	33
8	Cryptic sequence features in the active postmortem transcriptome. BMC Genomics, 2018, 19, 675.	2.8	4
9	Inhibiting crosstalk between MET signaling and mitochondrial dynamics and morphology: a novel therapeutic approach for lung cancer and mesothelioma. Cancer Biology and Therapy, 2018, 19, 1023-1032.	3.4	12
10	Differential Response of MET inhibition by Glesatinib (MGCD265) and Sitravatinib (MGCD516) in Nonâ€small Cell Lung Cancer and Malignant Mesothelioma. FASEB Journal, 2018, 32, 835.9.	0.5	0
11	Tracing the dynamics of gene transcripts after organismal death. Open Biology, 2017, 7, 160267.	3.6	72
12	Datasets used to discover the microbial signatures of oral dysbiosis, periodontitis and edentulism in humans. Data in Brief, 2017, 10, 30-32.	1.0	1
13	Gene Meter: Accurate abundance calculations of gene expression. Communicative and Integrative Biology, 2017, 10, e1329785.	1.4	4
14	Gene expression in the twilight of death. BioEssays, 2017, 39, 1700066.	2.5	8
15	Microbial signatures of oral dysbiosis, periodontitis and edentulism revealed by Gene Meter methodology. Journal of Microbiological Methods, 2016, 131, 85-101.	1.6	13
16	Interruption of Electrical Conductivity of Titanium Dental Implants Suggests a Path Towards Elimination Of Corrosion. PLoS ONE, 2015, 10, e0140393.	2.5	21
17	A Revised Design for Microarray Experiments to Account for Experimental Noise and Uncertainty of Probe Response. PLoS ONE, 2014, 9, e91295.	2.5	15
18	Distinctive thanatomicrobiome signatures found in the blood and internal organs of humans. Journal of Microbiological Methods, 2014, 106, 1-7.	1.6	108

#	ARTICLE	IF	CITATIONS
19	Physico-chemical foundations underpinning microarray and next-generation sequencing experiments. Nucleic Acids Research, 2013, 41, 2779-2796.	14.5	49
20	Transcriptome changes after genome‑wide admixture in invasive sculpins (*Cottus*). Molecular Ecology, 2012, 21, 4797-4810.	3.9	21
21	Scanner calibration revisited. BMC Bioinformatics, 2010, 11, 361.	2.6	2
22	Generation, analysis and functional annotation of expressed sequence tags from the sheepshead minnow (Cyprinodon variegatus). BMC Genomics, 2010, 11, S4.	2.8	3
23	Linking probe thermodynamics to microarray quantification. Physical Biology, 2010, 7, 048001.	1.8	3
24	Functioning *in situ*: gene expression in *Methylotenera mobilis* in its native environment as assessed through transcriptomics. ISME Journal, 2010, 4, 388-398.	9.8	38
25	Constructing a fish metabolic network model. Genome Biology, 2010, 11, R115.	9.6	47
26	Beyond Affymetrix arrays: expanding the set of known hybridization isotherms and observing pre-wash signal intensities. Nucleic Acids Research, 2010, 38, e28-e28.	14.5	25
27	Use of hidden correlations in short oligonucleotide array data are insufficient for accurate quantification of nucleic acid targets in complex target mixtures. Journal of Microbiological Methods, 2009, 76, 188-195.	1.6	6
28	Concentration dependency of nonequilibrium thermal dissociation curves in complex target samples. Journal of Microbiological Methods, 2008, 74, 82-88.	1.6	8
29	Simultaneous quantification of multiple nucleic acid targets in complex rRNA mixtures using high density microarrays and nonspecific hybridization as a source of information. Journal of Microbiological Methods, 2008, 75, 92-102.	1.6	9
30	A competitive hybridization model predicts probe signal intensity on high density DNA microarrays. Nucleic Acids Research, 2008, 36, 6585-6591.	14.5	19
31	Oligonucleotide microarrays: widely applied poorly understood. Briefings in Functional Genomics & Proteomics, 2007, 6, 141-148.	3.8	58
32	Revision of the nonequilibrium thermal dissociation and stringent washing approaches for identification of mixed nucleic acid targets by microarrays. Nucleic Acids Research, 2007, 35, e70.	14.5	27
33	Development of a statistically robust quantification method for microorganisms in mixtures using oligonucleotide microarrays. Journal of Microbiological Methods, 2007, 70, 292-300.	1.6	14
34	Comment on "Discrimination of Shifts in a Soil Microbial Community Associated with TNT-Contamination Using a Functional ANOVA of 16S rRNA Hybridized to Oligonucleotide Microarrays". Environmental Science & Technology, 2007, 41, 1797-1798.	10.0	7
35	Tests of rRNA hybridization to microarrays suggest that hybridization characteristics of oligonucleotide probes for species discrimination cannot be predicted. Nucleic Acids Research, 2006, 34, e66-e66.	14.5	101
36	An algorithm for the determination and quantification of components of nucleic acid mixtures based on single sequencing reactions. BMC Bioinformatics, 2005, 6, 281.	2.6	6

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37	Evaluation of Gel-Pad Oligonucleotide Microarray Technology by Using Artificial Neural Networks. Applied and Environmental Microbiology, 2005, 71, 8663-8676.	3.1	26
38	Effect of high pressure and reversed micelles on the fluorescent proteins. Biochimica Et Biophysica Acta - General Subjects, 2003, 1622, 192-195.	2.4	20
39	An algorithm and program for finding sequence specific oligonucleotide probes for species identification. BMC Bioinformatics, 2002, 3, 9.	2.6	26
40	Synthesis and X-ray structures of barium complexes with pivaloyltrifluoroacetone, [Ba(pta)2(H2O)] and Ba4(pta)8. Polyhedron, 1996, 15, 1731-1735.	2.2	12