

# Joanna Wysocka

## List of Publications by Year in descending order

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Version: 2024-02-01

60  
papers

12,510  
citations

71102

41  
h-index

138484

58  
g-index

73  
all docs

73  
docs citations

73  
times ranked

18883  
citing authors

#	ARTICLE	IF	CITATIONS
1	Roles of transposable elements in the regulation of mammalian transcription. <i>Nature Reviews Molecular Cell Biology</i> , 2022, 23, 481-497.	37.0	135
2	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.	6.2	20
3	Making the Human Face: Elucidating the Role of Enhancers in Hominid Craniofacial Evolution. <i>FASEB Journal</i> , 2022, 36, .	0.5	0
4	Insights into the genetic architecture of the human face. <i>Nature Genetics</i> , 2021, 53, 45-53.	21.4	94
5	Reactivation of the pluripotency program precedes formation of the cranial neural crest. <i>Science</i> , 2021, 371, .	12.6	84
6	The Intersection of the Genetic Architectures of Orofacial Clefts and Normal Facial Variation. <i>Frontiers in Genetics</i> , 2021, 12, 626403.	2.3	10
7	Human–chimpanzee fused cells reveal cis-regulatory divergence underlying skeletal evolution. <i>Nature Genetics</i> , 2021, 53, 467-476.	21.4	46
8	Temporal dissection of an enhancer cluster reveals distinct temporal and functional contributions of individual elements. <i>Molecular Cell</i> , 2021, 81, 969-982.e13.	9.7	47
9	Shared heritability of human face and brain shape. <i>Nature Genetics</i> , 2021, 53, 830-839.	21.4	57
10	3D facial phenotyping by biometric sibling matching used in contemporary genomic methodologies. <i>PLoS Genetics</i> , 2021, 17, e1009528.	3.5	13
11	Genome scans of facial features in East Africans and cross-population comparisons reveal novel associations. <i>PLoS Genetics</i> , 2021, 17, e1009695.	3.5	13
12	Enhancer-associated H3K4 methylation safeguards in vitro germline competence. <i>Nature Communications</i> , 2021, 12, 5771.	12.8	20
13	FaceBase 3: analytical tools and FAIR resources for craniofacial and dental research. <i>Development (Cambridge)</i> , 2020, 147, .	2.5	25
14	Loss of Extreme Long-Range Enhancers in Human Neural Crest Drives a Craniofacial Disorder. <i>Cell Stem Cell</i> , 2020, 27, 765-783.e14.	11.1	101
15	Opposing Effects of Cohesin and Transcription on CTCF Organization Revealed by Super-resolution Imaging. <i>Molecular Cell</i> , 2020, 80, 699-711.e7.	9.7	45
16	Transposable elements as a potent source of diverse cis-regulatory sequences in mammalian genomes. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190347.	4.0	141
17	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.	4.8	43
18	Zscan4 binds nucleosomal microsatellite DNA and protects mouse two-cell embryos from DNA damage. <i>Science Advances</i> , 2020, 6, eaaz9115.	10.3	39

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19	SATB1 Regulates GATA1 Protein Expression in Early Hematopoiesis and Is Deregulated in Diamond Blackfan Anemia. Blood, 2020, 136, 3-3.	1.4	0
20	Single Amino Acid Change Underlies Distinct Roles of H2A.Z Subtypes in Human Syndrome. Cell, 2019, 178, 1421-1436.e24.	28.9	65
21	The Spatiotemporal Pattern and Intensity of p53 Activation Dictates Phenotypic Diversity in p53-Driven Developmental Syndromes. Developmental Cell, 2019, 50, 212-228.e6.	7.0	48
22	2018 ISSCR Strategic Planning: Looking to the Future. Stem Cell Reports, 2019, 12, 1183-1185.	4.8	4
23	Hunting for genes that shape human faces: Initial successes and challenges for the future. Orthodontics and Craniofacial Research, 2019, 22, 207-212.	2.8	22
24	Heterogeneity in old fibroblasts is linked to variability in reprogramming and wound healing. Nature, 2019, 574, 553-558.	27.8	187
25	Genome-wide mapping of global-to-local genetic effects on human facial shape. Nature Genetics, 2018, 50, 414-423.	21.4	205
26	Tissue-selective effects of nucleolar stress and rDNA damage in developmental disorders. Nature, 2018, 554, 112-117.	27.8	125
27	Transcription-coupled changes in nuclear mobility of mammalian cis-regulatory elements. Science, 2018, 359, 1050-1055.	12.6	278
28	Histone H3 lysine 4 monomethylation modulates long-range chromatin interactions at enhancers. Cell Research, 2018, 28, 204-220.	12.0	131
29	Selective silencing of euchromatic L1s revealed by genome-wide screens for L1 regulators. Nature, 2018, 553, 228-232.	27.8	234
30	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. Heliyon, 2018, 4, e00667.	3.2	23
31	Systematic perturbation of retroviral LTRs reveals widespread long-range effects on human gene regulation. ELife, 2018, 7, .	6.0	146
32	Transcriptional Dependencies in Diffuse Intrinsic Pontine Glioma. Cancer Cell, 2017, 31, 635-652.e6.	16.8	290
33	MLL3 and MLL4 Facilitate Enhancer RNA Synthesis and Transcription from Promoters Independently of H3K4 Monomethylation. Molecular Cell, 2017, 66, 568-576.e4.	9.7	322
34	CSNK1a1 Regulates PRMT1 to Maintain the Progenitor State in Self-Renewing Somatic Tissue. Developmental Cell, 2017, 43, 227-239.e5.	7.0	48
35	CHARGE syndrome modeling using patient-iPSCs reveals defective migration of neural crest cells harboring CHD7 mutations. ELife, 2017, 6, .	6.0	52
36	Zika Virus Infection Induces Cranial Neural Crest Cells to Produce Cytokines at Levels Detrimental for Neurogenesis. Cell Host and Microbe, 2016, 20, 423-428.	11.0	113

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37	Ever-Changing Landscapes: Transcriptional Enhancers in Development and Evolution. <i>Cell</i> , 2016, 167, 1170-1187.	28.9	735
38	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.	3.3	35
39	The FaceBase Consortium: A comprehensive resource for craniofacial researchers. <i>Development (Cambridge)</i> , 2016, 143, 2677-88.	2.5	62
40	7SK-BAF axis controls pervasive transcription at enhancers. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 231-238.	8.2	92
41	Foxd3 Promotes Exit from Naive Pluripotency through Enhancer Decommissioning and Inhibits Germline Specification. <i>Cell Stem Cell</i> , 2016, 18, 118-133.	11.1	73
42	The primate-specific noncoding RNA HPAT5 regulates pluripotency during human preimplantation development and nuclear reprogramming. <i>Nature Genetics</i> , 2016, 48, 44-52.	21.4	153
43	Intrinsic retroviral reactivation in human preimplantation embryos and pluripotent cells. <i>Nature</i> , 2015, 522, 221-225.	27.8	507
44	Enhancer Divergence and cis-Regulatory Evolution in the Human and Chimp Neural Crest. <i>Cell</i> , 2015, 163, 68-83.	28.9	299
45	RNA helicase DDX21 coordinates transcription and ribosomal RNA processing. <i>Nature</i> , 2015, 518, 249-253.	27.8	232
46	ETO family protein Mtgr1 mediates Prdm14 functions in stem cell maintenance and primordial germ cell formation. <i>ELife</i> , 2015, 4, e10150.	6.0	51
47	Inappropriate p53 activation during development induces features of CHARGE syndrome. <i>Nature</i> , 2014, 514, 228-232.	27.8	117
48	Reorganization of Enhancer Patterns in Transition from Naive to Primed Pluripotency. <i>Cell Stem Cell</i> , 2014, 14, 838-853.	11.1	421
49	Modification of Enhancer Chromatin: What, How, and Why?. <i>Molecular Cell</i> , 2013, 49, 825-837.	9.7	1,200
50	Enhancer-mediated regulation of developmental gene expression. <i>FASEB Journal</i> , 2013, 27, 80.3.	0.5	0
51	Epigenomic Annotation of Enhancers Predicts Transcriptional Regulators of Human Neural Crest. <i>Cell Stem Cell</i> , 2012, 11, 633-648.	11.1	283
52	Enhancers as information integration hubs in development: lessons from genomics. <i>Trends in Genetics</i> , 2012, 28, 276-284.	6.7	248
53	A unique chromatin signature uncovers early developmental enhancers in humans. <i>Nature</i> , 2011, 470, 279-283.	27.8	1,949
54	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.	8.2	49

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55	CHD7 cooperates with PBAF to control multipotent neural crest formation. Nature, 2010, 463, 958-962.	27.8	527
56	Identifying novel proteins recognizing histone modifications using peptide pull-down assay. Methods, 2006, 40, 339-343.	3.8	76
57	Histone arginine methylation and its dynamic regulation. Frontiers in Bioscience - Landmark, 2006, 11, 344.	3.0	208
58	A PHD finger of NURF couples histone H3 lysine 4 trimethylation with chromatin remodelling. Nature, 2006, 442, 86-90.	27.8	1,008
59	WDR5 Associates with Histone H3 Methylated at K4 and Is Essential for H3 K4 Methylation and Vertebrate Development. Cell, 2005, 121, 859-872.	28.9	725
60	Loss of HCF-1â€“Chromatin Association Precedes Temperature-Induced Growth Arrest of tsBN67 Cells. Molecular and Cellular Biology, 2001, 21, 3820-3829.	2.3	175