Joanna Wysocka

Lorry Lokey Professor and Professor of Developmental Biology

Chemical and Systems Biology

CONTACT INFORMATION

- **Administrative Contact**

  Vanessa Perez - Administrative Associate

  Email vjperez@stanford.edu

  Tel 650-725-4209

Bio

ACADEMIC APPOINTMENTS

- Professor, Chemical and Systems Biology
- Professor, Developmental Biology
- Member, Bio-X
- Member, Cardiovascular Institute
- Member, Institute for Stem Cell Biology and Regenerative Medicine
- Member, Stanford Cancer Institute
- Member, Wu Tsai Neurosciences Institute

HONORS AND AWARDS

- Elected Member, National Academy of Sciences (2024)
- Momentum Award, International Society for Stem Cell Research (2022)
- Elected Member, EMBO (2019)
- Lorry Lokey Endowed Chair, Stanford University (2019)
- Elected Member, American Academy of Arts and Science (2018)
- Valkhof Chair Award, Radboud University Nijmegen, the Netherlands (2017)
- Investigator Award, Howard Hughes Medical Institute (2015)
- Harland Winfield Mossman Award in Developmental Biology, American Association of Anatomists (2013)
- Vilcek Prize for Creative Promise, Vilcek Foundation (2013)
- ISSCR Outstanding Young Investigator Award, International Society for Stem Cell Research (2010)
- Distinguished Young Scholar in Biomedical Research, W.M.Keck Foundation (2008-2013)
- New Faculty Award, California Institute for Regenerative Medicine (2008-2013)
- Searle Scholar, Chicago Community Trust (2007-2010)
- Faculty Scholar, Baxter Foundation (2007)

- Postdoctoral Fellowship, Damon Runyon Cancer Research Foundation (2004-2006)

PROFESSIONAL EDUCATION

- postdoctoral education, The Rockefeller University , Chromatin Biology (2006)
- PhD, IBB Polish Academy of Science & Cold Spring Harbor Laboratory , Biochemistry (2003)
- MSc, Warsaw University , Molecular Biology (1998)

LINKS

- Lab website: https://wysocka.stanford.edu

Research & Scholarship

CURRENT RESEARCH AND SCHOLARLY INTERESTS

We are employing a broad combination of genomic, genetic, biochemical, biophysical, single-cell and embryological approaches in number of cellular and organismal models to investigate functions of the non-coding parts of the genome, understand regulatory mechanisms underlying cellular plasticity and differentiation, investigate how quantitative changes in gene expression dictate differences in human traits, and study craniofacial development, evolution and disease.

MECHANISMS OF LONG RANGE GENE REGULATION

Central to the cell type-specific transcriptional regulation are distal cis-regulatory elements called enhancers. A major area of investigation in our laboratory is focused on general mechanisms of long-range gene regulation by enhancers, which can activate their target genes over tens of even hundreds of kilobases of genomic distances. We are striving to understand how enhancers are activated in response to developmental stimuli, how they communicate with target promoters, what is the dynamics of this process in living cells, and what is the role of chromatin context in priming or restricting enhancer activity.

HUMAN NEURAL CREST DEVELOPMENT, DISEASE AND EVOLUTION

Our laboratory uses Cranial Neural Crest Cells (CNCCs) as a paradigm to study how genetic information harbored by regulatory elements is decoded into a diversity of functions, behaviors and morphologies. CNCCs are a transient embryonic cell group which delaminates from the neural tube, migrates long distances and acquires an extraordinarily broad differentiation potential, ultimately giving rise to most of the craniofacial structures and determining their individual and species-specific variation. Over a third of human congenital malformations is linked to CNCC dysfunction, including over 700 syndromes with craniofacial manifestations.

The goal of our ongoing research effort is to understand how variation in gene dosage and expression translates into differences in CNCC behavior, leading to the emergence of normal-range and disease-associated morphological diversity in the craniofacial form. This gene expression variation can result both from the trans-regulatory differences, such as those associated with mutations of transcriptional and chromatin regulators in craniofacial syndromes, and from the variation in cis-regulatory sequences like enhancers. To understand both mechanisms of variation and their cell type specificity, we are using human pluripotent stem cell differentiation models that recapitulate induction, migration and differentiation of CNCCs in the dish and facilitate modeling of human neurocristopathies. To study impact of regulatory changes on facial morphology, we are combining these in vitro models with the in vivo work in mice and, in collaboration with human geneticists and anthropologists, with the genetic analysis and morphometric measurements of craniofacial features in human populations.

EXPLORING GENOMIC DARK MATTER: TRANSPOSABLE ELEMENTS

Transposable element (TE) derived sequences comprise nearly half of the human genome. It is not always appreciated, however, that most TEs that are present in modern humans invaded the ancestral genome at various points of primate evolution, but are typically not shared with more distal mammals such as rodents. Thus, TE derived sequences form a vast reservoir of largely primate-specific sequences from which novel regulatory functions can evolve. We are interested in understanding how TEs may serve as a substrate for evolution of species- and tissue-specific cis-regulatory elements for the host genes, and we are investigating a developmental aspect of transposon regulation.

Teaching

COURSES

2025-26

- Research Seminar: CSB 270 (Aut, Win, Spr)

2024-25

- Research Seminar: CSB 270 (Aut, Win, Spr)
- The Biology of Chromatin Templated Processes: CSB 250 (Win)

2023-24

- Research Seminar: CSB 270 (Aut, Win, Spr)

2022-23

- Research Seminar: CSB 270 (Aut, Win, Spr)
- The Biology of Chromatin Templated Processes: CSB 250 (Win)

STANFORD ADVISEES

Doctoral Dissertation Reader (AC)

Cecelia Andrews, Andrew Burden, Jada Lauren Garzon, Rayyan Jokhai, Angela Pogson, Achuthan Raja Venkatesh, Sicong Wang

Postdoctoral Faculty Sponsor

Kaelan Brennan, Tiffany Chern, Marko Dunjic, Lucia Ichino, Chunyang Ni

Doctoral Dissertation Advisor (AC)

Olivia Crocker, Gabriel Lopez Lopez, Emma Magee, Saman Tabatabaee, Jordan Valgardson

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Cancer Biology (Phd Program)
- Chemical and Systems Biology (Phd Program)
- Developmental Biology (Phd Program)
- Genetics (Phd Program)
- Stem Cell Biology and Regenerative Medicine (Phd Program)

Publications

PUBLICATIONS

- **DNA-guided transcription factor cooperativity shapes face and limb mesenchyme.** *Cell*
  Kim, S., Morgunova, E., Naqvi, S., Goovaerts, S., Bader, M., Koska, M., Popov, A., Luong, C., Pogson, A., Swigut, T., Claes, P., Taipale, J., Wysocka, et al
  2024

- **Precise modulation of transcription factor levels identifies features underlying dosage sensitivity.** *Nature genetics*
  Naqvi, S., Kim, S., Hoskens, H., Matthews, H. S., Spritz, R. A., Klein, O. D., Hallgrimsson, B., Swigut, T., Claes, P., Pritchard, J. K., Wysocka, J.
  2023
- **Structural elements promote architectural stripe formation and facilitate ultra-long-range gene regulation at a human disease locus.** *Molecular cell*
  Chen, L. F., Long, H. K., Park, M., Swigut, T., Boettiger, A. N., Wysocka, J.
  2023
- **Deciphering the multi-scale, quantitative cis-regulatory code.** *Molecular cell*
  Kim, S., Wysocka, J.
  2023
- **Reactivation of the pluripotency program precedes formation of the cranial neural crest.** *Science (New York, N.Y.)*
  Zalc, A., Sinha, R., Gulati, G. S., Wesche, D. J., Daszczuk, P., Swigut, T., Weissman, I. L., Wysocka, J.
  2021; 371 (6529)
- **Single Amino Acid Change Underlies Distinct Roles of H2A.Z Subtypes in Human Syndrome.** *Cell*
  Greenberg, R. S., Long, H. K., Swigut, T. n., Wysocka, J. n.
  2019; 178 (6): 1421–36.e24
- **Transcription-coupled changes in nuclear mobility of mammalian cis-regulatory elements** *SCIENCE*
  Gu, B., Swigut, T., Spencley, A., Bauer, M. R., Chung, M., Meyer, T., Wysocka, J.
  2018; 359 (6379): 1050–55
- **Selective silencing of euchromatic L1s revealed by genome-wide screens for L1 regulators.** *Nature*
  Liu, N. n., Lee, C. H., Swigut, T. n., Grow, E. n., Gu, B. n., Bassik, M. n., Wysocka, J. n.
  2017
- **Enhancer Divergence and cis-Regulatory Evolution in the Human and Chimp Neural Crest.** *Cell*
  Prescott, S. L., Srinivasan, R., Marchetto, M. C., Grishina, I., Narvaiza, I., Selleri, L., Gage, F. H., Swigut, T., Wysocka, J.
  2015; 163 (1): 68-83
- **Intrinsic retroviral reactivation in human preimplantation embryos and pluripotent cells.** *Nature*
  Grow, E. J., Flynn, R. A., Chavez, S. L., Bayless, N. L., Wossidlo, M., Wesche, D. J., Martin, L., Ware, C. B., Blish, C. A., Chang, H. Y., Pera, R. A., Wysocka, J.
  2015; 522 (7555): 221-225
- **Fibroblasts of disparate developmental origins harbor anatomically variant scarring potential** *Cell*
  Griffin, M., Li, D., Chen, K., Parker, J., Guo, J., Kim, S., Kraft, K., Downer, M., Morgan, A., Kuhnert, M., Jing, S., Yao, H., Valencia, et al
  2026
- **A commoncis-regulatory variant impacts normal-range and disease-associated human facial shape through regulation ofPKDCCduring chondrogenesis.** *eLife*
  Mohammed, J., Arora, N., Matthews, H. S., Hansen, K., Bader, M., Walsh, S., Shaffer, J. R., Weinberg, S. M., Swigut, T., Claes, P., Selleri, L., Wysocka, J.
  2024; 13
- **Structural elements facilitate 3D locus topology and regulation of a human disease gene**
  Long, H., Chen, L., Boettiger, A., Wysocka, J.
  SPRINGERNATURE.2024: 56-57
- **Joint multi-ancestry and admixed GWAS on 3D facial shape derived from MRI**
  Goovaerts, S., Hoskens, H., Matthews, H., Herrick, N., Vandermeulen, D., Yuan, M., Shaffer, J., Shriver, M., Wysocka, J., Walsh, S., Weinberg, S., Claes, P.
  SPRINGERNATURE.2024: 784
- **Joint multi-ancestry and admixed GWAS reveals the complex genetics behind human cranial vault shape.** *Nature communications*
  Goovaerts, S., Hoskens, H., Eller, R. J., Herrick, N., Musolf, A. M., Justice, C. M., Yuan, M., Naqvi, S., Lee, M. K., Vandermeulen, D., Szabo-Rogers, H. L., Romitti, P. A., Boyadjiev, et al

2023; 14 (1): 7436

- **A genome-wide genetic screen uncovers determinants of human pigmentation.** *Science (New York, N.Y.)*
  Bajpai, V. K., Swigut, T., Mohammed, J., Naqvi, S., Arreola, M., Tycko, J., Kim, T. C., Pritchard, J. K., Bassik, M. C., Wysocka, J.
  2023; 381 (6658): eade6289
- **DNA-guided transcription factor cooperativity shapes face and limb mesenchyme.** *bioRxiv : the preprint server for biology*
  Kim, S., Morgunova, E., Naqvi, S., Bader, M., Koska, M., Popov, A., Luong, C., Pogson, A., Claes, P., Taipale, J., Wysocka, J.
  2023
- **Extreme long-range gene regulatory perturbation drives a human craniofacial disorder**
  Long, H., Chen, L., Swigut, T., Boettiger, A., Wysocka, J.
  SPRINGERNATURE.2023: 14
- **Co-transcriptional genome surveillance by HUSH is coupled to termination machinery.** *Molecular cell*
  Spencley, A. L., Bar, S., Swigut, T., Flynn, R. A., Lee, C. H., Chen, L., Bassik, M. C., Wysocka, J.
  2023
- **C. David Allis (1951-2023).** *Cell*
  Bernstein, E., Dent, S., Dou, Y., Duncan, E. M., Hake, S. B., Strahl, B. D., Wysocka, J.
  2023; 186 (4): 663-667
- **C. David Allis (1951-2023).** *Molecular cell*
  Bernstein, E., Dent, S., Dou, Y., Duncan, E. M., Hake, S. B., Strahl, B. D., Wysocka, J.
  2023; 83 (4): 497-499
- **Making the Human Face: Elucidating the Role of Enhancers in Hominid Craniofacial Evolution.** *FASEB journal : official publication of the Federation of American Societies for Experimental Biology*
  Mohammed, J., Hansen, K., Claes, P., Weinberg, S., Selleri, L., Swigut, T., Wysocka, J.
  2022; 36 Suppl 1
- **Decoding the Human Face: Challenges and Progress in Understanding the Genetics of Craniofacial Morphology.** *Annual review of genomics and human genetics*
  Naqvi, S., Hoskens, H., Wilke, F., Weinberg, S. M., Shaffer, J. R., Walsh, S., Shriver, M. D., Wysocka, J., Claes, P.
  2022
- **Roles of transposable elements in the regulation of mammalian transcription.** *Nature reviews. Molecular cell biology*
  Fueyo, R., Judd, J., Feschotte, C., Wysocka, J.
  2022
- **Enhancer-associated H3K4 methylation safeguards in vitro germline competence.** *Nature communications*
  Bleckwehl, T., Crispatzu, G., Schaaf, K., Respuela, P., Bartusel, M., Benson, L., Clark, S. J., Dorighi, K. M., Barral, A., Laugsch, M., van IJcken, W. F., Manzanares, M., Wysocka, et al
  2021; 12 (1): 5771
- **Genome scans of facial features in East Africans and cross-population comparisons reveal novel associations.** *PLoS genetics*
  Liu, C., Lee, M. K., Naqvi, S., Hoskens, H., Liu, D., White, J. D., Indencleef, K., Matthews, H., Eller, R. J., Li, J., Mohammed, J., Swigut, T., Richmond, et al
  2021; 17 (8): e1009695
- **3D facial phenotyping by biometric sibling matching used in contemporary genomic methodologies.** *PLoS genetics*
  Hoskens, H., Liu, D., Naqvi, S., Lee, M. K., Eller, R. J., Indencleef, K., White, J. D., Li, J., Larmuseau, M. H., Hens, G., Wysocka, J., Walsh, S., Richmond, et al
  2021; 17 (5): e1009528
- **Shared heritability of human face and brain shape.** *Nature genetics*
  Naqvi, S., Sleyp, Y., Hoskens, H., Indencleef, K., Spence, J. P., Bruffaerts, R., Radwan, A., Eller, R. J., Richmond, S., Shriver, M. D., Shaffer, J. R., Weinberg, S. M., Walsh, et al
  2021
- **Temporal dissection of an enhancer cluster reveals distinct temporal and functional contributions of individual elements.** *Molecular cell*

Thomas, H. F., Kotova, E. n., Jayaram, S. n., Pilz, A. n., Romeike, M. n., Lackner, A. n., Penz, T. n., Bock, C. n., Leeb, M. n., Halbritter, F. n., Wysocka, J. n., Buecker, C. n.

2021

- **Human-chimpanzee fused cells reveal cis-regulatory divergence underlying skeletal evolution.** *Nature genetics*

  Gokhman, D. n., Agoglia, R. M., Kinnebrew, M. n., Gordon, W. n., Sun, D. n., Bajpai, V. K., Naqvi, S. n., Chen, C. n., Chan, A. n., Chen, C. n., Petrov, D. A., Ahituv, N. n., Zhang, et al

  2021

- **Publisher Correction: Human-chimpanzee fused cells reveal cis-regulatory divergence underlying skeletal evolution.** *Nature genetics*

  Gokhman, D. n., Agoglia, R. M., Kinnebrew, M. n., Gordon, W. n., Sun, D. n., Bajpai, V. K., Naqvi, S. n., Chen, C. n., Chan, A. n., Chen, C. n., Petrov, D. A., Ahituv, N. n., Zhang, et al

  2021

- **The Intersection of the Genetic Architectures of Orofacial Clefts and Normal Facial Variation.** *Frontiers in genetics*

  Indencleef, K., Hoskens, H., Lee, M. K., White, J. D., Liu, C., Eller, R. J., Naqvi, S., Wehby, G. L., Moreno Uribe, L. M., Hecht, J. T., Long, R. E., Christensen, K., Deleyiannis, et al

  2021; 12: 626403

- **Insights into the genetic architecture of the human face.** *Nature genetics*

  White, J. D., Indencleef, K., Naqvi, S., Eller, R. J., Hoskens, H., Roosenboom, J., Lee, M. K., Li, J., Mohammed, J., Richmond, S., Quillen, E. E., Norton, H. L., Feingold, et al

  2020

- **FaceBase 3: analytical tools and FAIR resources for craniofacial and dental research.** *Development (Cambridge, England)*

  Samuels, B. D., Aho, R., Brinkley, J. F., Bugacov, A., Feingold, E., Fisher, S., Gonzalez-Reiche, A. S., Hacia, J. G., Hallgrimsson, B., Hansen, K., Harris, M. P., Ho, T., Holmes, et al

  2020; 147 (18)

- **Loss of Extreme Long-Range Enhancers in Human Neural Crest Drives a Craniofacial Disorder.** *Cell stem cell*

  Long, H. K., Osterwalder, M. n., Welsh, I. C., Hansen, K. n., Davies, J. O., Liu, Y. E., Koska, M. n., Adams, A. T., Aho, R. n., Arora, N. n., Ikeda, K. n., Williams, R. M., Sauka-Spengler, et al

  2020

- **Transposable elements as a potent source of diverse cis-regulatory sequences in mammalian genomes.** *Philosophical transactions of the Royal Society of London. Series B, Biological sciences*

  Sundaram, V. n., Wysocka, J. n.

  2020; 375 (1795): 20190347

- **Opposing Effects of Cohesin and Transcription on CTCF Organization Revealed by Super-resolution Imaging.** *Molecular cell*

  Gu, B. n., Comerci, C. J., McCarthy, D. G., Saurabh, S. n., Moerner, W. E., Wysocka, J. n.

  2020

- **Epigenomic and Transcriptomic Changes During Human RPE EMT in a Stem Cell Model of Epiretinal Membrane Pathogenesis and Prevention by Nicotinamide.** *Stem cell reports*

  Boles, N. C., Fernandes, M. n., Swigut, T. n., Srinivasan, R. n., Schiff, L. n., Rada-Iglesias, A. n., Wang, Q. n., Saini, J. S., Kiehl, T. n., Stern, J. H., Wysocka, J. n., Blenkinsop, T. A., Temple, et al

  2020

- **Zscan4 binds nucleosomal microsatellite DNA and protects mouse two-cell embryos from DNA damage.** *Science advances*

  Srinivasan, R. n., Nady, N. n., Arora, N. n., Hsieh, L. J., Swigut, T. n., Narlikar, G. J., Wossidlo, M. n., Wysocka, J. n.

  2020; 6 (12): eaaz9115

- **The Spatiotemporal Pattern and Intensity of p53 Activation Dictates Phenotypic Diversity in p53-Driven Developmental Syndromes.** *Developmental cell*

  Bowen, M. E., McClendon, J., Long, H. K., Sorayya, A., Van Nostrand, J. L., Wysocka, J., Attardi, L. D.

  2019

- **Hunting for genes that shape human faces: Initial successes and challenges for the future**

  Weinberg, S. M., Roosenboom, J., Shaffer, J. R., Shriver, M. D., Wysocka, J., Claes, P.

  WILEY.2019: 207–12

- **SNPs discovered in European GWAS shape worldwide facial diversity**

  Shriver, M. D., White, J. D., Lasisi, T., Eller, R. J., Gonzalez-Zarzar, T., Indencleef, K., Li, J., Hoskens, H., Ortega-Castrillon, A., Zaidi, A., Weinberg, S. M., Wysocka, J., Walsh, et al

  WILEY.2019: 227

- **Meta-analysis identifies 48 SNPs with multiple independent effects on human facial features**

  White, J. D., Roosenboom, J., Indencleef, K., Mohammed, J., Li, J., Ortega-Castrillon, A., Swigut, T., Lee, M., Gonzalez-Zarzar, T., Zaidi, A. A., Shaffer, J. R., Feingold, E., Richmond, et al

  WILEY.2019: 267

- **Hunting for genes that shape human faces: Initial successes and challenges for the future.** *Orthodontics & craniofacial research*

  Weinberg, S. M., Roosenboom, J. n., Shaffer, J. R., Shriver, M. D., Wysocka, J. n., Claes, P. n.

  2019; 22 Suppl 1: 207–12

- **2018 ISSCR Strategic Planning: Looking to the Future.** *Stem cell reports*

  Wysocka, J. n., Rossant, J. n.

  2019; 12 (6): 1183–85

- **Heterogeneity in old fibroblasts is linked to variability in reprogramming and wound healing.** *Nature*

  Mahmoudi, S. n., Mancini, E. n., Xu, L. n., Moore, A. n., Jahanbani, F. n., Hebestreit, K. n., Srinivasan, R. n., Li, X. n., Devarajan, K. n., Prélot, L. n., Ang, C. E., Shibuya, Y. n., Benayoun, et al

  2019; 574 (7779): 553–58

- **Systematic perturbation of retroviral LTRs reveals widespread long-range effects on human gene regulation.** *eLife*

  Fuentes, D. R., Swigut, T., Wysocka, J.

  2018; 7

- **Nicotinamide protects against PVR by preventing RPE cells to undergo EMT**

  Fernandes, M., Schiff, L., Swigut, T., Boles, N., Srinivasan, R., Rada-Iglesias, A., Wang, Q., Saini, J., Kiehl, T., Stern, J., Wysocka, J., Temple, S., Blenkinsop, et al

  ASSOC RESEARCH VISION OPHTHALMOLOGY INC.2018

- **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*

  Glinsky, G., Durruthy-Durruthy, J., Wossidlo, M., Grow, E. J., Weirather, J. L., Au, K., Wysocka, J., Sebastiano, V.

  2018; 4 (6): e00667

- **Genome-wide mapping of global-to-local genetic effects on human facial shape** *NATURE GENETICS*

  Claes, P., Roosenboom, J., White, J. D., Swigut, T., Sero, D., Li, J., Lee, M., Zaidi, A., Mattern, B. C., Liebowitz, C., Pearson, L., Gonzalez, T., Leslie, et al

  2018; 50 (3): 414-+

- **Histone H3 lysine 4 monomethylation modulates longrange chromatin interactions at enhancers (vol 28, pg 204, 2018)** *CELL RESEARCH*

  Yan, J., Chen, S. A., Local, A., Liu, T., Qiu, Y., Dorighi, K. M., Preissl, S., Rivera, C. M., Wang, C., Ye, Z., Ge, K., Hu, M., Wysocka, et al

  2018; 28 (3): 387

- **Tissue-selective effects of nucleolar stress and rDNA damage in developmental disorders** *NATURE*

  Calo, E., Gu, B., Bowen, M. E., Aryan, F., Zalc, A., Liang, J., Flynn, R. A., Swigut, T., Chang, H. Y., Attardi, L. D., Wysocka, J.

  2018; 554 (7690): 112-+

- **Histone H3 lysine 4 monomethylation modulates long-range chromatin interactions at enhancers.** *Cell research*

  Yan, J. n., Chen, S. A., Local, A. n., Liu, T. n., Qiu, Y. n., Dorighi, K. M., Preissl, S. n., Rivera, C. M., Wang, C. n., Ye, Z. n., Ge, K. n., Hu, M. n., Wysocka, et al

  2018

- **Mll3 and Mll4 Facilitate Enhancer RNA Synthesis and Transcription from Promoters Independently of H3K4 Monomethylation** *MOLECULAR CELL*

  Dorighi, K. M., Swigut, T., Henriques, T., Bhanu, N. V., Scruggs, B. S., Nady, N., Still, C. D., Garcia, B. A., Adelman, K., Wysocka, J.

  2017; 66 (4): 568-?

- **Transcriptional Dependencies in Diffuse Intrinsic Pontine Glioma** *CANCER CELL*

Nagaraja, S., Vitanza, N. A., Woo, P. J., Taylor, K. R., Liu, F., Zhang, L., Li, M., Meng, W., Ponnuswami, A., Sun, W., Ma, J., Hulleman, E., Swigut, et al

2017; 31 (5): 635-?

- **Corrigendum: HIPSTR and thousands of lncRNAs are heterogeneously expressed in human embryos, primordial germ cells and stable cell lines.** *Scientific reports*

  Yunusov, D., Anderson, L., DaSilva, L. F., Wysocka, J., Ezashi, T., Roberts, R. M., Verjovski-Almeida, S.

  2017; 7: 44632-?

- **CHARGE syndrome modeling using patient-iPSCs reveals defective migration of neural crest cells harboring CHD7 mutations.** *eLife*

  Okuno, H. n., Renault Mihara, F. n., Ohta, S. n., Fukuda, K. n., Kurosawa, K. n., Akamatsu, W. n., Sanosaka, T. n., Kohyama, J. n., Hayashi, K. n., Nakajima, K. n., Takahashi, T. n., Wysocka, J. n., Kosaki, et al

  2017; 6

- **CSNK1a1 Regulates PRMT1 to Maintain the Progenitor State in Self-Renewing Somatic Tissue.** *Developmental cell*

  Bao, X. n., Siprashvili, Z. n., Zarnegar, B. J., Shenoy, R. M., Rios, E. J., Nady, N. n., Qu, K. n., Mah, A. n., Webster, D. E., Rubin, A. J., Wozniak, G. G., Tao, S. n., Wysocka, et al

  2017; 43 (2): 227–39.e5

- **Ever-Changing Landscapes: Transcriptional Enhancers in Development and Evolution** *CELL*

  Long, H. K., Prescott, S. L., Wysocka, J.

  2016; 167 (5): 1170-1187

- **Zika Virus Infection Induces Cranial Neural Crest Cells to Produce Cytokines at Levels Detrimental for Neurogenesis.** *Cell host & microbe*

  Bayless, N. L., Greenberg, R. S., Swigut, T., Wysocka, J., Blish, C. A.

  2016; 20 (4): 423-428

- **The FaceBase Consortium: a comprehensive resource for craniofacial researchers.** *Development*

  Brinkley, J. F., Fisher, S., Harris, M. P., Holmes, G., Hooper, J. E., Jabs, E. W., Jones, K. L., Kesselman, C., Klein, O. D., Maas, R. L., Marazita, M. L., Selleri, L., Spritz, et al

  2016; 143 (14): 2677-2688

- **The FaceBase Consortium: a comprehensive resource for craniofacial researchers** *DEVELOPMENT*

  Brinkley, J. F., Fisher, S., Harris, M. P., Holmes, G., Hooper, J. E., Jabs, E. W., Jones, K. L., Kesselman, C., Klein, O. D., Maas, R. L., Marazita, M. L., Selleri, L., Spritz, et al

  2016; 143 (14): 2677-2688

- **7SK-BAF axis controls pervasive transcription at enhancers.** *Nature structural & molecular biology*

  Flynn, R. A., Do, B. T., Rubin, A. J., Calo, E., Lee, B., Kuchelmeister, H., Rale, M., Chu, C., Kool, E. T., Wysocka, J., Khavari, P. A., Chang, H. Y.

  2016; 23 (3): 231-238

- **Foxd3 Promotes Exit from Naive Pluripotency through Enhancer Decommissioning and Inhibits Germline Specification** *CELL STEM CELL*

  Respuela, P., Nikolic, M., Tan, M., Frommolt, P., Zhao, Y., Wysocka, J., Rada-Iglesias, A.

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