

Publication

An atlas of combinatorial transcriptional regulation in mouse and man

JournalArticle (Originalarbeit in einer wissenschaftlichen Zeitschrift)**ID** 490900**Author(s)** Ravasi, Timothy; Suzuki, Harukazu; Cannistraci, Carlo Vittorio; Katayama, Shintaro; Bajic, Vladimir B; Tan, Kai; Akalin, Altuna; Schmeier, Sebastian; Kanamori-Katayama, Mutsumi; Bertin, Nicolas; Carninci, Piero; Daub, Carsten O; Forrest, Alistair R R; Gough, Julian; Grimmond, Sean; Han, Jung-Hoon; Hashimoto, Takehiro; Hide, Winston; Hofmann, Oliver; Kamburov, Atanas; Kaur, Mandeep; Kawaji, Hideya; Kubosaki, Atsutaka; Lassmann, Timo; van Nimwegen, Erik; MacPherson, Cameron Ross; Ogawa, Chihiro; Radovanovic, Aleksandar; Schwartz, Ariel; Teasdale, Rohan D; Tegnér, Jesper; Lenhard, Boris; Teichmann, Sarah A; Arakawa, Takahiro; Ninomiya, Noriko; Murakami, Kayoko; Tagami, Michihira; Fukuda, Shiro; Imamura, Kengo; Kai, Chikatoshi; Ishihara, Ryoko; Kitazume, Yayoi; Kawai, Jun; Hume, David A; Ideker, Trey; Hayashizaki, Yoshihide**Author(s) at UniBasel** [van Nimwegen, Erik](#) ;**Year** 2010**Title** An atlas of combinatorial transcriptional regulation in mouse and man**Journal** Cell**Volume** 140**Number** 5**Pages / Article-Number** 744-52

Combinatorial interactions among transcription factors are critical to directing tissue-specific gene expression. To build a global atlas of these combinations, we have screened for physical interactions among the majority of human and mouse DNA-binding transcription factors (TFs). The complete networks contain 762 human and 877 mouse interactions. Analysis of the networks reveals that highly connected TFs are broadly expressed across tissues, and that roughly half of the measured interactions are conserved between mouse and human. The data highlight the importance of TF combinations for determining cell fate, and they lead to the identification of a SMAD3/FLI1 complex expressed during development of immunity. The availability of large TF combinatorial networks in both human and mouse will provide many opportunities to study gene regulation, tissue differentiation, and mammalian evolution.

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