

Victor Segura

List of Publications by Year in descending order

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94
papers

4,466
citations

94433

37
h-index

110387

64
g-index

95
all docs

95
docs citations

95
times ranked

9540
citing authors

#	ARTICLE	IF	CITATIONS
1	Characterization of complete lncRNAs transcriptome reveals the functional and clinical impact of lncRNAs in multiple myeloma. <i>Leukemia</i> , 2021, 35, 1438-1450.	7.2	28
2	Long Noncoding RNA EGOT Responds to Stress Signals to Regulate Cell Inflammation and Growth. <i>Journal of Immunology</i> , 2021, 206, 1932-1942.	0.8	6
3	Dynamic Intracellular Metabolic Cell Signaling Profiles During Ag-Dependent B-Cell Differentiation. <i>Frontiers in Immunology</i> , 2021, 12, 637832.	4.8	4
4	Whole exome sequencing characterization of individuals presenting extreme phenotypes of high and low risk of developing tobacco-induced lung adenocarcinoma. <i>Translational Lung Cancer Research</i> , 2021, 10, 1327-1337.	2.8	3
5	DeepMSPeptide: peptide detectability prediction using deep learning. <i>Bioinformatics</i> , 2020, 36, 1279-1280.	4.1	21
6	MiTPeptideDB: a proteogenomic resource for the discovery of novel peptides. <i>Bioinformatics</i> , 2020, 36, 205-211.	4.1	7
7	UPEFinder: A Bioinformatic Tool for the Study of Uncharacterized Proteins Based on Gene Expression Correlation and the PageRank Algorithm. <i>Journal of Proteome Research</i> , 2020, 19, 4795-4807.	3.7	3
8	Identification of Coding and Long Noncoding RNAs Differentially Expressed in Tumors and Preferentially Expressed in Healthy Tissues. <i>Cancer Research</i> , 2019, 79, 5167-5180.	0.9	38
9	Taking Advantage of the Selectivity of Histone Deacetylases and Phosphodiesterase Inhibitors to Design Better Therapeutic Strategies to Treat Alzheimer's Disease. <i>Frontiers in Aging Neuroscience</i> , 2019, 11, 149.	3.4	32
10	The Mechanism of Action of the Anti-CD38 Monoclonal Antibody Isatuximab in Multiple Myeloma. <i>Clinical Cancer Research</i> , 2019, 25, 3176-3187.	7.0	156
11	Epigenomic profiling of myelofibrosis reveals widespread DNA methylation changes in enhancer elements and <i>ZFP36L1</i> as a potential tumor suppressor gene that is epigenetically regulated. <i>Haematologica</i> , 2019, 104, 1572-1579.	3.5	16
12	Identification of mutations associated with acquired resistance to sunitinib in renal cell cancer. <i>International Journal of Cancer</i> , 2019, 145, 1991-2001.	5.1	32
13	Proteogenomics in the context of the Human Proteome Project (HPP). <i>Expert Review of Proteomics</i> , 2019, 16, 267-275.	3.0	6
14	Richter transformation driven by Epstein-Barr virus reactivation during therapy-related immunosuppression in chronic lymphocytic leukaemia. <i>Journal of Pathology</i> , 2018, 245, 61-73.	4.5	24
15	The regulon of the RNA chaperone CspA and its auto-regulation in <i>Staphylococcus aureus</i> . <i>Nucleic Acids Research</i> , 2018, 46, 1345-1361.	14.5	44
16	Methylation changes and pathways affected in preterm birth: a role for <i>SLC6A3</i> in neurodevelopment. <i>Epigenomics</i> , 2018, 10, 91-103.	2.1	13
17	In-Depth Proteomic Characterization of Classical and Non-Classical Monocyte Subsets. <i>Proteomes</i> , 2018, 6, 8.	3.5	18
18	Deregulation of <i>linc-PINT</i> in acute lymphoblastic leukemia is implicated in abnormal proliferation of leukemic cells. <i>Oncotarget</i> , 2018, 9, 12842-12852.	1.8	43

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19	Strategies to design clinical studies to identify predictive biomarkers in cancer research. <i>Cancer Treatment Reviews</i> , 2017, 53, 79-97.	7.7	80
20	X-box Binding Protein 1 Regulates Unfolded Protein, Acute-Phase, and DNA Damage Responses During Regeneration of Mouse Liver. <i>Gastroenterology</i> , 2017, 152, 1203-1216.e15.	1.3	39
21	A new HDV mouse model identifies mitochondrial antiviral signaling protein (MAVS) as a key player in IFN- β induction. <i>Journal of Hepatology</i> , 2017, 67, 669-679.	3.7	47
22	Discovery of first-in-class reversible dual small molecule inhibitors against G9a and DNMTs in hematological malignancies. <i>Nature Communications</i> , 2017, 8, 15424.	12.8	109
23	Enhanced Missing Proteins Detection in NCI60 Cell Lines Using an Integrative Search Engine Approach. <i>Journal of Proteome Research</i> , 2017, 16, 4374-4390.	3.7	13
24	A First-in-Class Small-Molecule that Acts as a Dual Inhibitor of HDAC and PDE5 and that Rescues Hippocampal Synaptic Impairment in Alzheimer's Disease Mice. <i>Neuropsychopharmacology</i> , 2017, 42, 524-539.	5.4	86
25	Progress and pitfalls in finding the "missing proteins" from the human proteome map. <i>Expert Review of Proteomics</i> , 2017, 14, 9-14.	3.0	12
26	Progressive modulation of the human olfactory bulb transcriptome during Alzheimer's disease evolution: novel insights into the olfactory signaling across proteinopathies. <i>Oncotarget</i> , 2017, 8, 69663-69679.	1.8	36
27	Reversible dual inhibitor against G9a and DNMT1 improves human iPSC derivation enhancing MET and facilitating transcription factor engagement to the genome. <i>PLoS ONE</i> , 2017, 12, e0190275.	2.5	10
28	Homeobox NKX2-3 promotes marginal-zone lymphomagenesis by activating B-cell receptor signalling and shaping lymphocyte dynamics. <i>Nature Communications</i> , 2016, 7, 11889.	12.8	42
29	Detection of Missing Proteins Using the PRIDE Database as a Source of Mass Spectrometry Evidence. <i>Journal of Proteome Research</i> , 2016, 15, 4101-4115.	3.7	15
30	Proteogenomic Analysis of Single Amino Acid Polymorphisms in Cancer Research. <i>Advances in Experimental Medicine and Biology</i> , 2016, 926, 93-113.	1.6	7
31	Long noncoding RNA EGOT negatively affects the antiviral response and favors HCV replication. <i>EMBO Reports</i> , 2016, 17, 1013-1028.	4.5	109
32	Epigenetic alterations leading to TMPRSS4 promoter hypomethylation and protein overexpression predict poor prognosis in squamous lung cancer patients. <i>Oncotarget</i> , 2016, 7, 22752-22769.	1.8	29
33	Prediction of a Missing Protein Expression Map in the Context of the Human Proteome Project. <i>Journal of Proteome Research</i> , 2015, 14, 1350-1360.	3.7	18
34	Whole-epigenome analysis in multiple myeloma reveals DNA hypermethylation of B cell-specific enhancers. <i>Genome Research</i> , 2015, 25, 478-487.	5.5	118
35	Quest for Missing Proteins: Update 2015 on Chromosome-Centric Human Proteome Project. <i>Journal of Proteome Research</i> , 2015, 14, 3415-3431.	3.7	53
36	Virotherapy with a Semliki Forest Virus-Based Vector Encoding IL12 Synergizes with PD-1/PD-L1 Blockade. <i>Cancer Immunology Research</i> , 2015, 3, 449-454.	3.4	88

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37	Integration of Proteomics and Transcriptomics Data Sets for the Analysis of a Lymphoma B-Cell Line in the Context of the Chromosome-Centric Human Proteome Project. <i>Journal of Proteome Research</i> , 2015, 14, 3530-3540.	3.7	16
38	Genome Expression Profiling-Based Identification and Administration Efficacy of Host-Directed Antimicrobial Drugs against Respiratory Infection by Nontypeable <i>Haemophilus influenzae</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 7581-7592.	3.2	15
39	Proteogenomics Dashboard for the Human Proteome Project. <i>Journal of Proteome Research</i> , 2015, 14, 3738-3749.	3.7	11
40	Vitamin D-binding protein as a biomarker of active disease in acute intermittent porphyria. <i>Journal of Proteomics</i> , 2015, 127, 377-385.	2.4	3
41	Lineage-specific function of Engrailed-2 in the progression of chronic myelogenous leukemia to T-cell blast crisis. <i>Cell Cycle</i> , 2014, 13, 1717-1726.	2.6	7
42	Type I Interferon Regulates the Expression of Long Non-Coding RNAs. <i>Frontiers in Immunology</i> , 2014, 5, 548.	4.8	54
43	Genome-wide analysis of the human p53 transcriptional network unveils a lncRNA tumour suppressor signature. <i>Nature Communications</i> , 2014, 5, 5812.	12.8	172
44	A small noncoding RNA signature found in exosomes of GBM patient serum as a diagnostic tool. <i>Neuro-Oncology</i> , 2014, 16, 520-527.	1.2	298
45	Surfing Transcriptomic Landscapes. A Step beyond the Annotation of Chromosome 16 Proteome. <i>Journal of Proteome Research</i> , 2014, 13, 158-172.	3.7	26
46	Functional interpretation of microRNA-mRNA association in biological systems using R. <i>Computers in Biology and Medicine</i> , 2014, 44, 124-131.	7.0	6
47	Long Non-Coding RNA BST2/BISPR is Induced by IFN and Regulates the Expression of the Antiviral Factor Tetherin. <i>Frontiers in Immunology</i> , 2014, 5, 655.	4.8	92
48	Chromosome Transcriptome Profiling in the Context of High-Throughput Proteomics Studies. <i>Translational Bioinformatics</i> , 2014, , 19-40.	0.0	1
49	Splicing regulator SLU7 is essential for maintaining liver homeostasis. <i>Journal of Clinical Investigation</i> , 2014, 124, 2909-2920.	8.2	55
50	Abstract 1996: Inhibitor of differentiation-1 (Id1) expression deficiency in the tumor microenvironment impairs experimental hepatic metastasis of lung cancer. , 2014, , .		0
51	Whole-Genome Epigenomic Analysis in Multiple Myeloma Reveals DNA Hypermethylation of B-Cell Specific Enhancers. <i>Blood</i> , 2014, 124, 2032-2032.	1.4	0
52	Spanish Human Proteome Project: Dissection of Chromosome 16. <i>Journal of Proteome Research</i> , 2013, 12, 112-122.	3.7	17
53	Silica-induced Chronic Inflammation Promotes Lung Carcinogenesis in the Context of an Immunosuppressive Microenvironment. <i>Neoplasia</i> , 2013, 15, 913-918.	5.3	33
54	Cellular Plasticity Confers Migratory and Invasive Advantages to a Population of Glioblastoma-Initiating Cells that Infiltrate Peritumoral Tissue. <i>Stem Cells</i> , 2013, 31, 1075-1085.	3.2	83

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55	Base Pairing Interaction between 5â€™- and 3â€™-UTRs Controls icaR mRNA Translation in <i>Staphylococcus aureus</i> . <i>PLoS Genetics</i> , 2013, 9, e1004001.	3.5	123
56	Pint lincRNA connects the p53 pathway with epigenetic silencing by the Polycomb repressive complex 2. <i>Genome Biology</i> , 2013, 14, R104.	9.6	224
57	Germinal centre protein HGAL promotes lymphoid hyperplasia and amyloidosis via BCR-mediated Syk activation. <i>Nature Communications</i> , 2013, 4, 1338.	12.8	37
58	Unraveling a novel transcription factor code determining the human arterial-specific endothelial cell signature. <i>Blood</i> , 2013, 122, 3982-3992.	1.4	93
59	Aberrant DNA methylation profile of chronic and transformed classic Philadelphia-negative myeloproliferative neoplasms. <i>Haematologica</i> , 2013, 98, 1414-1420.	3.5	46
60	Smokers with CT Detected Emphysema and No Airway Obstruction Have Decreased Plasma Levels of EGF, IL-15, IL-8 and IL-1ra. <i>PLoS ONE</i> , 2013, 8, e60260.	2.5	9
61	Preclinical activity of LBH589 alone or in combination with chemotherapy in a xenogeneic mouse model of human acute lymphoblastic leukemia. <i>Leukemia</i> , 2012, 26, 1517-1526.	7.2	41
62	Expression of <i>MALT1</i> oncogene in hematopoietic stem/progenitor cells recapitulates the pathogenesis of human lymphoma in mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 10534-10539.	7.1	73
63	Prohibitin-1 deficiency promotes inflammation and increases sensitivity to liver injury. <i>Journal of Proteomics</i> , 2012, 75, 5783-5792.	2.4	23
64	TET2 Mutations Are Associated with Specific 5-Methylcytosine and 5-Hydroxymethylcytosine Profiles in Patients with Chronic Myelomonocytic Leukemia. <i>PLoS ONE</i> , 2012, 7, e31605.	2.5	70
65	Wavelet-based detection of transcriptional activity on a novel <i>Staphylococcus aureus</i> tiling microarray. <i>BMC Bioinformatics</i> , 2012, 13, 222.	2.6	3
66	Identification of Novel Deregulated RNA Metabolism-Related Genes in Non-Small Cell Lung Cancer. <i>PLoS ONE</i> , 2012, 7, e42086.	2.5	48
67	Atrial fibrillation in pigs induces left atrial endocardial transcriptional remodelling. <i>Thrombosis and Haemostasis</i> , 2012, 108, 742-749.	3.4	6
68	Receptor of Activated Protein C Promotes Metastasis and Correlates with Clinical Outcome in Lung Adenocarcinoma. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2012, 186, 96-105.	5.6	45
69	Differential expression of prostaglandin D2 synthase (PTGDS) in patients with attention deficitâ€“hyperactivity disorder and bipolar disorder. <i>Journal of Affective Disorders</i> , 2012, 138, 479-484.	4.1	20
70	Chronic stress and impaired glutamate function elicit a depressive-like phenotype and common changes in gene expression in the mouse frontal cortex. <i>European Neuropsychopharmacology</i> , 2011, 21, 23-32.	0.7	55
71	Blockade of the NFÎ±B pathway drives differentiating glioblastoma-initiating cells into senescence both in vitro and in vivo. <i>Oncogene</i> , 2011, 30, 3537-3548.	5.9	69
72	Genome-wide antisense transcription drives mRNA processing in bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 20172-20177.	7.1	231

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73	A signature of six genes highlights defects on cell growth and specific metabolic pathways in murine and human hepatocellular carcinoma. <i>Functional and Integrative Genomics</i> , 2011, 11, 419-429.	3.5	19
74	HSV-1 Cgal+ Infection Promotes Quaking RNA Binding Protein Production and Induces Nuclear-Cytoplasmic Shuttling of Quaking I-5 Isoform in Human Hepatoma Cells. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.009126.	3.8	22
75	HGAL-a Germinal Center Specific Protein, Enhances B-Cell Receptor Signaling by Activation of Syk, Leading to Follicular Lymphoproliferation. <i>Blood</i> , 2011, 118, 584-584.	1.4	1
76	Preclinical Activity of LBH589 Alone or in Combination with Chemotherapy in a Xenogeneic Mouse Model of Human Acute Lymphoblastic Leukemia. <i>Blood</i> , 2011, 118, 1520-1520.	1.4	0
77	Homeobox NKX2-3 Is Over-Expressed in Human B-Cell Lymphomas and Drives Marginal Zone B-Cell Lymphomagenesis in Mice. <i>Blood</i> , 2011, 118, 260-260.	1.4	0
78	VEGF elicits epithelial-mesenchymal transition (EMT) in prostate intraepithelial neoplasia (PIN)-like cells via an autocrine loop. <i>Experimental Cell Research</i> , 2010, 316, 554-567.	2.6	100
79	Molecular characterization of the GÎ³â€globinâ€tag transgenic mouse model of hormone refractory prostate cancer: Comparison to human prostate cancer. <i>Prostate</i> , 2010, 70, 630-645.	2.3	9
80	Prohibitin deficiency blocks proliferation and induces apoptosis in human hepatoma cells: Molecular mechanisms and functional implications. <i>Proteomics</i> , 2010, 10, 1609-1620.	2.2	55
81	Adenovirus VA RNA-derived miRNAs target cellular genes involved in cell growth, gene expression and DNA repair. <i>Nucleic Acids Research</i> , 2010, 38, 750-763.	14.5	210
82	Genome-Wide Proximal Promoter Analysis and Interpretation. <i>Methods in Molecular Biology</i> , 2010, 593, 157-174.	0.9	0
83	Wilms' Tumor 1 Gene Expression in Hepatocellular Carcinoma Promotes Cell Dedifferentiation and Resistance to Chemotherapy. <i>Cancer Research</i> , 2009, 69, 1358-1367.	0.9	46
84	Oncostatin M Enhances the Antiviral Effects of Type I Interferon and Activates Immunostimulatory Functions in Liver Epithelial Cells. <i>Journal of Virology</i> , 2009, 83, 3298-3311.	3.4	33
85	FactorY, a bioinformatic resource for genome-wide promoter analysis. <i>Computers in Biology and Medicine</i> , 2009, 39, 385-387.	7.0	10
86	Proteomic Analysis of ChemonaÃve Pediatric Osteosarcomas and Corresponding Normal Bone Reveals Multiple Altered Molecular Targets. <i>Journal of Proteome Research</i> , 2009, 8, 3882-3888.	3.7	36
87	Identification of TNF-Î± and MMP-9 as potential baseline predictive serum markers of sunitinib activity in patients with renal cell carcinoma using a human cytokine array. <i>British Journal of Cancer</i> , 2009, 101, 1876-1883.	6.4	79
88	SPACE: an algorithm to predict and quantify alternatively spliced isoforms using microarrays. <i>Genome Biology</i> , 2008, 9, R46.	9.6	26
89	Identification of a gene-pathway associated with non-alcoholic steatohepatitis. <i>Journal of Hepatology</i> , 2007, 46, 708-718.	3.7	52
90	Methylseleninic acid enhances the effect of etoposide to inhibit prostate cancer growth in vivo. <i>International Journal of Cancer</i> , 2007, 121, 1197-1204.	5.1	8

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91	GARBAN II: An integrative framework for extracting biological information from proteomic and genomic data. <i>Proteomics</i> , 2006, 6, S12-S15.	2.2	6
92	Correlation between Gene Expression and GO Semantic Similarity. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2005, 2, 330-338.	3.0	194
93	GARBAN: genomic analysis and rapid biological annotation of cDNA microarray and proteomic data. <i>Bioinformatics</i> , 2003, 19, 2158-2160.	4.1	27
94	Quantification of jiggle in real electromyographic signals. <i>Muscle and Nerve</i> , 2000, 23, 1022-1034.	2.2	22