Victor Trevino

List of Publications by Year in descending order

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279487 51492 9,039 101 23 86 citations h-index g-index papers 107 107 107 13844 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Generating human papillomavirus (HPV) reference databases to maximize genomic mapping. Archives of Virology, 2022, 167, 57-65.	0.9	О
2	Multiomics subtyping for clinically prognostic cancer subtypes and personalized therapy: A systematic review and meta-analysis. Genetics in Medicine, 2022, 24, 15-25.	1.1	5
3	Germline Variants in Cancer Genes from Young Breast Cancer Mexican Patients. Cancers, 2022, 14, 1647.	1.7	5
4	Multivariate genome-wide association study models to improve prediction of Crohn's disease risk and identification of potential novel variants. Computers in Biology and Medicine, 2022, 145, 105398.	3.9	4
5	A systematic review and functional bioinformatics analysis of genes associated with Crohn's disease identify more than 120 related genes. BMC Genomics, 2022, 23, 302.	1.2	7
6	The Enigmatic Aliphatic Acetogenins and Their Correlations With Lipids During Seed Germination and Leaf Development of Avocado (Persea americana Mill.). Frontiers in Plant Science, 2022, 13, 839326.	1.7	3
7	Characterizing genes associated with cancer using the CRISPR/Cas9 system: A systematic review of genes and methodological approaches. Gene, 2022, 833, 146595.	1.0	7
8	Identification of a Novel Pathogenic Rearrangement Variant of the APC Gene Associated with a Variable Spectrum of Familial Cancer. Diagnostics, $2021,11,411.$	1.3	3
9	Plasma and vacuolar membrane sphingolipidomes: composition and insights on the role of main molecular species. Plant Physiology, 2021, 186, 624-639.	2.3	15
10	Analysis of HPV Integrations in Mexican Pre-Tumoral Cervical Lesions Reveal Centromere-Enriched Breakpoints and Abundant Unspecific HPV Regions. International Journal of Molecular Sciences, 2021, 22, 3242.	1.8	7
11	Improvement of serum lipid parameters in consumers of Mexican Wagyu ross beef: A randomized controlled trial. Journal of Food Science, 2021, 86, 2713-2726.	1.5	3
12	Robust Discovery of Mild Cognitive Impairment Subtypes and Their Risk of Alzheimer's Disease Conversion Using Unsupervised Machine Learning and Gaussian Mixture Modeling. Current Alzheimer Research, 2021, 18, 595-606.	0.7	9
13	Dynamic landscape of chromatin accessibility and transcriptomic changes during differentiation of human embryonic stem cells into dopaminergic neurons. Scientific Reports, 2021, 11, 16977.	1.6	11
14	Chemosensitivity analysis and study of gene resistance on tumors and cancer stem cell isolates from patients with colorectal cancer. Molecular Medicine Reports, 2021, 24, .	1.1	2
15	Identification and analysis of 35 genes associated with vitamin D deficiency: A systematic review to identify genetic variants. Journal of Steroid Biochemistry and Molecular Biology, 2020, 196, 105516.	1.2	22
16	Modeling and analysis of site-specific mutations in cancer identifies known plus putative novel hotspots and bias due to contextual sequences. Computational and Structural Biotechnology Journal, 2020, 18, 1664-1675.	1.9	5
17	Unsupervised Hierarchical Clustering of Pancreatic Adenocarcinoma Dataset from TCGA Defines a Mucin Expression Profile that Impacts Overall Survival. Cancers, 2020, 12, 3309.	1.7	17
18	Computational methods for detecting cancer hotspots. Computational and Structural Biotechnology Journal, 2020, 18, 3567-3576.	1.9	12

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19	HotSpotAnnotations—a database for hotspot mutations and annotations in cancer. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	1.4	21
20	A systematic review of genes affecting mitochondrial processes in cancer. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2020, 1866, 165846.	1.8	2
21	Transcriptomic and cellular analyses of CRISPR/Cas9-mediated edition of FASN show inhibition of aggressive characteristics in breast cancer cells. Biochemical and Biophysical Research Communications, 2020, 529, 321-327.	1.0	12
22	Improving predictive models for Alzheimer's disease using GWAS data by incorporating misclassified samples modeling. PLoS ONE, 2020, 15, e0232103.	1.1	20
23	Multiple HPV Infections and Viral Load Association in Persistent Cervical Lesions in Mexican Women. Viruses, 2020, 12, 380.	1.5	50
24	Integrative Analysis of Lipid Profiles in Plasma Allows Cardiometabolic Risk Factor Clustering in Children with Metabolically Unhealthy Obesity. Oxidative Medicine and Cellular Longevity, 2020, 2020, 1-15.	1.9	7
25	Immunotyping of tumorâ€ʻinfiltrating lymphocytes in tripleâ€ʻnegative breast cancer and genetic characterization. Oncology Letters, 2020, 20, 1-1.	0.8	12
26	Integrative genomic analysis identifies associations of molecular alterations to APOBEC and BRCA1/2 mutational signatures in breast cancer. Molecular Genetics & Enomic Medicine, 2019, 7, e810.	0.6	7
27	PubTerm: a web tool for organizing, annotating and curating genes, diseases, molecules and other concepts from PubMed records. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.4	19
28	TSH levels, overweight, BMI, and skin expression levels of DCT and CCBL2 genes are related to vitiligo treatment response with narrow band UVB phototherapy. Dermatologic Therapy, 2019, 32, e12893.	0.8	0
29	Lipid and cholesterol metabolism gene expression in pterygium fibroblasts: comparative analysis with adipocytes and other fibroblasts. Revista Mexicana De OftalmologÃa (English Edition), 2019, 93, .	0.0	0
30	Understanding the HPV integration and its progression to cervical cancer. Infection, Genetics and Evolution, 2018, 61, 134-144.	1.0	97
31	CAPN3, DCT, MLANA and TYRP1 are overexpressed in skin of vitiligo vulgaris Mexican patients. Experimental and Therapeutic Medicine, 2018, 15, 2804-2811.	0.8	14
32	Variable selection in Logistic regression model with genetic algorithm. Annals of Translational Medicine, 2018, 6, 45-45.	0.7	20
33	Evaluation of skin expression profiles of patients with vitiligo treated with narrow-band UVB therapy by targeted RNA-seq. Anais Brasileiros De Dermatologia, 2018, 93, 843-851.	0.5	11
34	Computational approaches for predicting key transcription factors in targeted cell reprogramming (Review). Molecular Medicine Reports, 2018, 18, 1225-1237.	1.1	7
35	Primary explant culture and collagen I substrate enhances corneal endothelial cell morphology. BMC Research Notes, 2018, 11, 48.	0.6	1
36	Radiogenomics analysis identifies correlations of digital mammography with clinical molecular signatures in breast cancer. PLoS ONE, 2018, 13, e0193871.	1.1	15

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37	Identification and Temporal Characterization of Features Associated with the Conversion from Mild Cognitive Impairment to Alzheimer's Disease. Current Alzheimer Research, 2018, 15, 751-763.	0.7	7
38	Identification of outcome-related driver mutations in cancer using conditional co-occurrence distributions. Scientific Reports, 2017, 7, 43350.	1.6	8
39	VALORATE: fast and accurate log-rank test in balanced and unbalanced comparisons of survival curves and cancer genomics. Bioinformatics, 2017, 33, 1900-1901.	1.8	9
40	Integrated transcriptomic and metabolomic analysis shows that disturbances in metabolism of tumor cells contribute to poor survival of RCC patients. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2017, 1863, 744-752.	1.8	16
41	A systematic review of genetic mutations in pulmonary arterial hypertension. BMC Medical Genetics, 2017, 18, 82.	2.1	59
42	Avocado fruit maturation and ripening: dynamics of aliphatic acetogenins and lipidomic profiles from mesocarp, idioblasts and seed. BMC Plant Biology, 2017, 17, 159.	1.6	34
43	Entrainment of Breast Cell Lines Results in Rhythmic Fluctuations of MicroRNAs. International Journal of Molecular Sciences, 2017, 18, 1499.	1.8	14
44	Metrics to estimate differential co-expression networks. BioData Mining, 2017, 10, 32.	2.2	21
45	A New Gene Expression Signature for Triple-Negative Breast Cancer using Frozen Fresh Tissue before Neoadjuvant chemotherapy. Molecular Medicine, 2017, 23, 101-111.	1.9	41
46	Profiles of Amino Acids and Acylcarnitines Related with Insecticide Exposure in Culex quinquefasciatus (Say). PLoS ONE, 2017, 12, e0169514.	1.1	7
47	A robust biomarker of differential correlations improves the diagnosis of cytologically indeterminate thyroid cancers. International Journal of Molecular Medicine, 2016, 37, 1355-1362.	1.8	21
48	Identification of circadian-related gene expression profiles in entrained breast cancer cell lines. Chronobiology International, 2016, 33, 392-405.	0.9	28
49	A Network Biology Approach Identifies Molecular Cross-Talk between Normal Prostate Epithelial and Prostate Carcinoma Cells. PLoS Computational Biology, 2016, 12, e1004884.	1.5	5
50	Efficient Gene Selection for Cancer Prognostic Biomarkers Using Swarm Optimization and Survival Analysis. Current Bioinformatics, 2016, 11, 310-323.	0.7	3
51	Integration and comparison of different genomic data for outcome prediction in cancer. BioData Mining, 2015, 8, 32.	2.2	14
52	Circulating microRNA expression profile in B-cell acute lymphoblastic leukemia. Cancer Biomarkers, 2015, 15, 299-310.	0.8	39
53	Reference values for amino acids and acylcarnitines in peripheral blood in Quarter horses and American Miniature horses. Acta Veterinaria Scandinavica, 2015, 57, 62.	0.5	7
54	GridMass: a fast two-dimensional feature detection method for LC/MS. Journal of Mass Spectrometry, 2015, 50, 165-174.	0.7	52

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55	Bilateral Image Subtraction and Multivariate Models for the Automated Triaging of Screening Mammograms. BioMed Research International, 2015, 2015, 1-12.	0.9	9
56	Multivariate Radiological-Based Models for the Prediction of Future Knee Pain: Data from the OAI. Computational and Mathematical Methods in Medicine, 2015, 2015, 1-10.	0.7	5
57	Improved Diagnostic Multimodal Biomarkers for Alzheimer's Disease and Mild Cognitive Impairment. BioMed Research International, 2015, 2015, 1-11.	0.9	16
58	P1-168: A time series analysis of ADNI data reveals novel Alzheimer's-dementia-associated factors., 2015, 11, P408-P409.		0
59	Identification of a multi-cancer gene expression biomarker for cancer clinical outcomes using a network-based algorithm. Scientific Reports, 2015, 5, 11966.	1.6	93
60	Molecular evolution and expression profile of the chemerine encoding gene RARRES2 in baboon and chimpanzee. Biological Research, 2015, 48, 31.	1.5	11
61	Knee osteoarthritis image registration: data from the Osteoarthritis Initiative. Proceedings of SPIE, 2015, , .	0.8	0
62	Comparison of gene expression patterns across 12 tumor types identifies a cancer supercluster characterized by TP53 mutations and cell cycle defects. Oncogene, 2015, 34, 2732-2740.	2.6	46
63	Magnetization-prepared rapid acquisition with gradient echo magnetic resonance imaging signal and texture features for the prediction of mild cognitive impairment to Alzheimer's disease progression. Journal of Medical Imaging, 2014, 1, 031005.	0.8	15
64	MRI signal and texture features for the prediction of MCI to Alzheimer's disease progression. , 2014, , .		1
65	Bilateral image subtraction features for multivariate automated classification of breast cancer risk., 2014,,.		2
66	Wide association study of radiological features that predict future knee OA pain: data from the OAI. Proceedings of SPIE, 2014, , .	0.8	4
67	SurvMicro: assessment of miRNA-based prognostic signatures for cancer clinical outcomes by multivariate survival analysis. Bioinformatics, 2014, 30, 1630-1632.	1.8	46
68	Landscape of genomic alterations in cervical carcinomas. Nature, 2014, 506, 371-375.	13.7	708
69	Knee Osteoarthritis pain prediction from X-ray imaging: Data from Osteoarthritis Initiative. , 2014, , .		4
70	Osteoarthritis pain prediction using X-ray features: data from OAI. Osteoarthritis and Cartilage, 2014, 22, S275-S276.	0.6	1
71	IC-P-081: T2 AND PROTON DENSITY SIGNAL- AND TEXTURE-RELATED FEATURES FOR THE PREDICTION OF MCI TO ALZHEIMER'S DISEASE PROGRESSION. , 2014, 10, P45-P46.		0
72	P3-210: T2 AND PROTON DENSITY SIGNAL- AND TEXTURE-RELATED FEATURES FOR THE PREDICTION OF MCI TO ALZHEIMER'S DISEASE PROGRESSION. , 2014, 10, P707-P708.		0

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73	Radiological Pain Predictors in Knee Osteoarthritis, a Four Feature Selection Comparison: Data from the OAI. Lecture Notes in Computer Science, 2014, , 351-360.	1.0	1
74	Differential expression of miRâ€1, miRâ€125b and miRâ€191 in breast cancer tissue. Asia-Pacific Journal of Clinical Oncology, 2013, 9, 53-59.	0.7	60
75	Modelling gene expression profiles related to prostate tumor progression using binary states. Theoretical Biology and Medical Modelling, 2013, 10, 37.	2.1	4
76	Inferring tumour purity and stromal and immune cell admixture from expression data. Nature Communications, 2013, 4, 2612.	5.8	5,788
77	Improved multimodal biomarkers for Alzheimer's disease and mild cognitive impairment diagnosis: data from ADNI. Proceedings of SPIE, 2013, , .	0.8	2
78	Local image registration a comparison for bilateral registration mammography., 2013,,.		4
79	Predictive features of breast cancer on Mexican screening mammography patients. , 2013, , .		7
80	SurvExpress: An Online Biomarker Validation Tool and Database for Cancer Gene Expression Data Using Survival Analysis. PLoS ONE, 2013, 8, e74250.	1.1	646
81	Identification and Characterization of microRNAS from Entamoeba histolytica HM1-IMSS. PLoS ONE, 2013, 8, e68202.	1.1	18
82	Abstract 4604: Landscape of human and viral genomic alterations in cervical carcinomas, 2013, , .		0
83	COMPADRE: an R and web resource for pathway activity analysis by component decompositions. Bioinformatics, 2012, 28, 2701-2702.	1.8	9
84	Can T2 relaxation be used to predict koos other symptoms? - data from the osteoarthritis initiative. Osteoarthritis and Cartilage, 2012, 20, S208-S209.	0.6	2
85	Analysis of Normal-Tumour Tissue Interaction in Tumours: Prediction of Prostate Cancer Features from the Molecular Profile of Adjacent Normal Cells. PLoS ONE, 2011, 6, e16492.	1.1	17
86	420 ADVANCED MRI-BASED MEASUREMENTS AS SURROGATE MARKERS OF KOOS PAIN AND KOOS OTHER KNEE SYMPTOMS: DATA FROM THE OSTEOARTHRITIS INITIATIVE. Osteoarthritis and Cartilage, 2010, 18, \$187.	0.6	1
87	High-throughput profiling of the humoral immune responses against thirteen human papillomavirus types by proteome microarrays. Virology, 2010, 405, 31-40.	1.1	34
88	Compact cancer biomarkers discovery using a swarm intelligence feature selection algorithm. Computational Biology and Chemistry, 2010, 34, 244-250.	1.1	41
89	Simplified amplified-fragment length polymorphism method for genotyping Mycobacterium tuberculosis isolates. Journal of Microbiological Methods, 2009, 78, 331-338.	0.7	3
90	Metabolomic analysis of human vitreous humor differentiates ocular inflammatory disease. Molecular Vision, 2009, 15, 1210-7.	1.1	47

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91	Models and computational strategies linking physiological response to molecular networks from large-scale data. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2008, 366, 3067-3089.	1.6	11
92	DNA Microarrays: a Powerful Genomic Tool for Biomedical and Clinical Research. Molecular Medicine, 2007, 13, 527-541.	1.9	205
93	Synovial fluid leukocyte apoptosis is inhibited in patients with very early rheumatoid arthritis. Arthritis Research and Therapy, 2006, 8, R120.	1.6	80
94	Identification of VDR-Responsive Gene Signatures in Breast Cancer Cells. Oncology, 2006, 71, 111-123.	0.9	41
95	GALGO: an R package for multivariate variable selection using genetic algorithms. Bioinformatics, 2006, 22, 1154-1156.	1.8	136
96	Analysis of host response to bacterial infection using error model based gene expression microarray experiments. Nucleic Acids Research, 2005, 33, 2352-2353.	6.5	4
97	Analysis of host response to bacterial infection using error model based gene expression microarray experiments. Nucleic Acids Research, 2005, 33, e53-e53.	6.5	8
98	Making Sense of Molecular Signatures in The Immune System. Combinatorial Chemistry and High Throughput Screening, 2004, 7, 231-238.	0.6	4
99	Transcription unit conservation in the three domains of life: a perspective from Escherichia coli. Trends in Genetics, 2001, 17, 175-177.	2.9	46
100	Incorporating Breast Asymmetry Studies into CADx Systems., 0, , .		1
101	Under-Updated Particle Swarm Optimization for Small Feature Selection Subsets from Large-Scale Datasets., 0, , .		o