Stanford

Joanna Wysocka

Lorry Lokey Professor and Professor of Developmental Biology

Chemical and Systems Biology

CONTACT INFORMATION

- **Administrative Contact**

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Bio

ACADEMIC APPOINTMENTS

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

HONORS AND AWARDS

- 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, canonically defined as short noncoding DNA sequences that act to drive transcription independent of their relative distance, location or orientation to their cognate promoter. 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-speci#c 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 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 frogs and, in collaboration with human geneticists and anthropologists, with the 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

2019-20

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

2018-19

- The Biology of Chromatin Templated Processes: CSB 250 (Spr)

STANFORD ADVISEES

Doctoral Dissertation Reader (AC)

Veronica Behrens, Michael Bocek, Elizabeth Chen, Giovanni Diaz, Yilin Fan, Tony Gao, Fiorella Grandi, Bahareh Haddad Derafshi, Zachary Harvey, TzuChiao Hung, Dylan Husmann, Leslie Mateo, Sam Piekos, Suhas Rao, Owen Smith, Laura Spector, Chris Still, Mike Van, Wendy Wenderski, Daniel Wesche

Postdoctoral Faculty Sponsor

Vivek Bajpai, Liang-Fu Chen, Raquel Fueyo, Seungsoo Kim, Youngbin Lim, Hannah Long, Jaaved Mohammed, Sahin Naqvi, Antoine Zalc

Doctoral Dissertation Advisor (AC)

Alex Adams, Bo Gu, Christina Jensen, Naz Koska, Andrew Spencley

Orals Evaluator

Bo Gu, Zachary Harvey

Postdoctoral Research Mentor

Youngbin Lim

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

- **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-?
- **Selective silencing of euchromatic L1s revealed by genome-wide screens for L1 regulators.** *Nature*
  Liu, N., Lee, C. H., Swigut, T., Grow, E., Gu, B., Bassik, M., Wysocka, J.
  2017
- **Ever-Changing Landscapes: Transcriptional Enhancers in Development and Evolution** *CELL*
  Long, H. K., Prescott, S. L., Wysocka, J.
  2016; 167 (5): 1170-1187

- **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

- **CHARGE syndrome modeling using patient-iPSCs reveals defective migration of neural crest cells harboring CHD7 mutations.** *eLife*
  Okuno, H., Renault Mihara, F., Ohta, S., Fukuda, K., Kurosawa, K., Akamatsu, W., Sanosaka, T., Kohyama, J., Hayashi, K., Nakajima, K., Takahashi, T., Wysocka, J., Kosaki, et al
  2017; 6

- **CSNK1a1 Regulates PRMT1 to Maintain the Progenitor State in Self-Renewing Somatic Tissue.** *Developmental cell*
  Bao, X., Siprashvili, Z., Zarnegar, B. J., Shenoy, R. M., Rios, E. J., Nady, N., Qu, K., Mah, A., Webster, D. E., Rubin, A. J., Wozniak, G. G., Tao, S., Wysocka, et al
  2017; 43 (2): 227–39.e5

- **E2F activation of S phase promoters via association with HCF-1 and the MLL family of histone H3K4 methyltransferases** *MOLECULAR CELL*
  Tyagi, S., Chabes, A. L., Wysocka, J., Herr, W.
  2007; 27 (1): 107-119

- **Methylation of lysine 4 on histone H3: Intricacy of writing and reading a single epigenetic mark** *MOLECULAR CELL*
  Ruthenburg, A. J., Allis, C. D., Wysocka, J.
  2007; 25 (1): 15-30

- **Identifying novel proteins recognizing histone modifications using peptide pull-down assay** *METHODS*
  Wysocka, J.
  2006; 40 (4): 339-343

- **A PHD finger of NURF couples histone H3 lysine 4 trimethylation with chromatin remodelling** *NATURE*
  Wysocka, J., Swigut, T., Xiao, H., Milne, T. A., Kwon, S. Y., Landry, J., Kauer, M., Tackett, A. J., Chait, B. T., Badenhorst, P., Wu, C., Allis, C. D.
  2006; 442 (7098): 86-90

- **Molecular basis for site-specific read-out of histone H3K4me3 by the BPTF PHD finger of NURF** *NATURE*
  Li, H., Ilin, S., Wang, W., Duncan, E. M., Wysocka, J., Allis, C. D., Patel, D. J.
  2006; 442 (7098): 91-95

- **Histone arginine methylation and its dynamic regulation** *FRONTIERS IN BIOSCIENCE-LANDMARK*
  Wysocka, J., Allis, C. D., Coonrod, S.
  2006; 11: 344-355

- **Taking LSD1 to a new high** *CELL*
  Wysocka, J., Milne, T. A., Allis, C. D.
  2005; 122 (5): 654-658

- **Physical association and coordinate function of the H3K4 methyltransferase MLL1 and the H4K16 acetyltransferase MOF** *CELL*
  Dou, Y. L., Milne, T. A., Tackett, A. J., Smith, E. R., Fukuda, A., Wysocka, J., Allis, C. D., Chait, B. T., Hess, J. L., Roeder, R. G.
  2005; 121 (6): 873-885

- **WDR5 associates with histone H3 methylated at K4 and is essential for H3K4 methylation and vertebrate development** *CELL*
  Wysocka, J., Swigut, T., Milne, T. A., Dou, Y. L., Zhang, X., Burlingame, A. L., Roeder, R. G., Brivanlou, A. H., Allis, C. D.
  2005; 121 (6): 859-872

- **Human PAD4 regulates histone arginine methylation levels via demethylimination** *SCIENCE*
  Wang, Y., Wysocka, J., Sayegh, J., Lee, Y. H., Perlin, J. R., Leonelli, L., Sonbuchner, L. S., McDonald, C. H., COOK, R. G., Dou, Y., Roeder, R. G., Clarke, S., Stallcup, et al
  2004; 306 (5694): 279-283

- **Leukemia proto-oncoprotein MLL forms a SET1-like histone methyltransferase complex with menin to regulate Hox gene expression** *MOLECULAR AND CELLULAR BIOLOGY*

Yokoyama, A., Wang, Z., Wysocka, J., Sanyal, M., Aufiero, D. J., Kitabayashi, I., Herr, W., Cleary, M. L.
2004; 24 (13): 5639-5649

- **Linking covalent histone modifications to epigenetics: The rigidity and plasticity of the marks** *69th Cold Spring Harbor Symposium on Quantitative Biology*
  Wang, Y., Wysocka, J., Perlin, J. R., Leonelli, L., Allis, C. D., Coonrod, S. A.
  COLD SPRING HARBOR LAB PRESS, PUBLICATIONS DEPT.2004: 161–169

- **The herpes simplex virus VP16-induced complex: the makings of a regulatory switch** *TRENDS IN BIOCHEMICAL SCIENCES*
  Wysocka, J., Herr, W.
  2003; 28 (6): 294-304

- **Human Sin3 deacetylase and trithorax-related Set1/Ash2 histone H3-K4 methyltransferase are tethered together selectively by the cell-proliferation factor HCF-1** *GENES & DEVELOPMENT*
  Wysocka, J., Myers, M. P., Laherty, C. D., Eisenman, R. N., Herr, W.
  2003; 17 (7): 896-911

- **Inactivation of the retinoblastoma protein family can bypass the HCF-1 defect in tsBN67 cell proliferation and cytokinesis** *MOLECULAR AND CELLULAR BIOLOGY*
  Reilly, P. T., Wysocka, J., Herr, W.
  2002; 22 (19): 6767-6778

- **Loss of HCF-1-chromatin association precedes temperature-induced growth arrest of tsBN67 cells** *MOLECULAR AND CELLULAR BIOLOGY*
  Wysocka, J., Reilly, P. T., Herr, W.
  2001; 21 (11): 3820-3829

- **Developmental and cell-cycle regulation of Caenorhabditis elegans HCF phosphorylation** *BIOCHEMISTRY*
  Wysocka, J., Liu, Y., Kobayashi, R., Herr, W.
  2001; 40 (19): 5786-5794