# Victor Trevino

List of Publications by Year
in descending order

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|---|---|---|---|
| 101<br>papers | 9,039<br>citations | 279798<br>23<br>h-index | 51608<br>86<br>g-index |
| 107<br>all docs | 107<br>docs citations | 107<br>times ranked | 13844<br>citing authors |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 1 | Generating human papillomavirus (HPV) reference databases to maximize genomic mapping. Archives of Virology, 2022, 167, 57-65. | 2.1 | 0 |
| 2 | Multiomics subtyping for clinically prognostic cancer subtypes and personalized therapy: A systematic review and meta-analysis. Genetics in Medicine, 2022, 24, 15-25. | 2.4 | 5 |
| 3 | Germline Variants in Cancer Genes from Young Breast Cancer Mexican Patients. Cancers, 2022, 14, 1647. | 3.7 | 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. | 7.0 | 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. | 2.8 | 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. | 3.6 | 3 |
| 7 | Characterizing genes associated with cancer using the CRISPR/Cas9 system: A systematic review of genes and methodological approaches. Gene, 2022, 833, 146595. | 2.2 | 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. | 2.6 | 3 |
| 9 | Plasma and vacuolar membrane sphingolipidomes: composition and insights on the role of main molecular species. Plant Physiology, 2021, 186, 624-639. | 4.8 | 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. | 4.1 | 7 |
| 11 | Improvement of serum lipid parameters in consumers of Mexican Wagyu-Cross beef: A randomized controlled trial. Journal of Food Science, 2021, 86, 2713-2726. | 3.1 | 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. | 1.4 | 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. | 3.3 | 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, . | 2.4 | 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. | 2.5 | 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. | 4.1 | 5 |
| 17 | Unsupervised Hierarchical Clustering of Pancreatic Adenocarcinoma Dataset from TCGA Defines a Mucin Expression Profile that Impacts Overall Survival. Cancers, 2020, 12, 3309. | 3.7 | 17 |
| 18 | Computational methods for detecting cancer hotspots. Computational and Structural Biotechnology Journal, 2020, 18, 3567-3576. | 4.1 | 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, . | 3.0 | 21 |
| 20 | A systematic review of genes affecting mitochondrial processes in cancer. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2020, 1866, 165846. | 3.8 | 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. | 2.1 | 12 |
| 22 | Improving predictive models for Alzheimer's disease using GWAS data by incorporating misclassified samples modeling. PLoS ONE, 2020, 15, e0232103. | 2.5 | 20 |
| 23 | Multiple HPV Infections and Viral Load Association in Persistent Cervical Lesions in Mexican Women. Viruses, 2020, 12, 380. | 3.3 | 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. | 4.0 | 7 |
| 25 | Immunotyping of tumor-infiltrating lymphocytes in triple-negative breast cancer and genetic characterization. Oncology Letters, 2020, 20, 1-1. | 1.8 | 12 |
| 26 | Integrative genomic analysis identifies associations of molecular alterations to APOBEC and BRCA1/2 mutational signatures in breast cancer. Molecular Genetics &amp; Genomic Medicine, 2019, 7, e810. | 1.2 | 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, . | 3.0 | 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. | 1.7 | 0 |
| 29 | Lipid and cholesterol metabolism gene expression in pterygium fibroblasts: comparative analysis with adipocytes and other fibroblasts. Revista Mexicana De Oftalmología (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. | 2.3 | 97 |
| 31 | CAPN3, DCT, MLANA and TYRP1 are overexpressed in skin of vitiligo vulgaris Mexican patients. Experimental and Therapeutic Medicine, 2018, 15, 2804-2811. | 1.8 | 14 |
| 32 | Variable selection in Logistic regression model with genetic algorithm. Annals of Translational Medicine, 2018, 6, 45-45. | 1.7 | 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. | 1.1 | 11 |
| 34 | Computational approaches for predicting key transcription factors in targeted cell reprogramming (Review). Molecular Medicine Reports, 2018, 18, 1225-1237. | 2.4 | 7 |
| 35 | Primary explant culture and collagen I substrate enhances corneal endothelial cell morphology. BMC Research Notes, 2018, 11, 48. | 1.4 | 1 |
| 36 | Radiogenomics analysis identifies correlations of digital mammography with clinical molecular signatures in breast cancer. PLoS ONE, 2018, 13, e0193871. | 2.5 | 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. | 1.4 | 7 |
| 38 | Identification of outcome-related driver mutations in cancer using conditional co-occurrence distributions. Scientific Reports, 2017, 7, 43350. | 3.3 | 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. | 4.1 | 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. | 3.8 | 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. | 3.6 | 34 |
| 43 | Entrainment of Breast Cell Lines Results in Rhythmic Fluctuations of MicroRNAs. International Journal of Molecular Sciences, 2017, 18, 1499. | 4.1 | 14 |
| 44 | Metrics to estimate differential co-expression networks. BioData Mining, 2017, 10, 32. | 4.0 | 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. | 4.4 | 41 |
| 46 | Profiles of Amino Acids and Acylcarnitines Related with Insecticide Exposure in Culex quinquefasciatus (Say). PLoS ONE, 2017, 12, e0169514. | 2.5 | 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. | 4.0 | 21 |
| 48 | Identification of circadian-related gene expression profiles in entrained breast cancer cell lines. Chronobiology International, 2016, 33, 392-405. | 2.0 | 28 |
| 49 | A Network Biology Approach Identifies Molecular Cross-Talk between Normal Prostate Epithelial and Prostate Carcinoma Cells. PLoS Computational Biology, 2016, 12, e1004884. | 3.2 | 5 |
| 50 | Efficient Gene Selection for Cancer Prognostic Biomarkers Using Swarm Optimization and Survival Analysis. Current Bioinformatics, 2016, 11, 310-323. | 1.5 | 3 |
| 51 | Integration and comparison of different genomic data for outcome prediction in cancer. BioData Mining, 2015, 8, 32. | 4.0 | 14 |
| 52 | Circulating microRNA expression profile in B-cell acute lymphoblastic leukemia. Cancer Biomarkers, 2015, 15, 299-310. | 1.7 | 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. | 1.6 | 7 |
| 54 | GridMass: a fast two-dimensional feature detection method for LC/MS. Journal of Mass Spectrometry, 2015, 50, 165-174. | 1.6 | 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. | 1.9 | 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. | 1.3 | 5 |
| 57 | Improved Diagnostic Multimodal Biomarkers for Alzheimerâ€™s Disease and Mild Cognitive Impairment. BioMed Research International, 2015, 2015, 1-11. | 1.9 | 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. | 3.3 | 93 |
| 60 | Molecular evolution and expression profile of the chemerine encoding gene RARRES2 in baboon and chimpanzee. Biological Research, 2015, 48, 31. | 3.4 | 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. | 5.9 | 46 |
| 63 | Magnetization-prepared rapid acquisition with gradient echo magnetic resonance imaging signal and texture features for the prediction of mild cognitive impairment to Alzheimerâ€™s disease progression. Journal of Medical Imaging, 2014, 1, 031005. | 1.5 | 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. | 4.1 | 46 |
| 68 | Landscape of genomic alterations in cervical carcinomas. Nature, 2014, 506, 371-375. | 27.8 | 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. | 1.3 | 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. | 1.3 | 1 |
| 74 | Differential expression of miRâ€21, miRâ€125b and miRâ€191 in breast cancer tissue. Asia-Pacific Journal of Clinical Oncology, 2013, 9, 53-59. | 1.1 | 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. | 12.8 | 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. | 2.5 | 646 |
| 81 | Identification and Characterization of microRNAS from Entamoeba histolytica HM1-IMSS. PLoS ONE, 2013, 8, e68202. | 2.5 | 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. | 4.1 | 9 |
| 84 | Can T2 relaxation be used to predict koos other symptoms? - data from the osteoarthritis initiative. Osteoarthritis and Cartilage, 2012, 20, S208-S209. | 1.3 | 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. | 2.5 | 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, S187. | 1.3 | 1 |
| 87 | High-throughput profiling of the humoral immune responses against thirteen human papillomavirus types by proteome microarrays. Virology, 2010, 405, 31-40. | 2.4 | 34 |
| 88 | Compact cancer biomarkers discovery using a swarm intelligence feature selection algorithm. Computational Biology and Chemistry, 2010, 34, 244-250. | 2.3 | 41 |
| 89 | Simplified amplified-fragment length polymorphism method for genotyping Mycobacterium tuberculosis isolates. Journal of Microbiological Methods, 2009, 78, 331-338. | 1.6 | 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. | 3.4 | 11 |
| 92 | DNA Microarrays: a Powerful Genomic Tool for Biomedical and Clinical Research. Molecular Medicine, 2007, 13, 527-541. | 4.4 | 205 |
| 93 | Synovial fluid leukocyte apoptosis is inhibited in patients with very early rheumatoid arthritis. Arthritis Research and Therapy, 2006, 8, R120. | 3.5 | 80 |
| 94 | Identification of VDR-Responsive Gene Signatures in Breast Cancer Cells. Oncology, 2006, 71, 111-123. | 1.9 | 41 |
| 95 | GALGO: an R package for multivariate variable selection using genetic algorithms. Bioinformatics, 2006, 22, 1154-1156. | 4.1 | 136 |
| 96 | Analysis of host response to bacterial infection using error model based gene expression microarray experiments. Nucleic Acids Research, 2005, 33, 2352-2353. | 14.5 | 4 |
| 97 | Analysis of host response to bacterial infection using error model based gene expression microarray experiments. Nucleic Acids Research, 2005, 33, e53-e53. | 14.5 | 8 |
| 98 | Making Sense of Molecular Signatures in The Immune System. Combinatorial Chemistry and High Throughput Screening, 2004, 7, 231-238. | 1.1 | 4 |
| 99 | Transcription unit conservation in the three domains of life: a perspective from Escherichia coli. Trends in Genetics, 2001, 17, 175-177. | 6.7 | 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, , . | | 0 |