

# Joanna Wysocka

## List of Publications by Year in descending order

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Version: 2024-02-01

60  
papers

12,510  
citations

71061

41  
h-index

138417

58  
g-index

73  
all docs

73  
docs citations

73  
times ranked

18883  
citing authors

#	ARTICLE	IF	CITATIONS
1	A unique chromatin signature uncovers early developmental enhancers in humans. <i>Nature</i> , 2011, 470, 279-283.	13.7	1,949
2	Modification of Enhancer Chromatin: What, How, and Why?. <i>Molecular Cell</i> , 2013, 49, 825-837.	4.5	1,200
3	A PHD finger of NURF couples histone H3 lysine 4 trimethylation with chromatin remodelling. <i>Nature</i> , 2006, 442, 86-90.	13.7	1,008
4	Ever-Changing Landscapes: Transcriptional Enhancers in Development and Evolution. <i>Cell</i> , 2016, 167, 1170-1187.	13.5	735
5	WDR5 Associates with Histone H3 Methylated at K4 and Is Essential for H3 K4 Methylation and Vertebrate Development. <i>Cell</i> , 2005, 121, 859-872.	13.5	725
6	CHD7 cooperates with PBAF to control multipotent neural crest formation. <i>Nature</i> , 2010, 463, 958-962.	13.7	527
7	Intrinsic retroviral reactivation in human preimplantation embryos and pluripotent cells. <i>Nature</i> , 2015, 522, 221-225.	13.7	507
8	Reorganization of Enhancer Patterns in Transition from Naive to Primed Pluripotency. <i>Cell Stem Cell</i> , 2014, 14, 838-853.	5.2	421
9	Mll3 and Mll4 Facilitate Enhancer RNA Synthesis and Transcription from Promoters Independently of H3K4 Monomethylation. <i>Molecular Cell</i> , 2017, 66, 568-576.e4.	4.5	322
10	Enhancer Divergence and cis-Regulatory Evolution in the Human and Chimp Neural Crest. <i>Cell</i> , 2015, 163, 68-83.	13.5	299
11	Transcriptional Dependencies in Diffuse Intrinsic Pontine Glioma. <i>Cancer Cell</i> , 2017, 31, 635-652.e6.	7.7	290
12	Epigenomic Annotation of Enhancers Predicts Transcriptional Regulators of Human Neural Crest. <i>Cell Stem Cell</i> , 2012, 11, 633-648.	5.2	283
13	Transcription-coupled changes in nuclear mobility of mammalian cis-regulatory elements. <i>Science</i> , 2018, 359, 1050-1055.	6.0	278
14	Enhancers as information integration hubs in development: lessons from genomics. <i>Trends in Genetics</i> , 2012, 28, 276-284.	2.9	248
15	Selective silencing of euchromatic L1s revealed by genome-wide screens for L1 regulators. <i>Nature</i> , 2018, 553, 228-232.	13.7	234
16	RNA helicase DDX21 coordinates transcription and ribosomal RNA processing. <i>Nature</i> , 2015, 518, 249-253.	13.7	232
17	Histone arginine methylation and its dynamic regulation. <i>Frontiers in Bioscience - Landmark</i> , 2006, 11, 344.	3.0	208
18	Genome-wide mapping of global-to-local genetic effects on human facial shape. <i>Nature Genetics</i> , 2018, 50, 414-423.	9.4	205

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19	Heterogeneity in old fibroblasts is linked to variability in reprogramming and wound healing. <i>Nature</i> , 2019, 574, 553-558.	13.7	187
20	Loss of HCF-1â€‘Chromatin Association Precedes Temperature-Induced Growth Arrest of tsBN67 Cells. <i>Molecular and Cellular Biology</i> , 2001, 21, 3820-3829.	1.1	175
21	The primate-specific noncoding RNA HPAT5 regulates pluripotency during human preimplantation development and nuclear reprogramming. <i>Nature Genetics</i> , 2016, 48, 44-52.	9.4	153
22	Systematic perturbation of retroviral LTRs reveals widespread long-range effects on human gene regulation. <i>ELife</i> , 2018, 7, .	2.8	146
23	Transposable elements as a potent source of diverse <i>cis</i>-regulatory sequences in mammalian genomes. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190347.	1.8	141
24	Roles of transposable elements in the regulation of mammalian transcription. <i>Nature Reviews Molecular Cell Biology</i> , 2022, 23, 481-497.	16.1	135
25	Histone H3 lysine 4 monomethylation modulates long-range chromatin interactions at enhancers. <i>Cell Research</i> , 2018, 28, 204-220.	5.7	131
26	Tissue-selective effects of nucleolar stress and rDNA damage in developmental disorders. <i>Nature</i> , 2018, 554, 112-117.	13.7	125
27	Inappropriate p53 activation during development induces features of CHARGE syndrome. <i>Nature</i> , 2014, 514, 228-232.	13.7	117
28	Zika Virus Infection Induces Cranial Neural Crest Cells to Produce Cytokines at Levels Detrimental for Neurogenesis. <i>Cell Host and Microbe</i> , 2016, 20, 423-428.	5.1	113
29	Loss of Extreme Long-Range Enhancers in Human Neural Crest Drives a Craniofacial Disorder. <i>Cell Stem Cell</i> , 2020, 27, 765-783.e14.	5.2	101
30	Insights into the genetic architecture of the human face. <i>Nature Genetics</i> , 2021, 53, 45-53.	9.4	94
31	7SK-BAF axis controls pervasive transcription at enhancers. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 231-238.	3.6	92
32	Reactivation of the pluripotency program precedes formation of the cranial neural crest. <i>Science</i> , 2021, 371, .	6.0	84
33	Identifying novel proteins recognizing histone modifications using peptide pull-down assay. <i>Methods</i> , 2006, 40, 339-343.	1.9	76
34	Foxd3 Promotes Exit from Naive Pluripotency through Enhancer Decommissioning and Inhibits Germline Specification. <i>Cell Stem Cell</i> , 2016, 18, 118-133.	5.2	73
35	Single Amino Acid Change Underlies Distinct Roles of H2A.Z Subtypes in Human Syndrome. <i>Cell</i> , 2019, 178, 1421-1436.e24.	13.5	65
36	The FaceBase Consortium: A comprehensive resource for craniofacial researchers. <i>Development (Cambridge)</i> , 2016, 143, 2677-88.	1.2	62

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37	Shared heritability of human face and brain shape. <i>Nature Genetics</i> , 2021, 53, 830-839.	9.4	57
38	CHARGE syndrome modeling using patient-iPSCs reveals defective migration of neural crest cells harboring CHD7 mutations. <i>ELife</i> , 2017, 6, .	2.8	52
39	ETO family protein Mtgr1 mediates Prdm14 functions in stem cell maintenance and primordial germ cell formation. <i>ELife</i> , 2015, 4, e10150.	2.8	51
40	Epigenomics of human embryonic stem cells and induced pluripotent stem cells: insights into pluripotency and implications for disease. <i>Genome Medicine</i> , 2011, 3, 36.	3.6	49
41	CSNK1a1 Regulates PRMT1 to Maintain the Progenitor State in Self-Renewing Somatic Tissue. <i>Developmental Cell</i> , 2017, 43, 227-239.e5.	3.1	48
42	The Spatiotemporal Pattern and Intensity of p53 Activation Dictates Phenotypic Diversity in p53-Driven Developmental Syndromes. <i>Developmental Cell</i> , 2019, 50, 212-228.e6.	3.1	48
43	Temporal dissection of an enhancer cluster reveals distinct temporal and functional contributions of individual elements. <i>Molecular Cell</i> , 2021, 81, 969-982.e13.	4.5	47
44	Human-chimpanzee fused cells reveal cis-regulatory divergence underlying skeletal evolution. <i>Nature Genetics</i> , 2021, 53, 467-476.	9.4	46
45	Opposing Effects of Cohesin and Transcription on CTCF Organization Revealed by Super-resolution Imaging. <i>Molecular Cell</i> , 2020, 80, 699-711.e7.	4.5	45
46	Epigenomic and Transcriptomic Changes During Human RPE EMT in a Stem Cell Model of Epiretinal Membrane Pathogenesis and Prevention by Nicotinamide. <i>Stem Cell Reports</i> , 2020, 14, 631-647.	2.3	43
47	Zscan4 binds nucleosomal microsatellite DNA and protects mouse two-cell embryos from DNA damage. <i>Science Advances</i> , 2020, 6, eaaz9115.	4.7	39
48	HIPSTR and thousands of lncRNAs are heterogeneously expressed in human embryos, primordial germ cells and stable cell lines. <i>Scientific Reports</i> , 2016, 6, 32753.	1.6	35
49	FaceBase 3: analytical tools and FAIR resources for craniofacial and dental research. <i>Development (Cambridge)</i> , 2020, 147, .	1.2	25
50	Single cell expression analysis of primate-specific retroviruses-derived HPAT lincRNAs in viable human blastocysts identifies embryonic cells co-expressing genetic markers of multiple lineages. <i>Heliyon</i> , 2018, 4, e00667.	1.4	23
51	Hunting for genes that shape human faces: Initial successes and challenges for the future. <i>Orthodontics and Craniofacial Research</i> , 2019, 22, 207-212.	1.2	22
52	Enhancer-associated H3K4 methylation safeguards in vitro germline competence. <i>Nature Communications</i> , 2021, 12, 5771.	5.8	20
53	Decoding the Human Face: Progress and Challenges in Understanding the Genetics of Craniofacial Morphology. <i>Annual Review of Genomics and Human Genetics</i> , 2022, 23, 383-412.	2.5	20
54	3D facial phenotyping by biometric sibling matching used in contemporary genomic methodologies. <i>PLoS Genetics</i> , 2021, 17, e1009528.	1.5	13

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55	Genome scans of facial features in East Africans and cross-population comparisons reveal novel associations. PLoS Genetics, 2021, 17, e1009695.	1.5	13
56	The Intersection of the Genetic Architectures of Orofacial Clefts and Normal Facial Variation. Frontiers in Genetics, 2021, 12, 626403.	1.1	10
57	2018 ISSCR Strategic Planning: Looking to the Future. Stem Cell Reports, 2019, 12, 1183-1185.	2.3	4
58	Enhancer-mediated regulation of developmental gene expression. FASEB Journal, 2013, 27, 80.3.	0.2	0
59	SATB1 Regulates GATA1 Protein Expression in Early Hematopoiesis and Is Deregulated in Diamond Blackfan Anemia. Blood, 2020, 136, 3-3.	0.6	0
60	Making the Human Face: Elucidating the Role of Enhancers in Hominid Craniofacial Evolution. FASEB Journal, 2022, 36, .	0.2	0