**Genome editing *via* CRISPR/Cas system**

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Genome editing with engineered nucleases such as ZFNs (zinc finger nucleases), TALENs (transcription-activator-like effector nucleases), and RGENs (CRISPR/Cas-derived RNA-guided engineered nucleases) is broadly useful for biomedical research, biotechnology, and medicine. Unlike ZFNs and TALENs whose DNA specificities are determined by DNA-binding proteins, RGENs use complementary base pairing to recognize target sites. Custom-designed RGENs are produced simply by replacing guide RNAs, making this system easy to access. Unfortunately, RGENs cleave not only on-target sites but also off-target sites that differ by up to several nucleotides from the on-target sites, causing unwanted off-target mutations and chromosomal rearrangements. Furthermore, these nucleases often induce in-frame mutations in target genes, reducing the efficacy of nucleases in a population of cells and hampering the isolation of biallelic null clones. Here I present a novel potential off-target searching tool (Cas-OFFinder, Bioinformatics 2014) and a Microhomology-predictor for inducing more efficient knock out (Nature Methods 2014). Furthermore, I introduce a novel genome-wide profiling method of CRISPR-Cas9 off-target effects in human cells (Digenome-seq, Nature Methods 2015). These tools are indispensable for carrying out the genome-wide knock-out screening or gene therapy.