

Yolande Y F M Ramos

List of Publications by Year in descending order

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Version: 2024-02-01

66
papers

4,233
citations

218381

26
h-index

143772

57
g-index

74
all docs

74
docs citations

74
times ranked

6509
citing authors

#	ARTICLE	IF	CITATIONS
1	The cdk5/p35 kinase is essential for neurite outgrowth during neuronal differentiation.. Genes and Development, 1996, 10, 816-825.	2.7	562
2	Inactivation of the p53 pathway in retinoblastoma. Nature, 2006, 444, 61-66.	13.7	550
3	The transcriptional landscape of age in human peripheral blood. Nature Communications, 2015, 6, 8570.	5.8	533
4	Genome-wide analyses identify a role for SLC17A4 and AADAT in thyroid hormone regulation. Nature Communications, 2018, 9, 4455.	5.8	181
5	Comparative study of the p53-mdm2 and p53-MDMX interfaces. Oncogene, 1999, 18, 189-199.	2.6	172
6	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. Nature Communications, 2016, 7, 10494.	5.8	153
7	Genes Involved in the Osteoarthritis Process Identified through Genome Wide Expression Analysis in Articular Cartilage; the RAAK Study. PLoS ONE, 2014, 9, e103056.	1.1	142
8	Genome-wide assessment of differential roles for p300 and CBP in transcription regulation. Nucleic Acids Research, 2010, 38, 5396-5408.	6.5	133
9	RNA sequencing data integration reveals an miRNA interactome of osteoarthritis cartilage. Annals of the Rheumatic Diseases, 2019, 78, 270-277.	0.5	130
10	Isolation and Identification of the Human Homolog of a New p53-Binding Protein, Mdmx. Genomics, 1997, 43, 34-42.	1.3	125
11	Hdmx Protein Stability Is Regulated by the Ubiquitin Ligase Activity of Mdm2. Journal of Biological Chemistry, 2003, 278, 38315-38324.	1.6	124
12	Hdmx Stabilizes Mdm2 and p53. Journal of Biological Chemistry, 2000, 275, 28039-28044.	1.6	119
13	Assessment of Osteoarthritis Candidate Genes in a Meta-Analysis of Nine Genome-Wide Association Studies. Arthritis and Rheumatology, 2014, 66, 940-949.	2.9	108
14	A meta-analysis of genome-wide association studies identifies novel variants associated with osteoarthritis of the hip. Annals of the Rheumatic Diseases, 2014, 73, 2130-2136.	0.5	108
15	Knee and hip articular cartilage have distinct epigenomic landscapes: implications for future cartilage regeneration approaches. Annals of the Rheumatic Diseases, 2014, 73, 2208-2212.	0.5	96
16	Integrative epigenomics, transcriptomics and proteomics of patient chondrocytes reveal genes and pathways involved in osteoarthritis. Scientific Reports, 2017, 7, 8935.	1.6	90
17	Novel Genetic Variants for Cartilage Thickness and Hip Osteoarthritis. PLoS Genetics, 2016, 12, e1006260.	1.5	76
18	Underlying molecular mechanisms of <i>DIO2</i> susceptibility in symptomatic osteoarthritis. Annals of the Rheumatic Diseases, 2015, 74, 1571-1579.	0.5	75

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19	Genome-wide association and functional studies identify a role for matrix Gla protein in osteoarthritis of the hand. <i>Annals of the Rheumatic Diseases</i> , 2017, 76, 2046-2053.	0.5	64
20	Genes expressed in blood link osteoarthritis with apoptotic pathways. <i>Annals of the Rheumatic Diseases</i> , 2014, 73, 1844-1853.	0.5	61
21	Increased type II deiodinase protein in OA-affected cartilage and allelic imbalance of OA risk polymorphism rs225014 at DIO2 in human OA joint tissues. <i>Annals of the Rheumatic Diseases</i> , 2012, 71, 1254-1258.	0.5	53
22	Transcriptional Associations of Osteoarthritis-Mediated Loss of Epigenetic Control in Articular Cartilage. <i>Arthritis and Rheumatology</i> , 2015, 67, 2108-2116.	2.9	47
23	A gain of function mutation in <i>TNFRSF11B</i> encoding osteoprotegerin causes osteoarthritis with chondrocalcinosis. <i>Annals of the Rheumatic Diseases</i> , 2015, 74, 1756-1762.	0.5	44
24	RNA Sequencing Reveals Interacting Key Determinants of Osteoarthritis Acting in Subchondral Bone and Articular Cartilage: Identification of <i>IL11</i> and <i>CHADL</i> as Attractive Treatment Targets. <i>Arthritis and Rheumatology</i> , 2021, 73, 789-799.	2.9	38
25	Tissue-specific transcript annotation and expression profiling with complementary next-generation sequencing technologies. <i>Nucleic Acids Research</i> , 2010, 38, e165-e165.	6.5	32
26	The role of epigenetics in osteoarthritis: current perspective. <i>Current Opinion in Rheumatology</i> , 2017, 29, 119-129.	2.0	32
27	The effect of forced exercise on knee joints in <i>Dio2^{+/+}</i> mice: type II iodothyronine deiodinase-deficient mice are less prone to develop OA-like cartilage damage upon excessive mechanical stress. <i>Annals of the Rheumatic Diseases</i> , 2016, 75, 571-577.	0.5	31
28	Neo-cartilage engineered from primary chondrocytes is epigenetically similar to autologous cartilage, in contrast to using mesenchymal stem cells. <i>Osteoarthritis and Cartilage</i> , 2016, 24, 1423-1430.	0.6	29
29	Radiographic endophenotyping in hip osteoarthritis improves the precision of genetic association analysis. <i>Annals of the Rheumatic Diseases</i> , 2017, 76, 1199-1206.	0.5	29
30	Annotating Transcriptional Effects of Genetic Variants in Disease-Relevant Tissue: Transcriptome-Wide Allelic Imbalance in Osteoarthritic Cartilage. <i>Arthritis and Rheumatology</i> , 2019, 71, 561-570.	2.9	27
31	Elucidating Epigenetic Regulation by Identifying Functional <i>cis</i> -Acting Long Noncoding RNAs and Their Targets in Osteoarthritic Articular Cartilage. <i>Arthritis and Rheumatology</i> , 2020, 72, 1845-1854.	2.9	24
32	Identification and characterization of two consistent osteoarthritis subtypes by transcriptome and clinical data integration. <i>Rheumatology</i> , 2021, 60, 1166-1175.	0.9	23
33	Meta-analysis identifies loci affecting levels of the potential osteoarthritis biomarkers sCOMP and uCTX-II with genome wide significance. <i>Journal of Medical Genetics</i> , 2014, 51, 596-604.	1.5	18
34	Cartilage from human-induced pluripotent stem cells: comparison with neo-cartilage from chondrocytes and bone marrow mesenchymal stromal cells. <i>Cell and Tissue Research</i> , 2021, 386, 309-320.	1.5	17
35	Elucidating mechano-pathology of osteoarthritis: transcriptome-wide differences in mechanically stressed aged human cartilage explants. <i>Arthritis Research and Therapy</i> , 2021, 23, 215.	1.6	17
36	Implementation of Functional Genomics for Bench-to-Bedside Transition in Osteoarthritis. <i>Current Rheumatology Reports</i> , 2015, 17, 53.	2.1	15

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37	Increased WISP1 expression in human osteoarthritic articular cartilage is epigenetically regulated and decreases cartilage matrix production. <i>Rheumatology</i> , 2019, 58, 1065-1074.	0.9	13
38	High-impact <i>FN1</i> mutation decreases chondrogenic potential and affects cartilage deposition via decreased binding to collagen type II. <i>Science Advances</i> , 2021, 7, eabg8583.	4.7	13
39	The miRNA-mRNA interactome of murine induced pluripotent stem cell-derived chondrocytes in response to inflammatory cytokines. <i>FASEB Journal</i> , 2020, 34, 11546-11561.	0.2	12
40	Involvement of epigenetics in osteoarthritis. <i>Best Practice and Research in Clinical Rheumatology</i> , 2017, 31, 634-648.	1.4	11
41	Characterization of dynamic changes in Matrix Gla Protein (MGP) gene expression as function of genetic risk alleles, osteoarthritis relevant stimuli, and the vitamin K inhibitor warfarin. <i>Osteoarthritis and Cartilage</i> , 2021, 29, 1193-1202.	0.6	11
42	Cripto favors chondrocyte hypertrophy via <i>TGF-β2</i> <i>SMAD1/5</i> signaling during development of osteoarthritis. <i>Journal of Pathology</i> , 2021, 255, 330-342.	2.1	11
43	Translating genomics into mechanisms of disease: Osteoarthritis. <i>Best Practice and Research in Clinical Rheumatology</i> , 2015, 29, 683-691.	1.4	10
44	The role of <i>TNFRSF11B</i> in development of osteoarthritic cartilage. <i>Rheumatology</i> , 2022, 61, 856-864.	0.9	10
45	Human Osteochondral Explants: Reliable Biomimetic Models to Investigate Disease Mechanisms and Develop Personalized Treatments for Osteoarthritis. <i>Rheumatology and Therapy</i> , 2021, 8, 499-515.	1.1	9
46	Long non-coding RNA expression profiling of subchondral bone reveals <i>AC005165.1</i> modifying <i>FRZB</i> expression during osteoarthritis. <i>Rheumatology</i> , 2022, 61, 3023-3032.	0.9	9
47	A human in vitro 3D neo-cartilage model to explore the response of OA risk genes to hyper-physiological mechanical stress. <i>Osteoarthritis and Cartilage Open</i> , 2022, 4, 100231.	0.9	8
48	Capturing Essential Physiological Aspects of Interacting Cartilage and Bone Tissue with Osteoarthritis Pathophysiology: A Human Osteochondral Unit-on-a-Chip Model. <i>Advanced Materials Technologies</i> , 2022, 7, .	3.0	7
49	Associations between joint effusion in the knee and gene expression levels in the circulation: a meta-analysis. <i>F1000Research</i> , 2016, 5, 109.	0.8	6
50	Circulating MicroRNAs Highly Correlate to Expression of Cartilage Genes Potentially Reflecting OA Susceptibility—Towards Identification of Applicable Early OA Biomarkers. <i>Biomolecules</i> , 2021, 11, 1356.	1.8	4
51	Mutation in the <i>CCAL1</i> locus accounts for bidirectional process of human subchondral bone turnover and cartilage mineralization. <i>Rheumatology</i> , 2022, 62, 360-372.	0.9	4
52	Censoring exosomal crosstalk in osteoarthritis. <i>Nature Aging</i> , 2021, 1, 332-334.	5.3	3
53	MicroRNAs and Regulation of Autophagy in Chondrocytes. <i>Methods in Molecular Biology</i> , 2021, 2245, 179-194.	0.4	3
54	Identification and functional characterization of imbalanced osteoarthritis-associated fibronectin splice variants. <i>Rheumatology</i> , 2023, 62, 894-904.	0.9	3

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55	CpG sites of osteoarthritis susceptibility gene DIO2 are differentially methylated in arthritic compared to preserved cartilage. <i>Osteoarthritis and Cartilage</i> , 2012, 20, S196.	0.6	2
56	Aberrant Calreticulin Expression in Articular Cartilage of Dio2 Deficient Mice. <i>PLoS ONE</i> , 2016, 11, e0154999.	1.1	2
57	A gain of function mutation in TNFRSF11B causes osteoarthritis with chondrocalcinosis. <i>Osteoarthritis and Cartilage</i> , 2014, 22, S226.	0.6	1
58	Protocol for the Isolation of Intact Chondrons from Healthy and Osteoarthritic Human Articular Cartilage. <i>Methods in Molecular Biology</i> , 2021, 2245, 13-22.	0.4	1
59	353 GENOME WIDE EXPRESSION ANALYSIS OF OSTEOARTHRITIS AFFECTED AND PRESERVED CARTILAGE FROM JOINT REPLACEMENT SURGERY MATERIAL IN THE RAAK STUDY. <i>Osteoarthritis and Cartilage</i> , 2011, 19, S159-S160.	0.6	0
60	Genes associated with osteoarthritis identified by microarray-analysis of whole blood samples link oa to apoptotic pathways. <i>Osteoarthritis and Cartilage</i> , 2012, 20, S77-S78.	0.6	0
61	Risk prediction using epigenetic profiles in blood of osteoarthritis patients. <i>Osteoarthritis and Cartilage</i> , 2015, 23, A73-A74.	0.6	0
62	Novel susceptibility loci for osteoarthritis of the hand: Coding variants in MGP and ENPP3. <i>Osteoarthritis and Cartilage</i> , 2016, 24, S226-S227.	0.6	0
63	Molecular phenotyping of patient chondrocytes reveals genes and pathways involved in osteoarthritis. <i>Osteoarthritis and Cartilage</i> , 2017, 25, S209-S210.	0.6	0
64	THU0020â€¦Increased expression of CCN4/WISP1 in osteoarthritic articular cartilage is epigenetically regulated and disrupts cartilage homeostasis. , 2017, , .		0
65	Clock genes for joint health: if we could turn back time. <i>Rheumatology</i> , 2021, , .	0.9	0
66	Inhibiting thyroid activation in aged human explants prevents mechanical induced detrimental signalling by mitigating metabolic processes. <i>Rheumatology</i> , 2022, , .	0.9	0