

Yolande Y F M Ramos

List of Publications by Year in descending order

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66
papers

4,233
citations

218592

26
h-index

143943

57
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74
all docs

74
docs citations

74
times ranked

6509
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification and functional characterization of imbalanced osteoarthritis-associated fibronectin splice variants. <i>Rheumatology</i> , 2023, 62, 894-904.	0.9	3
2	The role of <i>TNFRSF11B</i> in development of osteoarthritic cartilage. <i>Rheumatology</i> , 2022, 61, 856-864.	0.9	10
3	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
4	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
5	Inhibiting thyroid activation in aged human explants prevents mechanical induced detrimental signalling by mitigating metabolic processes. <i>Rheumatology</i> , 2022, , .	0.9	0
6	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
7	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
8	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
9	Identification and characterization of two consistent osteoarthritis subtypes by transcriptome and clinical data integration. <i>Rheumatology</i> , 2021, 60, 1166-1175.	0.9	23
10	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
11	Censoring exosomal crosstalk in osteoarthritis. <i>Nature Aging</i> , 2021, 1, 332-334.	5.3	3
12	Clock genes for joint health: if we could turn back time. <i>Rheumatology</i> , 2021, , .	0.9	0
13	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
14	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
15	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
16	Cripto favors chondrocyte hypertrophy via $TGF\beta^2$ $SMAD1/5$ signaling during development of osteoarthritis. <i>Journal of Pathology</i> , 2021, 255, 330-342.	2.1	11
17	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
18	MicroRNAs and Regulation of Autophagy in Chondrocytes. <i>Methods in Molecular Biology</i> , 2021, 2245, 179-194.	0.4	3

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19	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
20	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
21	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
22	Elucidating Epigenetic Regulation by Identifying Functional cis-Acting Long Noncoding RNAs and Their Targets in Osteoarthritic Articular Cartilage. <i>Arthritis and Rheumatology</i> , 2020, 72, 1845-1854.	2.9	24
23	RNA sequencing data integration reveals an miRNA interactome of osteoarthritis cartilage. <i>Annals of the Rheumatic Diseases</i> , 2019, 78, 270-277.	0.5	130
24	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
25	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
26	Genome-wide analyses identify a role for SLC17A4 and AADAT in thyroid hormone regulation. <i>Nature Communications</i> , 2018, 9, 4455.	5.8	181
27	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
28	The role of epigenetics in osteoarthritis: current perspective. <i>Current Opinion in Rheumatology</i> , 2017, 29, 119-129.	2.0	32
29	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
30	Integrative epigenomics, transcriptomics and proteomics of patient chondrocytes reveal genes and pathways involved in osteoarthritis. <i>Scientific Reports</i> , 2017, 7, 8935.	1.6	90
31	Molecular phenotyping of patient chondrocytes reveals genes and pathways involved in osteoarthritis. <i>Osteoarthritis and Cartilage</i> , 2017, 25, S209-S210.	0.6	0
32	THU0020...Increased expression of CCN4/WISP1 in osteoarthritic articular cartilage is epigenetically regulated and disrupts cartilage homeostasis. , 2017, , .		0
33	Involvement of epigenetics in osteoarthritis. <i>Best Practice and Research in Clinical Rheumatology</i> , 2017, 31, 634-648.	1.4	11
34	Novel Genetic Variants for Cartilage Thickness and Hip Osteoarthritis. <i>PLoS Genetics</i> , 2016, 12, e1006260.	1.5	76
35	Aberrant Calreticulin Expression in Articular Cartilage of Dio2 Deficient Mice. <i>PLoS ONE</i> , 2016, 11, e0154999.	1.1	2
36	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

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37	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
38	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
39	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. <i>Nature Communications</i> , 2016, 7, 10494.	5.8	153
40	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
41	Translating genomics into mechanisms of disease: Osteoarthritis. <i>Best Practice and Research in Clinical Rheumatology</i> , 2015, 29, 683-691.	1.4	10
42	Transcriptional Associations of Osteoarthritis-Mediated Loss of Epigenetic Control in Articular Cartilage. <i>Arthritis and Rheumatology</i> , 2015, 67, 2108-2116.	2.9	47
43	Underlying molecular mechanisms of <i>DIO2</i> susceptibility in symptomatic osteoarthritis. <i>Annals of the Rheumatic Diseases</i> , 2015, 74, 1571-1579.	0.5	75
44	Risk prediction using epigenetic profiles in blood of osteoarthritis patients. <i>Osteoarthritis and Cartilage</i> , 2015, 23, A73-A74.	0.6	0
45	The transcriptional landscape of age in human peripheral blood. <i>Nature Communications</i> , 2015, 6, 8570.	5.8	533
46	Implementation of Functional Genomics for Bench-to-Bedside Transition in Osteoarthritis. <i>Current Rheumatology Reports</i> , 2015, 17, 53.	2.1	15
47	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
48	Genes Involved in the Osteoarthritis Process Identified through Genome Wide Expression Analysis in Articular Cartilage; the RAAK Study. <i>PLoS ONE</i> , 2014, 9, e103056.	1.1	142
49	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
50	Assessment of Osteoarthritis Candidate Genes in a Meta-Analysis of Nine Genome-Wide Association Studies. <i>Arthritis and Rheumatology</i> , 2014, 66, 940-949.	2.9	108
51	Knee and hip articular cartilage have distinct epigenomic landscapes: implications for future cartilage regeneration approaches. <i>Annals of the Rheumatic Diseases</i> , 2014, 73, 2208-2212.	0.5	96
52	A meta-analysis of genome-wide association studies identifies novel variants associated with osteoarthritis of the hip. <i>Annals of the Rheumatic Diseases</i> , 2014, 73, 2130-2136.	0.5	108
53	Genes expressed in blood link osteoarthritis with apoptotic pathways. <i>Annals of the Rheumatic Diseases</i> , 2014, 73, 1844-1853.	0.5	61
54	A gain of function mutation in <i>TNFRSF11B</i> causes osteoarthritis with chondrocalcinosis. <i>Osteoarthritis and Cartilage</i> , 2014, 22, S226.	0.6	1

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55	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
56	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
57	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
58	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
59	Genome-wide assessment of differential roles for p300 and CBP in transcription regulation. <i>Nucleic Acids Research</i> , 2010, 38, 5396-5408.	6.5	133
60	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
61	Inactivation of the p53 pathway in retinoblastoma. <i>Nature</i> , 2006, 444, 61-66.	13.7	550
62	Hdmx Protein Stability Is Regulated by the Ubiquitin Ligase Activity of Mdm2. <i>Journal of Biological Chemistry</i> , 2003, 278, 38315-38324.	1.6	124
63	Hdmx Stabilizes Mdm2 and p53. <i>Journal of Biological Chemistry</i> , 2000, 275, 28039-28044.	1.6	119
64	Comparative study of the p53-mdm2 and p53-MDMX interfaces. <i>Oncogene</i> , 1999, 18, 189-199.	2.6	172
65	Isolation and Identification of the Human Homolog of a New p53-Binding Protein, Mdmx. <i>Genomics</i> , 1997, 43, 34-42.	1.3	125
66	The cdk5/p35 kinase is essential for neurite outgrowth during neuronal differentiation.. <i>Genes and Development</i> , 1996, 10, 816-825.	2.7	562