The laboratories of David Suter (UPSUTER) and Sebastian Maerkl (LBNC) at the Ecole Polytechnique Fédérale de Lausanne (EPFL) are **looking for a joint Post-doctoral researcher** to develop a synthetic biology approach to understand the biophysical and quantitative properties of a transcription factor network in stem cells.

EPFL is a world-leading engineering school situated at the shore of Lake Geneva in Switzerland, and fosters interdisciplinarity across basic and engineering science. The Suter lab uses in vivo approaches to understand how transcription factors regulate gene expression and cell identity of embryonic stem cells. The Maerkl lab is developing approaches to characterize and re-engineer transcription factors in vitro and in vivo.

This project is part of a Sinergia Consortium funded by the Swiss National Science Foundation, and will involve interdisciplinary collaboration with our partner lab expert in computational modelling of biological networks (van Nimwegen lab, University of Basel). The project will involve cutting edge approaches such as genome editing, high throughput multicolor live cell fluorescence imaging of stem cells, construction of synthetic transcription factors, and biophysical approaches to measure their properties in vitro and in vivo. The overarching goal of this project is to reach a quantitative understanding of how transcription factor networks control cell identity.

If you have a background in genome editing, live cell imaging and microfluidics and are interested in this project, send a cover letter, CV and the contact information of 3 referees to david.suter@epfl.ch and sebastian.maerkl@epfl.ch. For more information please visit http://suter-lab.epfl.ch/ and http://lbnc.epfl.ch/ or contact us using the email addresses given above.

References:

Mitotic chromosome binding predicts transcription factor properties in interphase.
Raccaud M, Alber AB, Friman ET, Agarwal H, Deluz C, Kuhn T, Gebhardt JCM, Suter DM.
Nature Communications 2019 Jan 30

Endogenous fluctuations of OCT4 and SOX2 bias pluripotent cell fate decisions.
Strebinger D*, Deluz C*, Friman ET*, Govindan S, Alber AB, Suter DM[†]. *Equal contribution; [†]Corresponding author.
Molecular Systems Biology 2019 September 25

Dynamic regulation of chromatin accessibility around the cell cycle by pioneer transcription factors.
Friman ET, Deluz C, Mehreles-Filho A, Govindan S, Gardeux V, Deplancke B, Suter DM†. †Corresponding author.
eLife, in press (also see bioRxiv version: doi:10.1101/698571)

Z. Swank, N. Laohakunakorn, and S. J. Maerkl, “Cell-free gene-regulatory network engineering with synthetic transcription factors.,” *Proceedings of the National Academy of Sciences*, vol. 116, no. 13, pp. 5892–5901, Mar. 2019.

H. Niederholtmeyer, Z. Z. Sun, Y. Hori, E. Yeung, A. Verpoorte, R. M. Murray, and S. J. Maerkl, “Rapid cell-free forward engineering of novel genetic ring oscillators.,” *eLife*, vol. 4, p. e09771, Oct. 2015.

A. S. Rajkumar, N. Denervaud, and S. J. Maerkl, “Mapping the fine structure of a eukaryotic promoter input-output function.,” *Nat Genet*, vol. 45, no. 10, pp. 1207–1215, Oct. 2013.