

**Oudelaar, A.M.**, Beagrie, R.A., Gosden, M., De Ornellas, S., Georgiades, E., Kerry, J., Hidalgo, D., Carrelha, J., Shivalingam, A., El-Sagheer, A.H., et al. (2020). Dynamics of the 4D genome during in vivo lineage specification and differentiation. *Nature Communications* 11, 2722. <https://doi.org/10.1038/s41467-020-16598-7>

Chiariello, A.M., Bianco, S., **Oudelaar, A.M.**, Esposito, A., Annunziatella, C., Fiorillo, L., Conte, M., Corrado, A., Prisco, A., Larke, M.S.C., et al. (2020). A Dynamic Folded Hairpin Conformation Is Associated with  $\alpha$ -Globin Activation in Erythroid Cells. *Cell Reports* 30, 2125–2135.e2125. <https://doi.org/10.1016/j.celrep.2020.01.044>

**Oudelaar, A.M.**, Harrold, C.L., Hanssen, L.L.P., Telenius, J.M., Higgs, D.R., and Hughes, J.R. (2019). A revised model for promoter competition based on multi-way chromatin interactions at the  $\alpha$ -globin locus. *Nature Communications* 10, 5412. <https://doi.org/10.1038/s41467-019-13404-x>

Godfrey, L., Crump, N.T., Thorne, R., Lau, I.-J., Repapi, E., Dimou, D., Smith, A.L., Harman, J.R., Telenius, J.M., **Oudelaar, A.M.**, et al. (2019). DOT1L inhibition reveals a distinct subset of enhancers dependent on H3K79 methylation. *Nature Communications* 10, 2803. <https://doi.org/10.1038/s41467-019-10844-3>

**Oudelaar, A.M.**, Davies, J.O.J., Hanssen, L.L.P., Telenius, J.M., Schwessinger, R., Liu, Y., Brown, J.M., Downes, D.J., Chiariello, A.M., Bianco, S., et al. (2018). Single-allele chromatin interactions identify regulatory hubs in dynamic compartmentalized domains. *Nature Genetics* 50, 1744–1751. <https://doi.org/10.1038/s41588-018-0253-2>

Brown, J.M., Roberts, N.A., Graham, B., Waithe, D., Lagerholm, C., Telenius, J.M., De Ornellas, S., **Oudelaar, A.M.**, Scott, C., Szczerbal, I., et al. (2018). A tissue-specific self-interacting chromatin domain forms independently of enhancer-promoter interactions. *Nature Communications* 9, 376. <https://doi.org/10.1038/s41467-018-06248-4>

**Oudelaar, A.M.**, Downes, D.J., Davies, J.O.J., and Hughes, J.R. (2017). Low-input Capture-C: A Chromosome Conformation Capture Assay to Analyze Chromatin Architecture in Small Numbers of Cells. *Bio-Protocol* 7, 23. <https://doi.org/10.21769/bioprotoc.2645>

**Oudelaar, A.M.**, Davies, J.O.J., Downes, D.J., Higgs, D.R., and Hughes, J.R. (2017). Robust detection of chromosomal interactions from small numbers of cells using low-input Capture-C. *Nucleic Acids Research* 45, 22, e184. <https://doi.org/10.1093/nar/gkx1194>

**Oudelaar, A.M.**, Hanssen, L.L.P., Hardison, R.C., Kassouf, M.T., Hughes, J.R., and Higgs, D.R. (2017). Between form and function: the complexity of genome folding. *Human Molecular Genetics* 26, R208–R215. <https://doi.org/10.1093/hmg/ddx306>

Hanssen, L.L.P., Kassouf, M.T., **Oudelaar, A.M.**, Biggs, D., Preece, C., Downes, D.J., Gosden, M., Sharpe, J.A., Sloane-Stanley, J.A., Hughes, J.R., et al. (2017). Tissue-specific CTCF-cohesin-mediated chromatin architecture delimits enhancer interactions and function in vivo. *Nature Cell Biology* 19, 952–961. <https://doi.org/10.1038/ncb3573>

Davies, J.O.J., **Oudelaar, A.M.**, Higgs, D.R., and Hughes, J.R. (2017). How best to identify chromosomal interactions: a comparison of approaches. *Nature Methods* 14, 125–134. <https://doi.org/10.1038/nmeth.4146>

Hay, D., Hughes, J.R., Babbs, C., Davies, J.O.J., Graham, B.J., Hanssen, L.L.P., Kassouf, M.T., **Oudelaar, A.M.**, Sharpe, J.A., Suci, M.C., et al. (2016). Genetic dissection of the  $\alpha$ -globin super-enhancer in vivo. *Nature Genetics* 48, 895–903. <https://doi.org/10.1038/ng.3605>