

1. Techniques like Anchor-Away that disrupt protein function by directly disturbing or eliminating a target protein provide an advantage over techniques affecting the respective DNA or mRNA in that they do so in a much shorter time. (this thesis)

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2. Anchor-Away is a promising new technique to disturb the function of a nuclear protein within a few hours a time frame that is short enough to better discern primary effects of a knock down from secondary effects. (this thesis)

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3. Rapalog is able to diffuse through the plasma membrane of murine ES cells, but not through the plasma membrane of *in vitro* differentiated cells. (this thesis)

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4. Advances in genome-editing techniques, like the development of recombineering for fast generation of targeting constructs and the development of the zinc finger nuclease/TALEN/CRISPR systems, make it possible to homozygously target ES cells fast, making Anchor-Away a viable technique because both alleles need to carry the anchoring tag. (this thesis)

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5. Recombineering combined with linear integration of big-sized DNA constructs by transposons enables fast and reliable generation of mouse models for wild type and/or slightly mutated gene loci. (this thesis)

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6. Models of indirect cooperation between transcription factors proposed in literature suggest that a large proportion of the functional cooperativity that is detected between transcription factors bound to the same enhancer may occur through indirect effects rather than the formation of stable ternary complexes, and these mechanisms may help to convert low-affinity DNA interactions into robust binding events. (Spitz and Furlong, Nature Reviews Genetics, 2012)

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7. The regulation of essential developmental factors by LDB1 defines it as an upstream transcriptional regulator of hematopoietic/endothelial development. (Mylona et al, Blood, 2013)

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8. The requirements for Runx1 in erythroid/myeloid progenitor and hematopoietic stem cell formation are temporally distinct, and long term-hematopoietic stem cell function is highly reliant on continued core binding factor activity. (Tober et al, Development, 2013)

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9. It is estimated that an individual typically differs from the reference human genome sequence at 10,000–11,000 sites that lead to differences in the protein sequence in addition to 10,000–12,000 coding sites that do not lead to differences in the protein sequence and each genome is heterozygous for 50-100 variants classified by the Human Gene Mutation Database as causing inherited disorders. (The 1000 Genomes Project Consortium, Nature, 2010)

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10. Prediction is very difficult, especially about the future. (Niels Bohr)

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11. “If you’re scared to die you better not be scared to live” (taken from *A friendly ghost* by Eels)

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