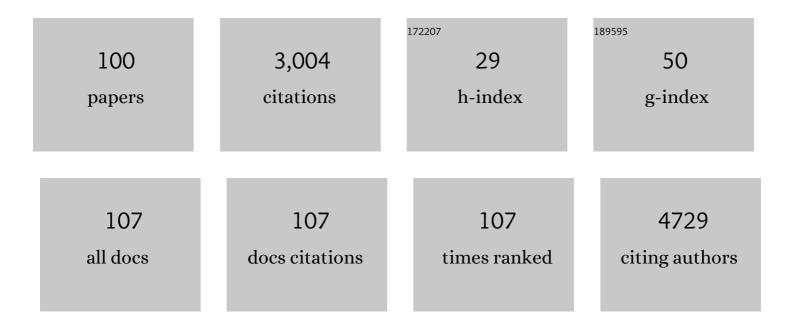
## Lorenzo L Pesce

List of Publications by Year in descending order

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LODENZO L DESCE

#	Article	IF	CITATIONS
1	Epithelial cell responses to rhinovirus identify an early-life–onset asthma phenotype in adults. Journal of Allergy and Clinical Immunology, 2022, 150, 604-611.	1.5	2
2	Comparative Effectiveness of Surgical Approaches for Lung Cancer. Journal of Surgical Research, 2021, 263, 274-284.	0.8	5
3	Genomic Context Differs Between Human Dilated Cardiomyopathy and Hypertrophic Cardiomyopathy. Journal of the American Heart Association, 2021, 10, e019944.	1.6	9
4	Patterns and persistence of SARS-CoV-2 IgG antibodies in Chicago to monitor COVID-19 exposure. JCI Insight, 2021, 6, .	2.3	24
5	COVID-19 mRNA Vaccination Generates Greater Immunoglobulin G Levels in Women Compared to Men. Journal of Infectious Diseases, 2021, 224, 793-797.	1.9	30
6	Genomic Autopsy of Sudden Deaths in Young Individuals. JAMA Cardiology, 2021, 6, 1247.	3.0	22
7	Bacterial Superinfection Pneumonia in Patients Mechanically Ventilated for COVID-19 Pneumonia. American Journal of Respiratory and Critical Care Medicine, 2021, 204, 921-932.	2.5	108
8	Personalized beyond Precision: Designing Unbiased Gold Standards to Improve Single-Subject Studies of Personal Genome Dynamics from Gene Products. Journal of Personalized Medicine, 2021, 11, 24.	1.1	3
9	The mechanism of cancer drug addiction in ALK-positive T-Cell lymphoma. Oncogene, 2020, 39, 2103-2117.	2.6	9
10	binomialRF: interpretable combinatoric efficiency of random forests to identify biomarker interactions. BMC Bioinformatics, 2020, 21, 374.	1.2	3
11	Pathogenic and Uncertain Genetic Variants Have Clinical Cardiac Correlates in Diverse Biobank Participants. Journal of the American Heart Association, 2020, 9, e013808.	1.6	27
12	Evaluating single-subject study methods for personal transcriptomic interpretations to advance precision medicine. BMC Medical Genomics, 2019, 12, 96.	0.7	8
13	A Single-Subject Method to Detect Pathways Enriched With Alternatively Spliced Genes. Frontiers in Genetics, 2019, 10, 414.	1.1	1
14	Developing a â€~personalome' for precision medicine: emerging methods that compute interpretable effect sizes from single-subject transcriptomes. Briefings in Bioinformatics, 2019, 20, 789-805.	3.2	24
15	Interpretation of 'Omics dynamics in a single subject using local estimates of dispersion between two transcriptomes. AMIA Annual Symposium proceedings, 2019, 2019, 582-591.	0.2	6
16	Convergent downstream candidate mechanisms of independent intergenic polymorphisms between co-classified diseases implicate epistasis among noncoding elements. , 2018, , .		1
17	Association of Cardiomyopathy With <i>MYBPC3</i> D389V and <i>MYBPC3<sup>Δ25bp</sup></i> Intronic Deletion in South Asian Descendants. JAMA Cardiology, 2018, 3, 481.	3.0	31
18	Testing for differentially expressed genetic pathways with single-subject N-of-1 data in the presence of inter-gene correlation. Statistical Methods in Medical Research, 2018, 27, 3797-3813.	0.7	13

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19	Novel disease syndromes unveiled by integrative multiscale network analysis of diseases sharing molecular effectors and comorbidities. BMC Medical Genomics, 2018, 11, 112.	0.7	8
20	Emergence of pathway-level composite biomarkers from converging gene set signals of heterogeneous transcriptomic responses. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2018, 23, 484-495.	0.7	7
21	Reading Between the Genes: Computational Models to Discover Function from Noncoding DNA. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2018, 23, 507-511.	0.7	0
22	kMEn: Analyzing noisy and bidirectional transcriptional pathway responses in single subjects. Journal of Biomedical Informatics, 2017, 66, 32-41.	2.5	15
23	A genome-by-environment interaction classifier for precision medicine: personal transcriptome response to rhinovirus identifies children prone to asthma exacerbations. Journal of the American Medical Informatics Association: JAMIA, 2017, 24, 1116-1126.	2.2	23
24	Experimental Modeling Supports a Role for MyBP-HL as a Novel Myofilament Component in Arrhythmia and Dilated Cardiomyopathy. Circulation, 2017, 136, 1477-1491.	1.6	34
25	N-of-1-pathways MixEnrich: advancing precision medicine via single-subject analysis in discovering dynamic changes of transcriptomes. BMC Medical Genomics, 2017, 10, 27.	0.7	29
26	Exploring Wound-Healing Genomic Machinery with a Network-Based Approach. Pharmaceuticals, 2017, 10, 55.	1.7	6
27	Network burst activity in hippocampal neuronal cultures: the role of synaptic and intrinsic currents. Journal of Neurophysiology, 2016, 115, 3073-3089.	0.9	66
28	Integrative genomics analyses unveil downstream biological effectors of disease-specific polymorphisms buried in intergenic regions. Npj Genomic Medicine, 2016, 1, .	1.7	19
29	Analysis of aggregated cell–cell statistical distances within pathways unveils therapeutic-resistance mechanisms in circulating tumor cells. Bioinformatics, 2016, 32, i80-i89.	1.8	15
30	Complex genetics of pulmonary diseases: lessons from genome-wide association studies and next-generation sequencing. Translational Research, 2016, 168, 22-39.	2.2	13
31	Multiscale Aspects of Generation of High-Gamma Activity during Seizures in Human Neocortex. ENeuro, 2016, 3, ENEURO.0141-15.2016.	0.9	30
32	eQTL networks unveil enriched mRNA master integrators downstream of complex disease-associated SNPs. Journal of Biomedical Informatics, 2015, 58, 226-234.	2.5	10
33	A functional genomic model for predicting prognosis in idiopathic pulmonary fibrosis. BMC Pulmonary Medicine, 2015, 15, 147.	0.8	42
34	Towards a PBMC "virogram assay―for precision medicine: Concordance between ex vivo and in vivo viral infection transcriptomes. Journal of Biomedical Informatics, 2015, 55, 94-103.	2.5	18
35	Estimating Screening-Mammography Receiver Operating Characteristic (ROC) Curves from Stratified Random Samples of Screening Mammograms. Academic Radiology, 2015, 22, 580-590.	1.3	1
36	Zodiac: A Comprehensive Depiction of Genetic Interactions in Cancer by Integrating TCGA Data. Journal of the National Cancer Institute, 2015, 107, .	3.0	27

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37	Dynamic changes of RNA-sequencing expression for precision medicine: N-of-1-pathways Mahalanobis distance within pathways of single subjects predicts breast cancer survival. Bioinformatics, 2015, 31, i293-i302.	1.8	30
38	Toward Networks from Spikes. Springer Series in Computational Neuroscience, 2015, , 277-292.	0.3	0
39	Supercomputing for the parallelization of whole genome analysis. Bioinformatics, 2014, 30, 1508-1513.	1.8	52
40	Targeted Analysis of Whole Genome Sequence Data to Diagnose Genetic Cardiomyopathy. Circulation: Cardiovascular Genetics, 2014, 7, 751-759.	5.1	53
41	â€~N-of-1- <i>pathways</i> ' unveils personal deregulated mechanisms from a single pair of RNA-Seq samples: towards precision medicine. Journal of the American Medical Informatics Association: JAMIA, 2014, 21, 1015-1025.	2.2	42
42	Concordance of deregulated mechanisms unveiled in underpowered experiments: PTBP1 knockdown case study. BMC Medical Genomics, 2014, 7, S1.	0.7	16
43	COPD Hospitalization Risk Increased with Distinct Patterns of Multiple Systems Comorbidities Unveiled by Network Modeling. AMIA Annual Symposium proceedings, 2014, 2014, 855-64.	0.2	1
44	Curation-free biomodules mechanisms in prostate cancer predict recurrent disease. BMC Medical Genomics, 2013, 6, S4.	0.7	9
45	Receiver-operating characteristic curves for somatic cell scores and California mastitis test in Valle del Belice dairy sheep. Veterinary Journal, 2013, 196, 528-532.	0.6	11
46	Interreader Scoring Variability in an Observer Study Using Dual-Modality Imaging for Breast Cancer Detection in Women with Dense Breasts. Academic Radiology, 2013, 20, 847-853.	1.3	17
47	Estimating Sensitivity and Specificity for Technology Assessment Based on Observer Studies. Academic Radiology, 2013, 20, 825-830.	1.3	2
48	Network models of genome-wide association studies uncover the topological centrality of protein interactions in complex diseases. Journal of the American Medical Informatics Association: JAMIA, 2013, 20, 619-629.	2.2	43
49	Large-Scale Modeling of Epileptic Seizures: Scaling Properties of Two Parallel Neuronal Network Simulation Algorithms. Computational and Mathematical Methods in Medicine, 2013, 2013, 1-10.	0.7	4
50	In Memory of Dr. Charles E. Metz. Japanese Journal of Radiological Technology, 2013, 69, 190-207.	0.0	0
51	Interpreting personal transcriptomes: personalized mechanism-scale profiling of RNA-seq data. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2013, , 159-70.	0.7	6
52	Variants Affecting Exon Skipping Contribute to Complex Traits. PLoS Genetics, 2012, 8, e1002998.	1.5	53
53	Granger causality analysis of state dependent functional connectivity of neurons in orofacial motor cortex during chewing and swallowing. , 2012, , .		2
54	Granger causality analysis of functional connectivity of spiking neurons in orofacial motor cortex during chewing and swallowing. , 2012, 2012, 4587-90.		3

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55	Translating Mendelian and complex inheritance of Alzheimer's disease genes for predicting unique personal genome variants. Journal of the American Medical Informatics Association: JAMIA, 2012, 19, 306-316.	2.2	18
56	Complex-disease networks of trait-associated single-nucleotide polymorphisms (SNPs) unveiled by information theory. Journal of the American Medical Informatics Association: JAMIA, 2012, 19, 295-305.	2.2	42
57	Improved detection of focal pneumonia by chest radiography with bone suppression imaging. European Radiology, 2012, 22, 2729-2735.	2.3	27
58	A scaling transformation for classifier output based on likelihood ratio: Applications to a CAD workstation for diagnosis of breast cancer. Medical Physics, 2012, 39, 2787-2804.	1.6	8
59	Risk Factors for Perioperative Acute Kidney Injury After Adult Cardiac Surgery: Role of Perioperative Management. Annals of Thoracic Surgery, 2012, 93, 584-591.	0.7	227
60	Single Sample Expression-Anchored Mechanisms Predict Survival in Head and Neck Cancer. PLoS Computational Biology, 2012, 8, e1002350.	1.5	75
61	Towards mechanism classifiers: expression-anchored Gene Ontology signature predicts clinical outcome in lung adenocarcinoma patients. AMIA Annual Symposium proceedings, 2012, 2012, 1040-9.	0.2	7
62	Semiparametric Estimation of the Relationship between ROC Operating Points and the Test-result Scale. Academic Radiology, 2011, 18, 1537-1548.	1.3	12
63	Non-contrast Enhanced MRI for Evaluation of Breast Lesions. Academic Radiology, 2011, 18, 1467-1474.	1.3	13
64	Fundamental limitations in developing computer-aided detection for mammography. Nuclear Instruments and Methods in Physics Research, Section A: Accelerators, Spectrometers, Detectors and Associated Equipment, 2011, 648, S251-S254.	0.7	0
65	Evaluation of Clinical Breast MR Imaging Performed with Prototype Computer-aided Diagnosis Breast MR Imaging Workstation: Reader Study. Radiology, 2011, 258, 696-704.	3.6	37
66	Small Lung Cancers: Improved Detection by Use of Bone Suppression Imaging—Comparison with Dual-Energy Subtraction Chest Radiography. Radiology, 2011, 261, 937-949.	3.6	51
67	Protein-network modeling of prostate cancer gene signatures reveals essential pathways in disease recurrence. Journal of the American Medical Informatics Association: JAMIA, 2011, 18, 392-402.	2.2	27
68	Repeatability and classifier bias in computer-aided diagnosis for breast ultrasound. Proceedings of SPIE, 2010, , .	0.8	0
69	Safety of Pregnancy After Primary Breast Carcinoma in Young Women: A Meta-Analysis to Overcome Bias of Healthy Mother Effect Studies. Obstetrical and Gynecological Survey, 2010, 65, 786-793.	0.2	69
70	Repeatability in computerâ€∎ided diagnosis: Application to breast cancer diagnosis on sonography. Medical Physics, 2010, 37, 2659-2669.	1.6	17
71		1.6	18
72	EuroSCORE Performance in Valve Surgery: A Meta-Analysis. Annals of Thoracic Surgery, 2010, 89, 787-793.e2.	0.7	91

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73	Network Modeling Identifies Molecular Functions Targeted by miR-204 to Suppress Head and Neck Tumor Metastasis. PLoS Computational Biology, 2010, 6, e1000730.	1.5	140
74	The Effect of Two Priors on Bayesian Estimation of "Proper―Binormal ROC Curves from Common and Degenerate Datasets. Academic Radiology, 2010, 17, 969-979.	1.3	3
75	On the Convexity of ROC Curves Estimated from Radiological Test Results. Academic Radiology, 2010, 17, 960-968.e4.	1.3	31
76	Stratified Sampling for Case Selection Criteria for Evaluating CAD. Lecture Notes in Computer Science, 2010, , 534-539.	1.0	0
77	SUâ€GCâ€Tâ€444: Normal Tissue Complication Probability (NTCP) Modeling Using Selfâ€Organizing Map (SOM). Medical Physics, 2010, 37, 3288-3288.	1.6	0
78	A study of the effect of noise injection on the training of artificial neural networks. , 2009, , .		23
79	Computer-aided Detection Evaluation Methods Are Not Created Equal. Radiology, 2009, 251, 634-636.	3.6	17
80	Experimental Design and Data Analysis in Receiver Operating Characteristic Studies: Lessons Learned from Reports in <i>Radiology</i> from 1997 to 2006. Radiology, 2009, 253, 822-830.	3.6	50
81	Breast US Computer-aided Diagnosis System: Robustness across Urban Populations in South Korea and the United States. Radiology, 2009, 253, 661-671.	3.6	24
82	Osteonecrosis of the jaw and use of bisphosphonates in adjuvant breast cancer treatment: a metanalysis. Breast Cancer Research and Treatment, 2009, 116, 433-439.	1.1	80
83	Comparison of spin echo T1-weighted sequences versus fast spin-echo proton density-weighted sequences for evaluation of meniscal tears at 1.5ÂT. Skeletal Radiology, 2009, 38, 21-29.	1.2	12
84	Noise injection for training artificial neural networks: A comparison with weight decay and early stopping. Medical Physics, 2009, 36, 4810-4818.	1.6	134
85	Comparison of ROC methods for partially paired data. , 2009, , .		1
86	Performance of Breast Ultrasound Computer-aided Diagnosis. Academic Radiology, 2008, 15, 1234-1245.	1.3	29
87	Performance of EuroSCORE in CABG and off-pump coronary artery bypass grafting: single institution experience and meta-analysis. European Heart Journal, 2008, 30, 297-304.	1.0	52
88	SUâ€GGâ€lâ€04: Gridâ€Computing for Optimization of CAD. Medical Physics, 2008, 35, 2643-2643.	1.6	0
89	Information theory applied to the sparse gene ontology annotation network to predict novel gene function. Bioinformatics, 2007, 23, i529-i538.	1.8	148
90	A Bayesian interpretation of the "proper" binormal ROC model using a uniform prior distribution for the area under the curve. , 2007, , .		2

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91	Imputation methods for temporal radiographic texture analysis in the detection of periprosthetic osteolysis. , 2007, , .		2
92	Usefulness of Temporal Subtraction Images for Identification of Interval Changes in Successive Whole-Body Bone Scans: JAFROC Analysis of Radiologists' Performance. Academic Radiology, 2007, 14, 959-966.	1.3	15
93	Reliable and Computationally Efficient Maximum-Likelihood Estimation of "Proper―Binormal ROC Curves. Academic Radiology, 2007, 14, 814-829.	1.3	112
94	The Structural Characterization of Oligonucleotide-Modified Gold Nanoparticle Networks Formed by DNA Hybridization. Journal of Physical Chemistry B, 2004, 108, 12375-12380.	1.2	145
95	Quantum dynamics simulation of the ultrafast photoionization of Li2. Journal of Chemical Physics, 2001, 114, 1259-1271.	1.2	31
96	Photodesorption of NO from a metal surface: quantum dynamical implications of a two-mode model. Chemical Physics, 2000, 251, 51-69.	0.9	28
97	Faber and Newton polynomial integrators for open-system density matrix propagation. Journal of Chemical Physics, 1999, 110, 5538-5547.	1.2	64
98	Variational wave packet method for dissipative photodesorption problems. Chemical Physics Letters, 1998, 288, 383-390.	1.2	17
99	The coupled channel density matrix method for open quantum systems: Formulation and application to the vibrational relaxation of molecules scattering from nonrigid surfaces. Journal of Chemical Physics, 1998, 108, 3045-3056.	1.2	24
100	"Free―nuclear density propagation in two dimensions the coupled-channel density matrix method and its application to inelastic molecule-surface scattering. Chemical Physics, 1997, 219, 43-55.	0.9	16