

# Sven Nelander

## List of Publications by Year in descending order

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Version: 2024-02-01

72  
papers

9,914  
citations

186265

28  
h-index

88630

70  
g-index

81  
all docs

81  
docs citations

81  
times ranked

20107  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Cancer Genome Atlas Pan-Cancer analysis project. <i>Nature Genetics</i> , 2013, 45, 1113-1120.	21.4	6,265
2	Subtype-specific genomic alterations define new targets for soft-tissue sarcoma therapy. <i>Nature Genetics</i> , 2010, 42, 715-721.	21.4	642
3	Origin of the U87MG glioma cell line: Good news and bad news. <i>Science Translational Medicine</i> , 2016, 8, 354re3.	12.4	313
4	The Human Glioblastoma Cell Culture Resource: Validated Cell Models Representing All Molecular Subtypes. <i>EBioMedicine</i> , 2015, 2, 1351-1363.	6.1	228
5	Simultaneous Multiplexed Measurement of RNA and Proteins in Single Cells. <i>Cell Reports</i> , 2016, 14, 380-389.	6.4	200
6	Models from experiments: combinatorial drug perturbations of cancer cells. <i>Molecular Systems Biology</i> , 2008, 4, 216.	7.2	168
7	Genome-wide association study identifies multiple susceptibility loci for multiple myeloma. <i>Nature Communications</i> , 2016, 7, 12050.	12.8	146
8	Clinically significant copy number alterations and complex rearrangements of <i>MYB</i> and <i>NFIB</i> in head and neck adenoid cystic carcinoma. <i>Genes Chromosomes and Cancer</i> , 2012, 51, 805-817.	2.8	136
9	Identification of Human Intestinal Alkaline Sphingomyelinase as a Novel Ecto-enzyme Related to the Nucleotide Phosphodiesterase Family. <i>Journal of Biological Chemistry</i> , 2003, 278, 38528-38536.	3.4	122
10	Variants in <i>ELL2</i> influencing immunoglobulin levels associate with multiple myeloma. <i>Nature Communications</i> , 2015, 6, 7213.	12.8	101
11	The Impact of Phenotypic Switching on Glioblastoma Growth and Invasion. <i>PLoS Computational Biology</i> , 2012, 8, e1002556.	3.2	90
12	Network modeling of the transcriptional effects of copy number aberrations in glioblastoma. <i>Molecular Systems Biology</i> , 2011, 7, 486.	7.2	80
13	Off-target effects dominate a large-scale RNAi screen for modulators of the TGF- $\beta$ 2 pathway and reveal microRNA regulation of <i>TGFBR2</i> . <i>Silence: A Journal of RNA Regulation</i> , 2011, 2, 3.	8.1	78
14	Human Mesenchymal glioblastomas are characterized by an increased immune cell presence compared to Proneural and Classical tumors. <i>Oncolmmunology</i> , 2019, 8, e1655360.	4.6	76
15	Gene expression analysis suggests that <i>EBF-1</i> and <i>PPAR<math>\gamma</math>32</i> induce adipogenesis of NIH-3T3 cells with similar efficiency and kinetics. <i>Physiological Genomics</i> , 2005, 23, 206-216.	2.3	53
16	Astrocytes enhance glioblastoma growth. <i>Glia</i> , 2020, 68, 316-327.	4.9	47
17	Glioblastoma Cell Malignancy and Drug Sensitivity Are Affected by the Cell of Origin. <i>Cell Reports</i> , 2017, 18, 977-990.	6.4	46
18	<i>ABCG2</i> regulates self-renewal and stem cell marker expression but not tumorigenicity or radiation resistance of glioma cells. <i>Scientific Reports</i> , 2016, 6, 25956.	3.3	45

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19	Safe and Effective Treatment of Experimental Neuroblastoma and Glioblastoma Using Systemically Delivered Triple MicroRNA-Detargeted Oncolytic Semliki Forest Virus. <i>Clinical Cancer Research</i> , 2017, 23, 1519-1530.	7.0	43
20	Integrative discovery of treatments for high-risk neuroblastoma. <i>Nature Communications</i> , 2020, 11, 71.	12.8	42
21	A Patient-Derived Cell Atlas Informs Precision Targeting of Glioblastoma. <i>Cell Reports</i> , 2020, 32, 107897.	6.4	41
22	NF1 regulates mesenchymal glioblastoma plasticity and aggressiveness through the AP-1 transcription factor FOSL1. <i>ELife</i> , 2021, 10, .	6.0	41
23	Functional association networks as priors for gene regulatory network inference. <i>Bioinformatics</i> , 2014, 30, i130-i138.	4.1	39
24	Bridging the gaps in systems biology. <i>Molecular Genetics and Genomics</i> , 2014, 289, 727-734.	2.1	38
25	Predictive screening for regulators of conserved functional gene modules (gene batteries) in mammals. <i>BMC Genomics</i> , 2005, 6, 68.	2.8	35
26	Batch-normalization of cerebellar and medulloblastoma gene expression datasets utilizing empirically defined negative control genes. <i>Bioinformatics</i> , 2019, 35, 3357-3364.	4.1	34
27	Prediction of Cell Type-Specific Gene Modules: Identification and Initial Characterization of a Core Set of Smooth Muscle-Specific Genes. <i>Genome Research</i> , 2003, 13, 1838-54.	5.5	32
28	Integrin $\alpha 10$ , a Novel Therapeutic Target in Glioblastoma, Regulates Cell Migration, Proliferation, and Survival. <i>Cancers</i> , 2019, 11, 587.	3.7	32
29	Glioma-derived plasminogen activator inhibitor-1 (PAI-1) regulates the recruitment of LRP1 positive mast cells. <i>Oncotarget</i> , 2015, 6, 23647-23661.	1.8	31
30	Epigenetic Regulation of ZBTB18 Promotes Glioblastoma Progression. <i>Molecular Cancer Research</i> , 2017, 15, 998-1011.	3.4	30
31	DNA microarray study on gene expression profiles in co-cultured endothelial and smooth muscle cells in response to 4- and 24-h shear stress. <i>Molecular and Cellular Biochemistry</i> , 2006, 281, 1-15.	3.1	28
32	High levels of WNT-5A in human glioma correlate with increased presence of tumor-associated microglia/monocytes. <i>Experimental Cell Research</i> , 2015, 339, 280-288.	2.6	28
33	Monotherapy efficacy of blood-brain barrier permeable small molecule reactivators of protein phosphatase 2A in glioblastoma. <i>Brain Communications</i> , 2020, 2, fcaa002.	3.3	28
34	Travelling wave analysis of a mathematical model of glioblastoma growth. <i>Mathematical Biosciences</i> , 2016, 276, 75-81.	1.9	26
35	BET and Aurora Kinase A inhibitors synergize against MYCN-positive human glioblastoma cells. <i>Cell Death and Disease</i> , 2019, 10, 881.	6.3	26
36	Selective Calcium Sensitivity in Immature Glioma Cancer Stem Cells. <i>PLoS ONE</i> , 2014, 9, e115698.	2.5	23

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37	Primary glioblastoma cells for precision medicine: a quantitative portrait of genomic (in)stability during the first 30 passages. <i>Neuro-Oncology</i> , 2018, 20, 1080-1091.	1.2	22
38	Integrative Modeling Reveals Annexin A2-mediated Epigenetic Control of Mesenchymal Glioblastoma. <i>EBioMedicine</i> , 2016, 12, 72-85.	6.1	21
39	Membrane-Depolarizing Channel Blockers Induce Selective Glioma Cell Death by Impairing Nutrient Transport and Unfolded Protein/Amino Acid Responses. <i>Cancer Research</i> , 2017, 77, 1741-1752.	0.9	21
40	c-Jun-N-terminal phosphorylation regulates DNMT1 expression and genome wide methylation in gliomas. <i>Oncotarget</i> , 2017, 8, 6940-6954.	1.8	21
41	Threshold-free high-power methods for the ontological analysis of genome-wide gene-expression studies. <i>Genome Biology</i> , 2007, 8, R74.	9.6	20
42	Comparative drug pair screening across multiple glioblastoma cell lines reveals novel drug-drug interactions. <i>Neuro-Oncology</i> , 2013, 15, 1469-1478.	1.2	19
43	LGR5 promotes tumorigenicity and invasion of glioblastoma stem-like cells and is a potential therapeutic target for a subset of glioblastoma patients. <i>Journal of Pathology</i> , 2019, 247, 228-240.	4.5	19
44	Modeling glioblastoma heterogeneity as a dynamic network of cell states. <i>Molecular Systems Biology</i> , 2021, 17, e10105.	7.2	19
45	Real-time evaluation of glioblastoma growth in patient-specific zebrafish xenografts. <i>Neuro-Oncology</i> , 2022, 24, 726-738.	1.2	19
46	Smooth Muscle Expression of Lipoma Preferred Partner Is Mediated by an Alternative Intronic Promoter That Is Regulated by Serum Response Factor/Myocardin. <i>Circulation Research</i> , 2008, 103, 61-69.	4.5	17
47	Avoiding pitfalls in L <sub>1</sub> -regularised inference of gene networks. <i>Molecular BioSystems</i> , 2015, 11, 287-296.	2.9	16
48	Efficient exploration of pan-cancer networks by generalized covariance selection and interactive web content. <i>Nucleic Acids Research</i> , 2015, 43, e98-e98.	14.5	16
49	Case-specific potentiation of glioblastoma drugs by pterostilbene. <i>Oncotarget</i> , 2016, 7, 73200-73215.	1.8	16
50	Do two mutually exclusive gene modules define the phenotypic diversity of mammalian smooth muscle?. <i>Molecular Genetics and Genomics</i> , 2008, 280, 127-37.	2.1	15
51	An improved method for detecting and delineating genomic regions with altered gene expression in cancer. <i>Genome Biology</i> , 2008, 9, R13.	9.6	15
52	Comparative epigenetic analysis of tumour initiating cells and syngeneic EPSC-derived neural stem cells in glioblastoma. <i>Nature Communications</i> , 2021, 12, 6130.	12.8	14
53	High sensitivity isoelectric focusing to establish a signaling biomarker for the diagnosis of human colorectal cancer. <i>BMC Cancer</i> , 2016, 16, 683.	2.6	12
54	Uncovering cancer gene regulation by accurate regulatory network inference from uninformative data. <i>Npj Systems Biology and Applications</i> , 2020, 6, 37.	3.0	12

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55	Neural Cell Adhesion Molecule-Deficient $\beta$ -Cell Tumorigenesis Results in Diminished Extracellular Matrix Molecule Expression and Tumour Cell-Matrix Adhesion. <i>Tumor Biology</i> , 2005, 26, 103-112.	1.8	8
56	Growth-Inhibitory Activity of Bone Morphogenetic Protein 4 in Human Glioblastoma Cell Lines Is Heterogeneous and Dependent on Reduced SOX2 Expression. <i>Molecular Cancer Research</i> , 2020, 18, 981-991.	3.4	8
57	HCN Channel Activity Balances Quiescence and Proliferation in Neural Stem Cells and Is a Selective Target for Neuroprotection During Cancer Treatment. <i>Molecular Cancer Research</i> , 2020, 18, 1522-1533.	3.4	6
58	Searching for Synergies: Matrix Algebraic Approaches for Efficient Pair Screening. <i>PLoS ONE</i> , 2013, 8, e68598.	2.5	6
59	Fast and accurate gene regulatory network inference by normalized least squares regression. <i>Bioinformatics</i> , 2022, 38, 2263-2268.	4.1	6
60	Autocrine signaling can explain the emergence of Allee effects in cancer cell populations. <i>PLoS Computational Biology</i> , 2022, 18, e1009844.	3.2	6
61	MYCMI-7: A Small MYC-Binding Compound that Inhibits MYC: MAX Interaction and Tumor Growth in a MYC-Dependent Manner. <i>Cancer Research Communications</i> , 2022, 2, 182-201.	1.7	6
62	Single-cell RNAseq and longitudinal proteomic analysis of a novel semi-spontaneous urothelial cancer model reveals tumor cell heterogeneity and pretumoral urine protein alterations. <i>PLoS ONE</i> , 2021, 16, e0253178.	2.5	4
63	p53-Mediated Radiosensitization of 177Lu-DOTATATE in Neuroblastoma Tumor Spheroids. <i>Biomolecules</i> , 2021, 11, 1695.	4.0	4
64	FC1000: normalized gene expression changes of systematically perturbed human cells. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2017, 16, 217-242.	0.6	3
65	Inferring the experimental design for accurate gene regulatory network inference. <i>Bioinformatics</i> , 2021, 37, 3553-3559.	4.1	3
66	Loss of Conservation of Graph Centralities in Reverse-engineered Transcriptional Regulatory Networks. <i>Methodology and Computing in Applied Probability</i> , 2017, 19, 1089-1105.	1.2	1
67	Increasing the accuracy of glioblastoma subtypes: Factoring in the tumor's cell of origin. <i>Molecular and Cellular Oncology</i> , 2019, 6, 1302907.	0.7	1
68	System-Scale Network Modeling of Cancer Using EPoC. <i>Advances in Experimental Medicine and Biology</i> , 2012, 736, 617-643.	1.6	1
69	Identification of Biomarkers and Signatures in Protein Data. , 2015, , .		0
70	Image-Based Detection of Patient-Specific Drug-Induced Cell-Cycle Effects in Glioblastoma. <i>SLAS Discovery</i> , 2018, 23, 1030-1039.	2.7	0
71	Graph Centrality Based Prediction of Cancer Genes. <i>Springer Proceedings in Mathematics and Statistics</i> , 2016, , 275-311.	0.2	0
72	Optimal Sparsity Selection Based on an Information Criterion for Accurate Gene Regulatory Network Inference. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	0