Gregg B Morin

List of Publications by Year in descending order

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Version: 2024-02-01

91 papers

20,218 citations

76326 40 h-index 91 g-index

102 all docs $\begin{array}{c} 102 \\ \\ \text{docs citations} \end{array}$

102 times ranked 25346 citing authors

#	Article	IF	CITATIONS
1	Characterization of a small molecule inhibitor of disulfide reductases that induces oxidative stress and lethality in lung cancer cells. Cell Reports, 2022, 38, 110343.	6.4	14
2	Proteomic analysis of archival breast cancer clinical specimens identifies biological subtypes with distinct survival outcomes. Nature Communications, 2022, 13, 896.	12.8	46
3	Chloroquine treatment induces secretion of autophagy-related proteins and inclusion of Atg8-family proteins in distinct extracellular vesicle populations. Autophagy, 2022, 18, 2547-2560.	9.1	18
4	Elucidating the importance and regulation of key enhancers for human MEIS1 expression. Leukemia, 2022, 36, 1980-1989.	7.2	6
5	Whole-proteome analysis of mesonephric-derived cancers describes new potential biomarkers. Human Pathology, 2021, 108, 1-11.	2.0	8
6	Protein feature analysis of heat shock induced ubiquitination sites reveals preferential modification site localization. Journal of Proteomics, 2021, 239, 104182.	2.4	3
7	Proteomic Screens for Suppressors of Anoikis Identify IL1RAP as a Promising Surface Target in Ewing Sarcoma. Cancer Discovery, 2021, 11, 2884-2903.	9.4	51
8	De novo and cell line models of human mammary cell transformation reveal an essential role for Yb-1 in multiple stages of human breast cancer. Cell Death and Differentiation, 2021, , .	11.2	2
9	Multiomics Characterization of Low-Grade Serous Ovarian Carcinoma Identifies Potential Biomarkers of MEK Inhibitor Sensitivity and Therapeutic Vulnerability. Cancer Research, 2021, 81, 1681-1694.	0.9	19
10	Proteotranscriptomic classification and characterization of pancreatic neuroendocrine neoplasms. Cell Reports, 2021, 37, 109817.	6.4	14
11	Bottomâ€up proteomics of envelope proteins extracted from spinach chloroplast via high organic content CEâ€MS. Electrophoresis, 2020, 41, 370-378.	2.4	12
12	Proteomic analysis of transitional cell carcinoma–like variant of tubo-ovarian high-grade serous carcinoma. Human Pathology, 2020, 101, 40-52.	2.0	4
13	Arginine Depletion Therapy with ADI-PEG20 Limits Tumor Growth in Argininosuccinate Synthase–Deficient Ovarian Cancer, Including Small-Cell Carcinoma of the Ovary, Hypercalcemic Type. Clinical Cancer Research, 2020, 26, 4402-4413.	7.0	21
14	Dynamic pH barrage junction focusing of amino acids, peptides, and digested monoclonal antibodies in capillary electrophoresis–mass spectrometry. Electrophoresis, 2020, 41, 1832-1842.	2.4	12
15	Loss of m1acp3Î ⁻ Ribosomal RNA Modification Is a Major Feature of Cancer. Cell Reports, 2020, 31, 107611.	6.4	64
16	The Pathognomonic FOXL2 C134W Mutation Alters DNA-Binding Specificity. Cancer Research, 2020, 80, 3480-3491.	0.9	19
17	Complementary Methods for de Novo Monoclonal Antibody Sequencing to Achieve Complete Sequence Coverage. Journal of Proteome Research, 2020, 19, 2700-2707.	3.7	12
18	Re-expression of SMARCA4/BRG1 in small cell carcinoma of ovary, hypercalcemic type (SCCOHT) promotes an epithelial-like gene signature through an AP-1-dependent mechanism. ELife, 2020, 9, .	6.0	19

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19	The interaction between SPARC and GRP78 interferes with ER stress signaling and potentiates apoptosis via PERK/eIF2α and IRE1α/XBP-1 in colorectal cancer. Cell Death and Disease, 2019, 10, 504.	6.3	61
20	Response to Comment on "PP2A inhibition sensitizes cancer stem cells to ABL tyrosine kinase inhibitors in BCR-ABL ⁺ human leukemiaâ€. Science Translational Medicine, 2019, 11, .	12.4	3
21	The FUS-DDIT3 Interactome in Myxoid Liposarcoma. Neoplasia, 2019, 21, 740-751.	5.3	26
22	A Standardized and Reproducible Proteomics Protocol for Bottom-Up Quantitative Analysis of Protein Samples Using SP3 and Mass Spectrometry. Methods in Molecular Biology, 2019, 1959, 65-87.	0.9	25
23	BAP1 haploinsufficiency predicts a distinct immunogenic class of malignant peritoneal mesothelioma. Genome Medicine, 2019, 11, 8.	8.2	88
24	Class I <scp>HDAC</scp> inhibitors enhance <scp>YB</scp> â€1 acetylation and oxidative stress to block sarcoma metastasis. EMBO Reports, 2019, 20, e48375.	4.5	78
25	RawTools: Rapid and Dynamic Interrogation of Orbitrap Data Files for Mass Spectrometer System Management. Journal of Proteome Research, 2019, 18, 700-708.	3.7	20
26	Single-pot, solid-phase-enhanced sample preparation for proteomics experiments. Nature Protocols, 2019, 14, 68-85.	12.0	802
27	The SNAP25 Interactome in Ventromedial Caudate in Schizophrenia Includes the Mitochondrial Protein ARF1. Neuroscience, 2019, 420, 97-111.	2.3	10
28	Molecular characterization of <i>ERBB2</i> -amplified colorectal cancer identifies potential mechanisms of resistance to targeted therapies: a report of two instructive cases. Journal of Physical Education and Sports Management, 2018, 4, a002535.	1.2	16
29	Parsing and Quantification of Raw Orbitrap Mass Spectrometer Data Using RawQuant. Journal of Proteome Research, 2018, 17, 2237-2247.	3.7	10
30	PP2A inhibition sensitizes cancer stem cells to ABL tyrosine kinase inhibitors in BCR-ABL $<$ sup $>+sup>human leukemia. Science Translational Medicine, 2018, 10, .$	12.4	37
31	Extending the Compatibility of the SP3 Paramagnetic Bead Processing Approach for Proteomics. Journal of Proteome Research, 2018, 17, 1730-1740.	3.7	186
32	Using Public Data for Comparative Proteome Analysis in Precision Medicine Programs. Proteomics - Clinical Applications, 2018, 12, 1600179.	1.6	2
33	Histone Deacetylase Inhibitors Synergize with Catalytic Inhibitors of EZH2 to Exhibit Antitumor Activity in Small Cell Carcinoma of the Ovary, Hypercalcemic Type. Molecular Cancer Therapeutics, 2018, 17, 2767-2779.	4.1	50
34	Genome-wide discovery of somatic regulatory variants in diffuse large B-cell lymphoma. Nature Communications, 2018, 9, 4001.	12.8	102
35	Discovery of 3-Benzyl-1-(<i>trans</i> -4-((5-cyanopyridin-2-yl)amino)cyclohexyl)-1-arylurea Derivatives as Novel and Selective Cyclin-Dependent Kinase 12 (CDK12) Inhibitors. Journal of Medicinal Chemistry, 2018, 61, 7710-7728.	6.4	38
36	Investigating Acquisition Performance on the Orbitrap Fusion When Using Tandem MS/MS/MS Scanning with Isobaric Tags. Journal of Proteome Research, 2017, 16, 1839-1846.	3.7	20

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37	Evaluating the Characteristics of Reporter Ion Signal Acquired in the Orbitrap Analyzer for Isobaric Mass Tag Proteome Quantification Experiments. Journal of Proteome Research, 2017, 16, 1831-1838.	3.7	8
38	The histone methyltransferase <scp>EZH2</scp> is a therapeutic target in small cell carcinoma of the ovary, hypercalcaemic type. Journal of Pathology, 2017, 242, 371-383.	4. 5	78
39	CDK12 regulates alternative last exon mRNA splicing and promotes breast cancer cell invasion. Nucleic Acids Research, 2017, 45, 6698-6716.	14.5	114
40	CLK-dependent exon recognition and conjoined gene formation revealed with a novel small molecule inhibitor. Nature Communications, 2017, 8, 7.	12.8	108
41	Selective aggregation of the splicing factor Hsh155 suppresses splicing upon genotoxic stress. Journal of Cell Biology, 2017, 216, 4027-4040.	5.2	10
42	Hsp83 loss suppresses proteasomal activity resulting in an upregulation of caspase-dependent compensatory autophagy. Autophagy, 2017, 13, 1573-1589.	9.1	12
43	Quantitative Profiling of Single Formalin Fixed Tumour Sections: proteomics for translational research. Scientific Reports, 2016, 6, 34949.	3.3	100
44	Quantitative mass spectrometry reveals changes in SNAP-25 isoforms in schizophrenia. Schizophrenia Research, 2016, 177, 44-51.	2.0	17
45	Structures of the CDK12/CycK complex with AMP-PNP reveal a flexible C-terminal kinase extension important for ATP binding. Scientific Reports, 2015, 5, 17122.	3.3	30
46	Recurrent <i><scp>DICER1</scp></i> hotspot mutations in endometrial tumours and their impact on <scp>microRNA</scp> biogenesis. Journal of Pathology, 2015, 237, 215-225.	4.5	38
47	The <i>Drosophila</i> TIPE family member Sigmar interacts with the Ste20-like kinase Misshapen and modulates JNK signaling, cytoskeletal remodeling and autophagy. Biology Open, 2015, 4, 672-684.	1.2	10
48	Activation of an endogenous retrovirus-associated long non-coding RNA in human adenocarcinoma. Genome Medicine, 2015, 7, 22.	8.2	45
49	MEF2B mutations in non-Hodgkin lymphoma dysregulate cell migration by decreasing MEF2B target gene activation. Nature Communications, 2015, 6, 7953.	12.8	50
50	The Oncogenic Roles of DICER1 RNase IIIb Domain Mutations in Ovarian Sertoli-Leydig Cell Tumors. Neoplasia, 2015, 17, 650-660.	5.3	59
51	The 3′ Overhangs at Tetrahymena thermophila Telomeres Are Packaged by Four Proteins, Pot1a, Tpt1, Pat1, and Pat2. Eukaryotic Cell, 2014, 13, 240-245.	3.4	9
52	The <i>Drosophila</i> effector caspase Dcp-1 regulates mitochondrial dynamics and autophagic flux via SesB. Journal of Cell Biology, 2014, 205, 477-492.	5. 2	43
53	A transgenic mouse model demonstrating the oncogenic role of mutations in the polycomb-group gene EZH2 in lymphomagenesis. Blood, 2014, 123, 3914-3924.	1.4	69
54	Mutations in CIC and IDH1 cooperatively regulate 2-hydroxyglutarate levels and cell clonogenicity. Oncotarget, 2014, 5, 7960-7979.	1.8	35

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55	Novel mRNA isoforms and mutations of uridine monophosphate synthetase and 5-fluorouracil resistance in colorectal cancer. Pharmacogenomics Journal, 2013, 13, 148-158.	2.0	29
56	Cancerâ€associated somatic <i><scp>DICER1</scp></i> hotspot mutations cause defective <scp>miRNA</scp> processing and reverseâ€strand expression bias to predominantly mature 3p strands through loss of 5p strand cleavage. Journal of Pathology, 2013, 229, 400-409.	4.5	135
57	Interaction of Cyclin-Dependent Kinase 12/CrkRS with Cyclin K1 Is Required for the Phosphorylation of the C-Terminal Domain of RNA Polymerase II. Molecular and Cellular Biology, 2012, 32, 4691-4704.	2.3	93
58	Recurrent Somatic <i>DICER1</i> Mutations in Nonepithelial Ovarian Cancers. New England Journal of Medicine, 2012, 366, 234-242.	27.0	401
59	A tripartite complex composed of ETV6-NTRK3, IRS1 and IGF1R is required for ETV6-NTRK3-mediated membrane localization and transformation. Oncogene, 2012, 31, 1334-1340.	5.9	19
60	The Mammalian Proteins MMS19, MIP18, and ANT2 Are Involved in Cytoplasmic Iron-Sulfur Cluster Protein Assembly. Journal of Biological Chemistry, 2012, 287, 43351-43358.	3.4	39
61	Concurrent <i>CIC</i> mutations, <i>IDH</i> mutations, and 1p/19q loss distinguish oligodendrogliomas from other cancers. Journal of Pathology, 2012, 226, 7-16.	4.5	272
62	Molecular and structural characterization of the <scp>SH</scp> 3 domain of <scp>AHI</scp> â€1 in regulation of cellular resistance of <scp>BCR</scp> â€ <scp>ABL</scp> ⁺ chronic myeloid leukemia cells to tyrosine kinase inhibitors. Proteomics, 2012, 12, 2094-2106.	2.2	8
63	The clonal and mutational evolution spectrum of primary triple-negative breast cancers. Nature, 2012, 486, 395-399.	27.8	1,778
64	Somatic mutations at EZH2 Y641 act dominantly through a mechanism of selectively altered PRC2 catalytic activity, to increase H3K27 trimethylation. Blood, 2011, 117, 2451-2459.	1.4	556
65	Subtypeâ€specific mutation of <i>PPP2R1A</i> in endometrial and ovarian carcinomas. Journal of Pathology, 2011, 223, 567-573.	4.5	114
66	The Pot1a-associated proteins Tpt1 and Pat1 coordinate telomere protection and length regulation in <i>Tetrahymena</i> . Molecular Biology of the Cell, 2011, 22, 4161-4170.	2.1	21
67	Mutated EZH2 Collaborates with Myc in Inducing Lymphoma in a Mouse Model. Blood, 2011, 118, 227-227.	1.4	3
68	Cytosolic protein interactions of the schizophrenia susceptibility gene dysbindin. Journal of Neurochemistry, 2010, 113, 1491-1503.	3.9	33
69	Alternative expression analysis by RNA sequencing. Nature Methods, 2010, 7, 843-847.	19.0	283
70	<i>ARID1A</i> Mutations in Endometriosis-Associated Ovarian Carcinomas. New England Journal of Medicine, 2010, 363, 1532-1543.	27.0	1,460
71	ALEXA: a microarray design platform for alternative expression analysis. Nature Methods, 2008, 5, 118-118.	19.0	19
72	Largeâ€scale mapping of human protein–protein interactions by mass spectrometry. Molecular Systems Biology, 2007, 3, 89.	7.2	850

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73	Modification of the Creator recombination system for proteomics applicationsimproved expression by addition of splice sites. BMC Biotechnology, 2006, 6, 13.	3.3	41
74	Effect of TERT over-expression on the long-term transplantation capacity of hematopoietic stem cells. Nature Medicine, 2003, 9, 369-371.	30.7	149
75	Telomerase is required to slow telomere shortening and extend replicative lifespan of HSCs during serial transplantation. Blood, 2003, 102, 517-520.	1.4	294
76	TANK2, a New TRF1-associated Poly(ADP-ribose) Polymerase, Causes Rapid Induction of Cell Death upon Overexpression. Journal of Biological Chemistry, 2001, 276, 35891-35899.	3.4	188
77	Telomerase reverse transcriptase gene is a direct target of c-Myc but is not functionally equivalent in cellular transformation. Oncogene, 1999, 18, 1219-1226.	5.9	368
78	Functional requirement of p23 and Hsp90 in telomerase complexes. Genes and Development, 1999, 13, 817-826.	5.9	475
79	Extension of Life-Span by Introduction of Telomerase into Normal Human Cells. Science, 1998, 279, 349-352.	12.6	4,536
80	Expression of mouse telomerase reverse transcriptase during development, differentiation and proliferation. Oncogene, 1998, 16, 1723-1730.	5.9	307
81	The implications of telomerase biochemistry for human disease. European Journal of Cancer, 1997, 33, 750-760.	2.8	24
82	Telomerase Catalytic Subunit Homologs from Fission Yeast and Human. Science, 1997, 277, 955-959.	12.6	2,138
83	Reconstitution of human telomerase with the template RNA component hTR and the catalytic protein subunit hTRT. Nature Genetics, 1997, 17, 498-502.	21.4	881
84	Telomere control of replicative lifespan. Experimental Gerontology, 1997, 32, 375-382.	2.8	30
85	Recognition of a chromosome truncation site associated with \hat{l}_{\pm} -thalassaemia by human telomerase. Nature, 1991, 353, 454-456.	27.8	215
86	ATetrahymenaintron nucleotide connected to the GTP/arginine site. Nucleic Acids Research, 1989, 17, 6969-6981.	14.5	11
87	The human telomere terminal transferase enzyme is a ribonucleoprotein that synthesizes TTAGGG repeats. Cell, 1989, 59, 521-529.	28.9	1,466
88	Mitochondrial telomeres: Surprising diversity of repeated telomeric DNA sequences among six species of Tetrahymena. Cell, 1988, 52, 367-374.	28.9	83
89	Phylogenetic relationships and altered genome structures amongTetrahymenamitochondrial DNAs. Nucleic Acids Research, 1988, 16, 327-346.	14.5	52
90	The telomeres of the linear mitochondrial DNA of tetrahymena thermophila consist of 53 bp tandem repeats. Cell, 1986, 46, 873-883.	28.9	79

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91	Syn and anti stereochemistry in elimination reactions producing acyclic conjugated thioesters. Journal of the American Chemical Society, 1983, 105, 5150-5151.	13.7	8