Irina Gromova

List of Publications by Year in descending order

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IDINA CROMOVA

#	Article	IF	CITATIONS
1	Highâ€ŧhroughput proteomics of breast cancer interstitial fluid: identification of tumor subtypeâ€specific serologically relevant biomarkers. Molecular Oncology, 2021, 15, 429-461.	2.1	19
2	Noninvasive profiling of serum cytokines in breast cancer patients and clinicopathological characteristics. Oncolmmunology, 2019, 8, e1537691.	2.1	27
3	Let-7 microRNA controls invasion-promoting lysosomal changes via the oncogenic transcription factor myeloid zinc finger-1. Oncogenesis, 2018, 7, 14.	2.1	20
4	<i>N</i> â€glycan signatures identified in tumor interstitial fluid and serum of breast cancer patients: association with tumor biology and clinical outcome. Molecular Oncology, 2018, 12, 972-990.	2.1	24
5	Selective Loss of PARG Restores PARylation and Counteracts PARP Inhibitor-Mediated Synthetic Lethality. Cancer Cell, 2018, 33, 1078-1093.e12.	7.7	238
6	Profiling of micro <scp>RNA</scp> s in tumor interstitial fluid of breast tumors – a novel resource to identify biomarkers for prognostic classification and detection of cancer. Molecular Oncology, 2017, 11, 220-234.	2.1	50
7	Gaining insights into cancer biology through exploration of the cancer secretome using proteomic and bioinformatic tools. Expert Review of Proteomics, 2017, 14, 1021-1035.	1.3	21
8	Identification of BLCAP as a novel STAT3 interaction partner in bladder cancer. PLoS ONE, 2017, 12, e0188827.	1.1	9
9	Characterization of the Tumor Secretome from Tumor Interstitial Fluid (TIF). Methods in Molecular Biology, 2016, 1459, 231-247.	0.4	7
10	DNA replication stress mediates APOBEC3 family mutagenesis in breast cancer. Genome Biology, 2016, 17, 185.	3.8	140
11	Cytokine profiling of tumor interstitial fluid of the breast and its relationship with lymphocyte infiltration and clinicopathological characteristics. Oncolmmunology, 2016, 5, e1248015.	2.1	48
12	High level PHGDH expression in breast is predominantly associated with keratin 5â€positive cell lineage independently of malignancy. Molecular Oncology, 2015, 9, 1636-1654.	2.1	34
13	Molecular and diagnostic features of apocrine breast lesions. Expert Review of Molecular Diagnostics, 2015, 15, 1011-1022.	1.5	14
14	Sensitive detection of lysosomal membrane permeabilization by lysosomal galectin puncta assay. Autophagy, 2015, 11, 1408-1424.	4.3	281
15	FABP7 and HMGCS2 Are Novel Protein Markers for Apocrine Differentiation Categorizing Apocrine Carcinoma of the Breast. PLoS ONE, 2014, 9, e112024.	1.1	23
16	Proteomic analysis of tissue samples in translational breast cancer research. Expert Review of Proteomics, 2014, 11, 285-302.	1.3	12
17	Decreased Camptothecin Sensitivity of the Stem-Cell-Like Fraction of Caco2 Cells Correlates with an Altered Phosphorylation Pattern of Topoisomerase I. PLoS ONE, 2014, 9, e99628.	1.1	22
18	Tumor interstitial fluid — A treasure trove of cancer biomarkers. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 2259-2270.	1.1	64

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19	TIMP-1 Increases Expression and Phosphorylation of Proteins Associated with Drug Resistance in Breast Cancer Cells. Journal of Proteome Research, 2013, 12, 4136-4151.	1.8	36
20	Proteomic Profiling of Triple-negative Breast Carcinomas in Combination With a Three-tier Orthogonal Technology Approach Identifies Mage-A4 as Potential Therapeutic Target in Estrogen Receptor Negative Breast Cancer. Molecular and Cellular Proteomics, 2013, 12, 381-394.	2.5	40
21	Immunoexpression Analysis and Prognostic Value of BLCAP in Breast Cancer. PLoS ONE, 2012, 7, e45967.	1.1	8
22	Human <i>BLCAP</i> transcript: new editing events in normal and cancerous tissues. International Journal of Cancer, 2010, 127, 127-137.	2.3	56
23	HERC2 coordinates ubiquitin-dependent assembly of DNA repair factors on damaged chromosomes. Nature Cell Biology, 2010, 12, 80-86.	4.6	239
24	Bladder Cancer-associated Protein, a Potential Prognostic Biomarker in Human Bladder Cancer. Molecular and Cellular Proteomics, 2010, 9, 161-177.	2.5	45
25	Upâ€regulated Proteins in the Fluid Bathing the Tumour Cell Microenvironment as Potential Serological Markers for Early Detection of Cancer of the Breast. Molecular Oncology, 2010, 4, 65-89.	2.1	88
26	Tissue proteomics of the human mammary gland: Towards an abridged definition of the molecular phenotypes underlying epithelial normalcy. Molecular Oncology, 2010, 4, 539-561.	2.1	24
27	Proteomic Profiling of Mammary Carcinomas Identifies C7orf24, a γ-Glutamyl Cyclotransferase, as a Potential Cancer Biomarker. Journal of Proteome Research, 2010, 9, 3941-3953.	1.8	55
28	Molecular characterization of apocrine carcinoma of the breast: Validation of an apocrine protein signature in a wellâ€defined cohort. Molecular Oncology, 2009, 3, 220-237.	2.1	43
29	Omicsâ€based profiling of carcinoma of the breast and matched regional lymph node metastasis. Proteomics, 2008, 8, 5038-5052.	1.3	26
30	Proteomic strategies in bladder cancer: From tissue to fluid and back. Proteomics - Clinical Applications, 2008, 2, 974-988.	0.8	11
31	A single lysis solution for the analysis of tissue samples by different proteomic technologies. Molecular Oncology, 2008, 2, 368-379.	2.1	31
32	A Combined Proteome and Ultrastructural Localization Analysis of 14-3-3 Proteins in Transformed Human Amnion (AMA) Cells. Molecular and Cellular Proteomics, 2008, 7, 1225-1240.	2.5	23
33	IKAP localizes to membrane ruffles with filamin A and regulates actin cytoskeleton organization and cell migration. Journal of Cell Science, 2008, 121, 854-864.	1.2	90
34	15-Prostaglandin Dehydrogenase Expression Alone or in Combination with ACSM1 Defines a Subgroup of the Apocrine Molecular Subtype of Breast Carcinoma. Molecular and Cellular Proteomics, 2008, 7, 1795-1809.	2.5	31
35	Human Xip1 (C2orf13) Is a Novel Regulator of Cellular Responses to DNA Strand Breaks. Journal of Biological Chemistry, 2007, 282, 19638-19643.	1.6	68
36	Characterization of breast precancerous lesions and myoepithelial hyperplasia in sclerosing adenosis with apocrine metaplasia. Molecular Oncology, 2007, 1, 97-119.	2.1	32

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37	Identification of a subset of breast carcinomas characterized by expression of cytokeratin 15: Relationship between CK15+ progenitor/amplified cells and preâ€malignant lesions and invasive disease. Molecular Oncology, 2007, 1, 321-349.	2.1	24
38	Protein Detection in Gels by Silver StainingA Procedure Compatible with Mass Spectrometry. , 2006, , 219-223.		23
39	Molecular pathology of breast apocrine carcinomas: A protein expression signature specific for benign apocrine metaplasia. FEBS Letters, 2006, 580, 2935-2944.	1.3	48
40	Proteomic Analysis by Two-Dimensional Polyacrylamide Gel Electrophoresis. , 2006, , 19-46.		1
41	Proteomic analysis of urinary fibrinogen degradation products in patients with urothelial carcinomas. Clinical Proteomics, 2006, 2, 45-65.	1.1	4
42	Apocrine Cysts of the Breast. Molecular and Cellular Proteomics, 2006, 5, 462-483.	2.5	33
43	Immediate and Delayed Effects of E-Cadherin Inhibition on Gene Regulation and Cell Motility in Human Epidermoid Carcinoma Cells. Molecular and Cellular Biology, 2005, 25, 9138-9150.	1.1	48
44	Identification of Extracellular and Intracellular Signaling Components of the Mammary Adipose Tissue and Its Interstitial Fluid in High Risk Breast Cancer Patients. Molecular and Cellular Proteomics, 2005, 4, 492-522.	2.5	200
45	Impact of proteomics on bladder cancer research. Pharmacogenomics, 2004, 5, 381-394.	0.6	37
46	Proteomic Characterization of the Interstitial Fluid Perfusing the Breast Tumor Microenvironment. Molecular and Cellular Proteomics, 2004, 3, 327-344.	2.5	278
47	Towards discovery-driven translational research in breast cancer. FEBS Journal, 2004, 272, 2-15.	2.2	45
48	Protein Profiling of the Human Epidermis from the Elderly Reveals Up-regulation of a Signature of Interferon-Î ³ -induced Polypeptides That Includes Manganese-superoxide Dismutase and the p85β Subunit of Phosphatidylinositol 3-Kinase. Molecular and Cellular Proteomics, 2003, 2, 70-84.	2.5	38
49	Integrating Proteomic and Functional Genomic Technologies in Discovery-driven Translational Breast Cancer Research. Molecular and Cellular Proteomics, 2003, 2, 369-377.	2.5	44
50	Proteomic Strategies to Reveal Tumor Heterogeneity among Urothelial Papillomas. Molecular and Cellular Proteomics, 2002, 1, 269-279.	2.5	56
51	Human proteomic databases: a powerful resource for functional genomics in health and disease. Progress in Biophysics and Molecular Biology, 2002, 80, 3-22.	1.4	43
52	bc10: A novel human bladder cancer-associated protein with a conserved genomic structure downregulated in invasive cancer. International Journal of Cancer, 2002, 98, 539-546.	2.3	48
53	A novel member of the glycosyltransferase family, ?3Gn-T2, highly downregulated in invasive human bladder transitional cell carcinomas. Molecular Carcinogenesis, 2001, 32, 61-72.	1.3	22
54	Gene expression profiling: monitoring transcription and translation products using DNA microarrays and proteomics. FEBS Letters, 2000, 480, 2-16.	1.3	291

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55	Identification of true differentially expressed mRNAs in a pair of human bladder transitional cell carcinomas using an improved differential display procedure. Electrophoresis, 1999, 20, 241-248.	1.3	42
56	A comprehensive protein ressource for the study of bladder cancer: http://biobase.dk/cgi-bin/celis. Electrophoresis, 1999, 20, 300-309.	1.3	68
57	Human and mouse proteomic databases: novel resources in the protein universe. FEBS Letters, 1998, 430, 64-72.	1.3	139
58	Human rab11a: transcription, chromosome mapping and effect on the expression levels of host GTP-binding proteins. FEBS Letters, 1998, 429, 359-364.	1.3	11
59	Characterization of DNA Topoisomerase Ilα/β Heterodimers in HeLa Cells. Biochemistry, 1998, 37, 16645-16652.	1.2	9
60	Human 2-D PAGE databases for proteome analysis in health and disease: http ://biobase.dk/cgi-bin/celis. FEBS Letters, 1996, 398, 129-134.	1.3	75
61	Specificity and Functional Significance of DNA Interaction with the Nuclear Matrix: New Approaches to Clarify the Old Questions. International Review of Cytology, 1996, 162B, 405-448.	6.2	81
62	The channels model of nuclear matrix structure. BioEssays, 1995, 17, 443-450.	1.2	78
63	Long-range Fragmentation of the Eukaryotic Genome by Exogenous and Endogenous Nucleases Proceeds in a Specific Fashion via Preferential DNA Cleavage at Matrix Attachment Sites. Journal of Biological Chemistry, 1995, 270, 18685-18690.	1.6	50
64	Characterization of an altered DNA catalysis of a camptothecin-resistant eukaryotic topoisomerase I. Nucleic Acids Research, 1993, 21, 593-600.	6.5	41
65	DNA-specific antiidiotypic antibodies in the sera of patients with autoimmune diseases. FEBS Letters, 1992, 314, 259-263.	1.3	38
66	Camptothecin inhibits both the cleavage and religation reactions of eukaryotic DNA topoisomerase I. Journal of Molecular Biology, 1992, 228, 1025-1030.	2.0	81
67	New technique for uncoupling the cleavage and religation reactions of Eukaryotic Topoisomerase I Journal of Molecular Biology, 1991, 222, 669-678.	2.0	150