dCas9: A Versatile Tool For Epigenome Editing

Daan J.W. Brocken[1], Mariliis Tark-Dame[2]* and Remus T. Dame[1,3]*

[1]Leiden Institute of Chemistry, Gorlaeus Laboratories, Leiden University, Leiden, The Netherlands.
[2]Swammerdam Institute for Life Sciences, University of Amsterdam, Amsterdam, The Netherlands.
[3]Centre for Microbial Cell Biology, Leiden University, Leiden, The Netherlands.

*Correspondence: m.tark@uva.nl and rtdame@chem.leidenuniv.nl

Abstract

The epigenome is a heritable layer of information not encoded in the DNA sequence of the genome, but in chemical modifications of DNA or histones. These chemical modifications, together with transcription factors, operate as spatiotemporal regulators of genome activity. Dissecting epigenome function requires controlled site-specific alteration of epigenetic information. Such control can be obtained using designed DNA-binding platforms associated with effector domains to function as targeted transcription factors or epigenetic modifiers. Here, we review the use of dCas9 as a novel and versatile tool for fundamental studies on epigenetic landscapes, chromatin structure and transcription regulation, and the potential of this approach in basic research in these fields.

Introduction

The epigenome is a layer of information that, together with transcription factors, defines the cell-type-specific gene expression pattern of a genome. By definition, epigenetic information is mitotically and/or meiotically heritable, but not directly encoded in the DNA sequence (Bird, 2007; Berger et al., 2009). Epigenetic information consists of covalent chemical modifications [post-translational modification of histone proteins that include, but are not limited to, methyl, acetyl, phosphoryl and ubiquitin groups (Turner, 2012) and methylation of cytosine bases (Vardimon et al., 1982; Schübeler, 2015)] that alter the structure and physicochemical properties of DNA or DNA-bound histones (Bird, 2002; Kouzarides, 2007). Epigenetic modification states are dynamic by nature and depend on enzymes transferring or removing these modifications (Holliday, 1987; Cubas et al., 1999; Chong and Whitelaw, 2004; Youngson and Whitelaw, 2008). The epigenetic state of a genomic region is determined by combinations of modifications, but how exactly the resulting code is determined remains poorly understood (Gardner et al., 2011). These states correlate with gene expression and chromatin structure, and link the modification pattern of DNA and histones of genomic regions to states of development and differentiation (Holliday, 2006; Henikoff and Shilatifard, 2011; Zhou et al., 2011; Turner, 2012; Smith and Meissner, 2013).

A variety of diseases has been linked to mutations in epigenetic maintenance enzymes or to misregulation of genes following aberrations in the epigenetic code (Kelly et al., 2010; Baylin and Jones, 2011; Plass et al., 2013). Epigenome editing could develop into a tool used to revert aberrations in this code that lead to disease. Due to the lack of knowledge of rare modifications and the combinatorics of DNA and histone modifications, it is unclear by what exact mechanisms epigenetic signals lead to downstream effects on gene regulation and chromatin conformation and whether as yet unknown

functional elements exist in genomes. To be able to provide answers to these questions, especially those on causality and the order of concerted processes, epigenetic effectors have been employed to study the implications of modification of the epigenome. Sequence-specific targeting of epigenetic modifiers has been instrumental in understanding the roles of epigenetic modifications on gene regulation. Here, we review current efforts aimed at manipulating the epigenome, focusing on the nuclease-deactivated Cas9 (dCas9) as versatile tool for sequence-specific recruitment of effector proteins.

Epigenome editing

Numerous studies have established correlations between epigenetic state and genome activity (Bernstein *et al.*, 2010; Rivera and Ren, 2013; Roadmaps Epigenomics Consortium *et al.*, 2015). Investigating the epigenome and establishing causal relationships rather than correlations will benefit from site-specific targeting of enzymes involved in establishing, disrupting and maintaining epigenetic states. Ideally, approaches to achieve this aim are readily adaptable to accommodate different target specificity and functionality.

The earliest efforts to edit epigenetic states and determine the effects of alterations therein involved gene knock-out or knock-down of specific epigenetic modifiers (Stancheva and Meehan, 2000; Webster *et al.*, 2005), or the use of compounds inhibiting the activity of these modifiers or their targets (Lyko and Brown, 2005). Such global strategies, due to their pleiotropic impact, do not permit direct specific changes to be distinguished from secondary effects of the perturbation. Epigenetic modifiers – or their isolated functional domains – have been fused to DNA-binding proteins targeted at specific loci. Zinc finger proteins (ZFPs), transcription activator-like effectors (TALEs) and nuclease-deactivated Cas9 (dCas9) have thus been employed successfully as tools for direct control of transcription, and – combined with a domain containing nuclease activity – for genome editing (Gaj *et al.*, 2013). These DNA-binding proteins have also been used as vehicles to target epigenetic modifiers to specific loci. This application has been a major step forward in editing the epigenome (de Groote *et al.*, 2012; Thakore *et al.*, 2016). Below, we describe the three adaptable DNA-binding vehicles

currently available for targeted recruitment of effectors at designated genomic loci.

ZFPs

Zinc finger proteins (ZFPs) form a large class of DNA-binding proteins that use coordinated zinc ions to stabilize the typical $\beta\beta\alpha$ fold in their modular DNA-recognition domains. Each zinc finger domain consists of about 30 amino acids, capable of sequence-specific recognition of a 3–4 base pair sequence (Pavletich and Pabo, 1991). The canonical zinc finger protein harbours three such domains. For increased target specificity, synthetic zinc finger proteins generally consist of 4–6 zinc finger domains arranged in tandem. Choo *et al.* (1994) demonstrated in 1994 that it is possible to specifically target an oncogenic gene and reduce its transcription through transcriptional blockage by ZFP. This is the first instance of the use of a designed protein for manipulating gene expression at a defined locus. By targeting the histone methyltransferase (HMT) catalytic core using synthetic ZFPs to an endogenous genomic reporter system the causality of histone modifications in inducing repression of transcription was established (Snowden *et al.*, 2002). Histone 3 Lysine 9 methylation (H3K9me) was found to become enriched throughout a 500–1000 bp region around the target site. This spreading of the H3K9me mark, attributed to HP1, a protein associated with heterochromatin and mediator of gene silencing, resulted in repression of transcription (Snowden *et al.*, 2002). These applications of synthetic ZFPs are key examples of an adaptable DNA-binding platform tool, unique at the time, and laid the basis for the use of ZFP fusions in a wide range of applications (Klug, 2010; Urnov *et al.*, 2010; Gersbach *et al.*, 2014).

TALEs

Transcription activator-like effectors (TALEs) are DNA-binding proteins originating from plant pathogenic bacteria that consist of repeated motifs of 33 or 34 amino acids, with residues 12 and 13 – so-called repeat variable di-residues (RVDs) – in each otherwise conserved repeat recognizing one particular base in double stranded DNA (Boch *et al.*, 2009; Moscou and Bogdanove, 2009; Deng *et al.*, 2012). TALE repeats can – by analogy with ZFPs – be designed in tandem to recognize

any DNA sequence of interest, with each repeat recognizing one base via its RVD (Zhang *et al.*, 2011; Mussolino and Cathomen, 2012). Since di-residues specific for each nucleotide have been identified, the rational design of DNA recognition is straightforward (Zhang *et al.*, 2011; Reyon *et al.*, 2012). Nevertheless, target specificity of designed TALEs generally needs to be verified *in vitro* or *in vivo* (Morbitzer *et al.*, 2010; Zhang *et al.*, 2011; Grau *et al.*, 2013; Guilinger *et al.*, 2014). However, also TALEs and TALE–effector fusions verified to be target specific and active in a reporter assay may exhibit different activities when targeted at chromosomal sites, attributed to altered chromatin accessibility (Zhang *et al.*, 2011). Although quite recently discovered, TALEs have proven their value next to ZFPs in gene expression modulation and genome editing (Sanjana *et al.*, 2012; Gaj *et al.*, 2013). TALE fusions have also been used to target epigenetic modifiers to genomic loci. TALEs fused to the synthetic transactivation domain VP64 have been shown to up-regulate transcription of the endogenous pluripotency genes *SOX2* and *KLF4* in human 293FT cells, whereas TALE-VP64 targeted *c-MYC* and *OCT4* genes were unaffected (Zhang *et al.*, 2011). A TALE–TET1 fusion has been shown to decrease methylation of specific CpG dinucleotides in the targeted promoter regions, resulting in increased mRNA expression levels of the targeted genes (Maeder *et al.*, 2013a).

The use of both ZFPs and TALEs has been instrumental in achieving systematic and controlled targeting of effectors to defined genomic loci. However, there are some drawbacks to the use of these DNA-binding proteins. The design of ZFPs to target specific DNA sequences is not as straightforward and modular as suggested above, as side chain–side chain interactions within and between adjacent zinc fingers complicate DNA recognition (Wolfe *et al.*, 2000, 2001), precluding a robust 'recognition code', permitting reliable engineering of highly specific DNA-recognition proteins. Although the DNA recognition via defined RVDs is more modular compared to ZFPs, TALE arrays also suffer from off-target binding (Guilinger *et al.*, 2014; Rogers *et al.*, 2015). In fact, it has been shown that the protein context of a TALE repeat influences the DNA-binding specificity of the array (Rogers *et al.*, 2015). A related drawback is that DNA binding of TALEs (Bultmann *et al.*, 2012) and ZFPs (Choo,

1998; Daniel *et al.*, 2002; Vandevenne *et al.*, 2013) is affected by the presence of methylated cytosines in target sequences, making application in genomic contexts more complicated and less flexible. Independent of these drawbacks limiting application, it is important to realize that both tools require re-design of the protein sequence and validation for individual constructs targeting distinct DNA sequences. This process makes adaptation uncertain as well as time and resource consuming. The capability of employing these proteins in multiplex or high-throughput screening applications is limited by this inflexibility of target adaptation.

dCas9

The CRIPSR-associated protein 9 (Cas9) is an antiviral enzyme of the Type II clustered regularly interspaced short palindromic repeat (CRISPR) adaptive immune system in prokaryotes (Barrangou *et al.*, 2007; Bhaya *et al.*, 2011). The endogenous enzyme introduces double-strand breaks in DNA using two catalytic domains (RuvC and HNH). Two RNA molecules – a CRISPR RNA (crRNA) and a trans-activating crRNA (tracrRNA) – are used to guide Cas9 to its target sequence. A protospacer adjacent motif (PAM) flanking the target sequence recognized by the crRNA acts as an additional determinant in target recognition (Jinek *et al.*, 2012). In biotechnological applications the protein is generally guided by a chimeric single-guide RNA (sgRNA), a hybrid of crRNA and tracrRNA (Fig. 2.1).

Cas9 has been very rapidly and widely adopted (Doudna and Charpentier, 2014) as tool for genome editing (Cho *et al.*, 2013a; Cong *et al.*, 2013; Hwang *et al.*, 2013; Jinek *et al.*, 2013; Mali *et al.*, 2013b). The nuclease-deactivated variant, dCas9 (Fig. 2.1), initially created to establish which catalytic amino acids are necessary for dsDNA cleavage (Jinek *et al.*, 2012), laid the foundation for a whole range of new applications needing site-specific targeting. The dCas9 protein has been adopted as DNA-binding platform for applications as diverse as transcriptional blockage (Bikard *et al.*, 2013; Qi *et al.*, 2013), gene expression modulation (Cheng *et al.*, 2013; Gilbert *et al.*, 2013), epigenetic editing (Hilton *et al.*, 2015; Kearns *et al.*, 2015) and staining of chromosomal regions for live cell imaging (Chen *et al.*, 2013; Anton *et al.*, 2014; Ma *et al.*, 2015). In the next sections we discuss in detail
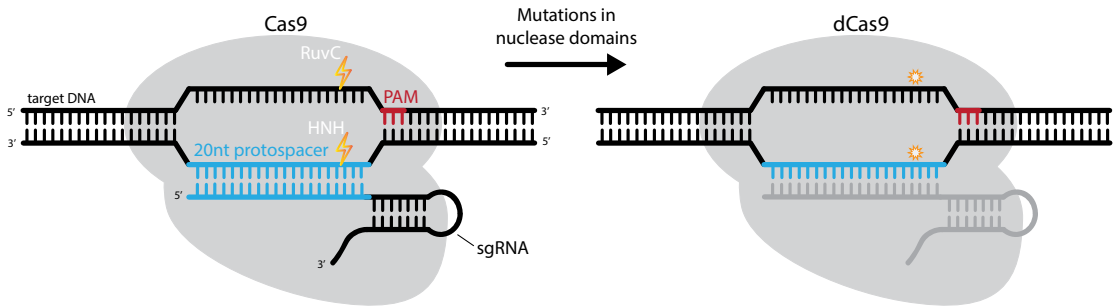
Figure 2.1 The Cas9 endonuclease and its nuclease-deactivated variant dCas9. The CRISPR-associated protein 9 (Cas9) is a prokaryotic antiviral protein that is guided by two RNA molecules (not shown) or, alternatively, one chimeric single-guide RNA (sgRNA) to cleave (using its RuvC and HNH catalytic domains) a target sequence containing a proper protospacer adjacent motif (PAM, in red) and matching the 20 nucleotide protospacer (in blue). Mutations in the nuclease domains (D10A and H840A in the commonly used *Streptococcus pyogenes* Cas9) result in a Cas9 variant, referred to as dCas9, capable of binding to the target sequence, but unable to cleave its target.

design strategies and applications of dCas9 for gene expression modulation and epigenetic editing.

dCas9 design strategies

Different strategies of varying complexity and efficacy for the use of dCas9 to manipulate the epigenome in controlled manner have been developed. In essence all these strategies belong to one of three categories discussed below (Fig. 2.2). Notably, some strategies discussed below have only been used for Cas9, but are equally suitable for use with dCas9.

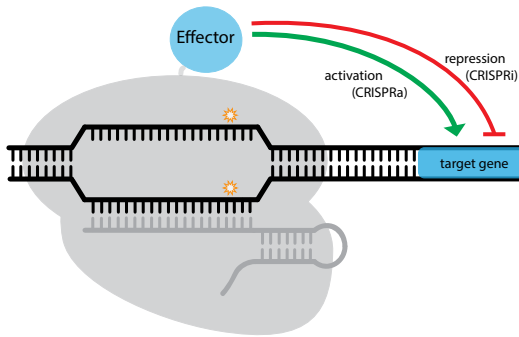### Class I – direct effector fusion

In the most straightforward design, the dCas9 protein (with no effector fused) is used to interfere with transcription via steric blockage of RNA polymerase binding or transcription elongation (Bikard *et al.*, 2013; Qi *et al.*, 2013). This strategy is successful in prokaryotes leading up to ~300-fold mRNA reduction when a single sgRNA is used to target dCas9 or even ~1000-fold when two sgRNAs are combined to block transcription elongation (Qi *et al.*, 2013). However, interference with transcription has not been successful in mammalian cells yielding only ~2-fold reduction in transcript levels (Qi *et al.*, 2013). For potent modulation of gene expression in mammalian cells by dCas9, specific effectors are implied. Down-regulation (CRISPRi) or activation (CRISPRa) of targeted genes is achieved by genetically fusing effector proteins – or

their active domains – to dCas9 and expressing them as a single recombinant protein (Fig. 2.2A). Transcription activator domains (VP64, p65) or repressor domains (KRAB, SID) have been fused to dCas9 to specifically increase or decrease target gene expression (Gilbert *et al.*, 2013; Maeder *et al.*, 2013b; Perez-Pinera *et al.*, 2013; Lawhorn *et al.*, 2014). Single dCas9–effector fusions are commonly targeted to adjacent sites using multiple different sgRNAs for maximum impact. In an effort to obtain maximum activation a combination of three different effectors (VP64, p65 and Rta) has been fused in succession to dCas9, resulting in a ~100-fold increase in transactivation of the target genes compared to dCas9-VP64 alone (Chavez *et al.*, 2015). A basic strategy towards achieving temporal control of dCas9–effector target binding is inducible expression of dCas9 or the sgRNA, e.g. by using a doxycycline (González *et al.*, 2014; Wang *et al.*, 2014; Dow *et al.*, 2015) or IPTG-responsive promoter. However, this approach suffers from leaky expression in the absence of an inducer.
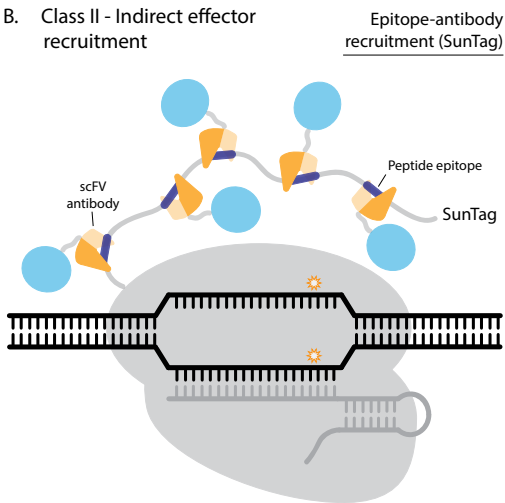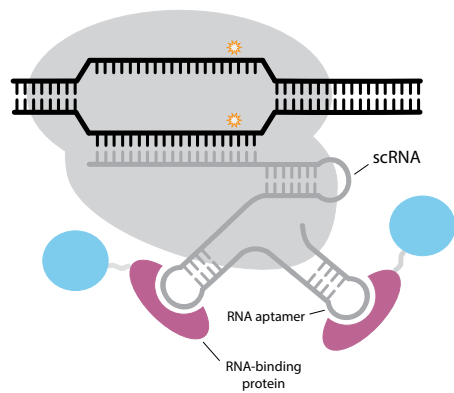
Class II – indirect effector recruitment

Class II strategies incorporate into the basic design additional motifs that recruit effector proteins (Fig. 2.2B). An example of such a motif is the SunTag (Tanenbaum *et al.*, 2014), a protein scaffold containing peptide epitopes (a variant with 10 and one with 24 epitopes is available) able to recruit effector domains via specific single-chain variable fragment (scFv) antibodies (Fig. 2.2B). The SunTag-carrying
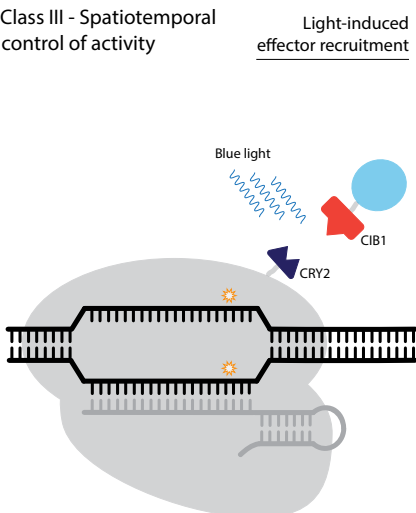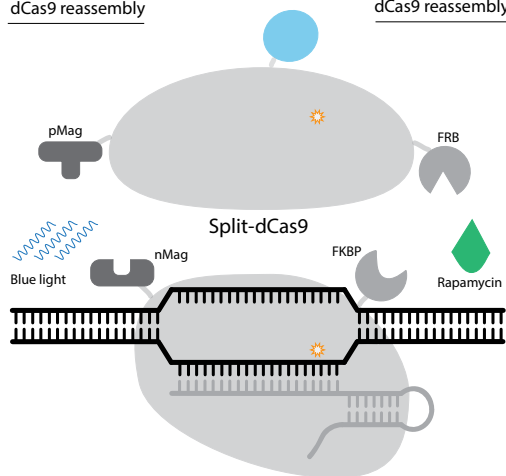
Figure 2.2 Design strategies of using dCas9 to target effector domains to specific DNA sequences. (A) The effector domain is directly fused to dCas9 to recruit it to sequences specified by the sgRNA. (B) The effector domain(s) is recruited via functional scaffolds incorporated in the sgRNA–dCas9 complex, either via fusion to dCas9 (left) or via RNA aptamers in a scaffolding RNA (scRNA, right). (C) Spatiotemporal control of effector activity is obtained via controlled recruitment of effectors to the sgRNA–dCas9 complex (left) or the reconstitution of split-dCas9 directly fused to effectors (right) via light- or chemical-inducible heterodimerization partners.

dCas9 has been shown to successfully recruit scFv–VP64 fusions and to increase target gene expression more than the simple dCas9–VP64 fusion (Tanenbaum *et al.*, 2014).

More complex systems with added functionality are not limited to direct genetic fusion of effector domains to dCas9. The sgRNA can be extended to include RNA aptamers (Fig. 2.2B), secondary RNA structures specifically recognized by RNA-binding proteins, to form a scaffolding RNA (scRNA) (Mali *et al.*, 2013a; Konermann *et al.*, 2015; Zalatan *et al.*, 2015). Using scRNAs with RNA aptamers such as MS2, PP7, com or the PUF binding site (PBS), effectors can be recruited to the dCas9–sgRNA complex indirectly via fusion to corresponding RNA-binding proteins (Mali *et al.*, 2013a; Zalatan *et al.*, 2015; Cheng *et al.*, 2016). Recruiting effectors simultaneously via a dCas9 gene fusion and via aptamers present in the sgRNA has been shown to yield strong synergistic transactivation (Konermann *et al.*, 2015; Xu *et al.*, 2016). For example, recruiting two MS2–p65-HSF1 fusions to dCas9-VP64 via an scRNA containing two MS2 hairpin aptamers resulted in a 100-fold enhancement of transactivation compared to just dCas9-VP64. Using just one scRNA this system outperformed a pool of eight sgRNAs targeting dCas9-VP64 to distinct sites along the proximal promoter region of target genes (Konermann *et al.*, 2015).

Class III – spatiotemporal control of activity

In a third class, dCas9 strategies are aimed at precisely controlling effector recruitment or dCas9 DNA-binding activity in space and/or time (Fig. 2.2C). Such control has been achieved by using split-(d)Cas9 or split-(d)Cas9-effector proteins that are conditionally assembled into a functional DNA-binding complex in the presence of sgRNA (Wright *et al.*, 2015), upon chemical induction (Zetsche *et al.*, 2015b) or light induction (Nihongaki *et al.*, 2015a). (d)Cas9, split in two individual domains, is assembled into a functional complex in the presence of full-length sgRNA. Truncated sgRNA prevents complex formation and can be used to disassemble the two Cas9 domains (Wright *et al.*, 2015). For chemical induction C- and N-terminal Cas9 (and dCas9) fragments have been fused to FK506 binding protein 12 (FKBP) and FKBP rapamycin binding (FRB) domains, respectively, that

dimerize upon rapamycin induction (Banaszynski *et al.*, 2005; Zetsche *et al.*, 2015b) (Fig. 2.2C). Using a split-dCas9 system fused to VP64, expression of target genes was shown to be specifically induced in the presence of rapamycin (Zetsche *et al.*, 2015b). Another strategy involves reassembly of split-dCas9 by photoinducible dimerization domains termed Magnets (pMag and nMag) (Fig. 2.2C) in response to exposure to blue light (Kawano *et al.*, 2015; Nihongaki *et al.*, 2015a).

In order to control effector recruitment rather than split-(d)Cas9 reconstitution, the heterodimerization partners CRY2 and CIB1 have been used to bring together full-length dCas9 and effectors such as VP64 or p65 upon blue light irradiation (Konermann *et al.*, 2013; Nihongaki *et al.*, 2015b; Polstein and Gersbach, 2015) (Fig. 2.2C). Although the light-inducible CRY2–CIB1 pair works well to bring together dCas9 and effectors, the use of these partners was unsuccessful when applied to reassembly of split-(d)Cas9 (Nihongaki *et al.*, 2015a).

An alternative strategy to control the binding of Cas9 to its target sequence relies on intein-mediated splicing (Davis *et al.*, 2015; Truong *et al.*, 2015). Designs with intein in the reading frame of full-length Cas9 or fused to both fragments of split-Cas9 have been used. In both cases, after intein trans-splicing is induced full-length functional Cas9 is obtained (Davis *et al.*, 2015; Truong *et al.*, 2015). An other, less common approach, is to use Cas9 inactive due to caging of lysine residues necessary for Cas9 function (Hemphill *et al.*, 2015). Exposure to UV light removes the caging group (Riggsbee and Deiters, 2010) and recovers an active Cas9 (Hemphill *et al.*, 2015).

Due to the availability of Cas9 orthologues (Chylinski *et al.*, 2014) and redesigned synthetic Cas9 proteins (Kleinstiver *et al.*, 2015; Hirano *et al.*, 2016) with different PAM recognition sequences (Table 2.1), combinations of multiple dCas9 orthologues and matching sgRNAs can be used in parallel to perform distinct activities. In *E. coli* two orthologues have been used to simultaneously cleave viral dsDNA and repress a reporter gene via transcriptional blockage (using a nuclease-active SpyCas9 and a deactivated NmCas9 protein respectively) (Esvelt *et al.*, 2013). In this study it was established that *N. meningitidis*, S. *thermophilus* CRISPR1 and S. *pyogenes* Cas9 function fully orthogonal to one another in *E. coli* as well as in

Table 2.1 Overview of Cas9 orthologues and synthetic redesigned Cas9s. Orthologues indicated with a + have been used as dCas9 systems. Abbreviations: N = any base; D = A, G or T; Y = C or T; R = G or A; W = A or T. Note: PAM sequences shown here are consensus sequences derived from sequence logos (i.e. nucleotide frequency plots) retrieved from bioinformatics analyses and/or cleavage assays using libraries of putative PAMs

Cas9	Origin	5′-PAM-3′	References
BlCas9	*Brevibacillus laterosporus*	NNNNCNDD	Karvelis *et al*., 2015
CdCas9	*Corynebacterium diphtheriae*	NGG	Ran *et al*., 2015
CjCas9	*Campylobacter jejuni*	NNNNACA	Fonfara *et al*., 2014
ClCas9	*Campylobacter lari*	NNGGG	Ran *et al*., 2015
FnCas9	*Francisella novicida*	NG	Fonfara *et al*., 2014
FnCas9$_{RHA}$	Mutant E1369<u>R</u>/E1449<u>H</u>/R1556<u>A</u>	YG	Hirano *et al*., 2016
LiCas9	*Listeria innocua*	NGG	Esvelt *et al*., 2013
NcCas9	*Neisseria cinerea*	NNNNGTA	Ran *et al*., 2015
NmCas9+	*Neisseria meningitidis*	NNNNGATT	Hou *et al*., 2013; Zhang *et al*., 2013
PlCas9	*Parvibaculum lavamentivorans*	NNNCAT	Ran *et al*., 2015
PmCas9	*Pasteurella multocida*	GNNNCNNA	Fonfara *et al*., 2014
SaCas9	*Staphylococcus aureus*	NNGRR(T)	Kleinstiver *et al*., 2015; Ran *et al*., 2015
SmCas9	*Streptococcus mutans*	NGG	Fonfara *et al*., 2014; van der Ploeg, 2009
SpaCas9	*Streptococcus pasteurianus*	NNGTGA	Ran *et al*., 2015
SpyCas9+	*Streptococcus pyogenes*	NGG	Jinek *et al*., 2012
SpyCas9$_{EQR}$	Mutant D1135<u>E</u>/R1335<u>Q</u>/T1337<u>R</u>	NGG (increased specificity)	Kleinstiver *et al*., 2015
SpyCas9$_{QQR1}$	Mutant G1218R/N1286Q/I1331F/D1332K/R1333<u>Q</u>/R1335<u>Q</u>/T1337<u>R</u>	NAAG	Anders *et al*., 2016
SpyCas9$_{VQR}$	Mutant D1135<u>V</u>/R1335<u>Q</u>/T1337<u>R</u>	NGAN	Kleinstiver *et al*., 2015
SpyCas9$_{VRER}$	Mutant D1135<u>V</u>/G1218<u>R</u>/R1335<u>E</u>/T1337<u>R</u>	NGCG	Kleinstiver *et al*., 2015
St1Cas9+	*Streptococcus thermophilus*** (CRISPR 1)	NNARAAW	Deveau *et al*., 2008; Fonfara *et al*., 2014; Horvath *et al*., 2008
St3Cas9	*Streptococcus thermophilus** (CRISPR 3)	NGG(NG)	Fonfara *et al*., 2014; Horvath *et al*., 2008
TdCas9+	*Treponema denticola*	NAAAAN	Esvelt *et al*., 2013

human cells, allowing for targeting distinct and non-overlapping sets of sequences within the same cell (Esvelt *et al*., 2013). The three catalytically deactivated Cas9 orthologues from the same three species have been used to label distinct chromosomal loci in live human cells (Ma *et al*., 2015).

Applications of the dCas9 tool

Targetable DNA-binding proteins with additional activity in epigenetic editing and/or gene expression modulation can be divided in two categories based on the nature of the effector: (i) targeted transcription factors (TTFs) and (ii) targeted epigenetic modifiers (TEMs) (Table 2.2). Effectors used in TTFs are (derivatives of) natural abundant and potent transcription factors that affect gene expression, but also often have indirect and multilateral effects on the states of the epigenome through recruitment of (multiple) effector partners. Commonly used effectors are herpes simplex viral protein 16, VP16 (Wang *et al*., 2000; Memedula and Belmont, 2003) – better known in tetrameric form as VP64 (Beerli *et al*., 1998) – and p65, a subunit of the human NF-κB transcription factor (Schmitz and Baeuerle, 1991). Both effectors exhibit complex mechanisms of transactivation via recruitment of secondary transcription factors (Mittler *et al*., 2003;

Table 2.2 An overview of effectors used in dCas9 systems

| | Direct fusion | Indirect recruitment | | | References |
		scRNA	SunTag	Light-induced	
Targeted transcription factors (TTFs)					
Activating	VP64				Chavez *et al*., 2015; Farzadfard *et al*., 2013; Gao *et al*., 2014; Gilbert *et al*., 2013; Hilton *et al*., 2015; Hu *et al*., 2014; Kearns *et al*., 2014; Maeder *et al*., 2013b; Mali *et al*., 2013b; Perez-Pinera *et al*., 2013; Polstein and Gersbach, 2015; Zetsche *et al*., 2015a
		VP64			Cheng *et al*., 2016; Mali *et al*., 2013b; Zalatan *et al*., 2015
			VP64		Gilbert *et al*., 2014; Tanenbaum *et al*., 2014
				VP64	Konermann *et al*., 2013; Nihongaki *et al*., 2015b; Polstein and Gersbach, 2015
	VP48				Cheng *et al*., 2013
	VP120				Cheng *et al*., 2013; Gao *et al*., 2014
	VP64	VP64 or p65 +/- HSF1 or MyoD1			Konermann *et al*., 2015
	p65				Gilbert *et al*., 2013
	p65	p65 or VP64			Konermann *et al*., 2015
				p65	Nihongaki *et al*., 2015b
	P65-HSF1				Cheng *et al*., 2016
		P65-HSF1			Cheng *et al*., 2016
	VP64-p65-Rta				Chavez *et al*., 2015
Repressing	KRAB				Farzadfard *et al*., 2013; Gao *et al*., 2014; Gilbert *et al*., 2013; Hu *et al*., 2014; Kearns *et al*., 2014, 2015; Lawhorn *et al*., 2014; Thakore *et al*., 2015
		KRAB			Cheng *et al*., 2016; Zalatan *et al*., 2015
	SID4x				Konermann *et al*., 2013
	Mxi1				Gilbert *et al*., 2013
Targeted epigenetic modifiers (TEMs)					
Histone acetylation	p300				Hilton *et al*., 2015
	CBP				Cheng *et al*., 2016
		CBP			Cheng *et al*., 2016
Histone demethylation	LSD1				Kearns *et al*., 2015
DNA methylation	DNMT3A				McDonald *et al*., 2016; Vojta *et al*., 2016
DNA demethylation	TET1	TET1			Xu *et al*., 2016

van Essen e*t al.*, 2009). As transcription repressor the Krüppel-associated box (KRAB), a domain found in numerous mammalian repressors, is commonly used. Together with recruited co-repressor KAP1, KRAB attracts a variety of epigenetic modifiers and chromatin remodelling proteins to induce heterochromatin and block transcription (Groner *et al.*, 2010). TEMs are designed based

on epigenetic effectors, i.e. (derivatives of or active domains of) enzymes that catalyse the transfer or removal of epigenetic modifications. Epigenetic effectors that have been used as TEMs are DNA methyltransferase 3A (DMT3A) (McDonald *et al.*, 2016; Vojta *et al.*, 2016), TET1 5mC-hydroxylase (Maeder *et al.*, 2013a; Xu *et al.*, 2016), LSD1 histone demethylase (Mendenhall *et al.*, 2013; Kearns *et al.*, 2015) and the p300 and CBP histone acetyltransferases (Hilton *et al.*, 2015; Cheng *et al.*, 2016). Below, we discuss applications of epigenetic editing by TEMs or indirect modulation by TTFs using dCas9 as DNA-binding platform.

Manipulating the epigenome and gene expression using TEMs and TTFs

So far only a few studies have been published reporting the use of dCas9 fusions for epigenome editing and manipulating gene expression. The catalytic histone acetyltransferase (HAT) core domain p300 has been used to catalyse acetylation of histones in human HEK293T cells (Hilton *et al.*, 2015). Targeting dCas9–p300 fusions to promoter regions or proximal or distant enhancers caused activation of gene expression. Increased expression upon enhancer-targeting was concomitant with enrichment in H3K27ac at the corresponding genomic target sites (Hilton *et al.*, 2015). In most cases the same genes could be transactivated by dCas9-VP64 when targeted at promoters. To achieve transactivation both effectors can thus be used. The two effectors behave somewhat differently in terms of their impact on histone acetylation state, as p300 directly catalyses H3K27ac (Ogryzko *et al.*, 1996; Delvecchio *et al.*, 2013), whereas VP64 recruits subsequent transactivation components, amongst which is p300 (Memedula and Belmont, 2003). Also the histone acetyltransferase domain of the CREB-binding protein has been fused to dCas9 (dCas9-CBPHAT) and has been used to catalyse locus-specific acetylation of histones (Cheng *et al.*, 2016). dCas9-CBPHAT was targeted using the Casilio (CRISPR/Cas9-Pumilio) system, which harbours an scRNA containing multiple PUF binding sites (PBS), to recruit additional CBPHAT domains via fusions with Pumilio/FBF (PUF) RNA-binding domains. Similar to dCas9-p300, targeting dCas9-CBPHAT to promoters or proximal and distal enhancer

caused increased expression of the target genes (Cheng *et al.*, 2016).

dCas9 has also been used to introduce DNA methylation by targeting the catalytic domain of the *de novo* DNA methyltransferase 3A (DNMT3A) to specific loci. dCas9-DNMT3A has been used to methylate cytosines around the transcription start site (TSS) of human and mice genes (McDonald *et al.*, 2016; Vojta *et al.*, 2016). Using this strategy, the methylation status of the CpG island spanning the TSS of the tumour-suppressor gene *CDKN2A* increased by 20%, resulting in 40% reduction in *CDKN2A* mRNA levels (McDonald *et al.*, 2016). Targeting the unmethylated promoter regions of the *BACH* or *IL6ST* genes increased CpG methylation by 50% and reduced expression 2-fold (Vojta *et al.*, 2016). However, this increase in methylation is not the only cause of reduced expression; catalytically inactive DNMT3A also induced repression, attributed to steric hindrance of the transcription machinery (McDonald *et al.*, 2016; Vojta *et al.*, 2016). In contrast, when dCas9-DNMT3A was targeted to a CpG island 100–400 bp downstream of the TSS, resulting in an increase of 20–35% methylation of CpG residues, no significant change in *CDKN2A* mRNA expression was observed (McDonald *et al.*, 2016). Upon targeting dCas9-DNMT3A to the unmethylated *Cdkn1a* gene in mouse myeloid progenitor cells resulting in *Cdkn1a* repression, proliferation was enhanced. In these studies dCas9 was as effective in introducing DNA methylation as ZFP- or TALE-based DNMT3A systems. The highest efficiency of methylation of targeted CpG residues was obtained when target sites are bracketed by inwardly directed sgRNAs (i.e. target CpGs are downstream of the PAM) and within ~50 bp of the sgRNA binding site (McDonald *et al.*, 2016; Vojta *et al.*, 2016).

Recently the catalytic domain of TET1 was used to induce demethylation of DNA (Xu *et al.*, 2016). In this study the catalytic domain of TET1 was fused to dCas9 and two additional copies of the same effector were directed to the target location via two MS2 aptamers integrated in the sgRNA design (Xu *et al.*, 2016). Transiently delivered scRNA/dCas9-TET1 induced demethylation of the targeted *RANKL* gene, a gene silenced through hypermethylation in HEK-293FT cells, and about 2-fold increased *RANKL* mRNA levels. Stable expression of the system yielded stronger effects:

10- to 20-fold transactivation (Xu *et al.*, 2016). To demonstrate the generic applicability of this epigenome editing strategy, expression of *MAGEB2* and *MMP2*, which are both silenced by hypermethylation in HeLa cells, was shown to be up-regulated by targeted demethylation. Interestingly, combining multiple sgRNAs that target distinct sites in the *RANKL* and *MAGE* genes does not result in significant additive or synergistic increase in transactivation (Xu *et al.*, 2016). A similar non-additive effect in transactivation was observed for dCas9-p300 targeted to multiple adjacent sites to induce histone acetylation (Hilton *et al.*, 2015).

Characterizing known or discovering new regulatory elements in the genome

Large-scale mapping of the human epigenome and chromatin states reveals vast numbers of putative regulatory elements (ENCODE Project Consortium, 2012; Thurman *et al.*, 2012; Roadmaps Epigenomics Consortium *et al.*, 2015). The validation and characterization of these elements benefits from the use of targetable epigenetic effectors to establish the functions of these regions in the genome.

In order to establish whether dCas9-LSD1 can be used to investigate enhancer function, the fusion protein has been targeted at well-characterized and putative enhancers in mouse embryonic stem cells. Before the introduction of dCas9, TALE–LSD1 fusion proteins had been already used to target endogenous candidate regulatory elements enriched for H3K4me2 and H3K27ac (Mendenhall *et al.*, 2013). These studies established that at a subset of putative enhancers the epigenetic state was altered following LSD1 targeting, permitting identification of the down-regulated target genes (Mendenhall *et al.*, 2013). Targeting of LSD1 to eight putative pluripotency-specific enhancers using dCas9 resulted in the discovery of four enhancers regulating the expression of genes critical in maintaining embryonic state (Kearns *et al.*, 2015). Chromosome conformation capture (3C) confirmed that the target gene was not down-regulated through enhancer–promoter loop disturbance of dCas9-LSD1 binding *per se*. A reduction in H3K4me2 and H3K27ac was observed around the sgRNA-dCas9-LSD1 target site in the identified *Tbx3*-enhancer. In contrast,

dCas9-KRAB targeted to the same site in the *Tbx3*-enhancer resulted in a reduction of H3K27ac and an increase of H3K27me3 and H3K9me3 at the *Tbx3* proximal promoter region. However, neither dCas9-KRAB nor dCas9-LSD1 was able to increase the level of the repressive marks H3K27me3 and H3K9me3 at the *Tbx3*-enhancer region. In a different study, in which the KRAB domain was targeted at the HS2 enhancer in the globin locus control region (LCR) in human K562 cells, H3K9me3 marks were effectively introduced at the target enhancer region (Thakore *et al.*, 2015). The introduction of these repressive marks was concurrent with decreased chromatin accessibility at the target site in the enhancer as well as in several other parts of the LCR (Thakore *et al.*, 2015). These findings suggest pleiotropic effects of dCas9-KRAB at the targeted enhancer–promoter loop or as yet uncharacterized downstream mechanisms of chromatin reorganization.

Genome-wide forward screening

Using libraries of targeted DNA-binding platforms fused to effectors the epigenetic states and/or expression levels of genes can be altered to study their impact on selected downstream processes or phenotypes in genome-wide forward screens. Such screening applications gain momentum due to expanding number of high-resolution techniques to measure epigenetic landscapes and chromatin states (Zentner and Henikoff, 2014; Ramani *et al.*, 2016), including the introduction of novel methods for mapping epigenetic modifications in the genomes of single cells (Angermueller *et al.*, 2016; Song *et al.*, 2016).

The application of dCas9 in forward screening using targeted transcription factors (TTFs) was shown to permit highly specific genome-scale transcription modulation (Gilbert *et al.*, 2014; Konermann *et al.*, 2015). Using combinations of 10 sgRNAs per gene, tiling −50 to +300 bp for repression (CRISPRi) or −400 to −50 bp for activation (CRISPRa) around the TSS to target nearly 1600 protein-encoding genes, human K562 cells were screened for growth phenotypes. In this study transcription was repressed using dCas9-KRAB and activated using dCas9-SunTag recruiting scFv–VP64 fusions (Gilbert *et al.*, 2014). In a second screen, known as well as novel complexes and pathways involved in the response to a chimeric

cholera–diphtheria toxin were identified (Gilbert *et al.*, 2014). Using next-generation sequencing, sgRNAs guiding the dCas9-effectors could afterwards be identified to determine the genomic locus responsible for the screened phenotypic characteristics (Gilbert *et al.*, 2014; Konermann *et al.*, 2015). A crucial aspect of screening studies using dCas9–effector fusions is that due to improved sgRNA design and more effective dCas9 design strategies, one dCas9 recruited by a single sgRNA now suffices in modulating a specific locus (Konermann *et al.*, 2015).

Current hurdles in application of dCas9

dCas9 has been shown to exhibit off-target binding at genome-wide scale (Kuscu *et al.*, 2014; Tsai *et al.*, 2015). Studies on target specificity have mainly been done on Cas9 (Fu *et al.*, 2014; Slaymaker *et al.*, 2016; Kleinstiver *et al.*, 2016); these findings can be extrapolated to dCas9 and dCas9-based effectors. The ability of the Cas9–sgRNA complex to localize and bind at a target sequence could be altered by genome accessibility as a consequence of local chromatin environment (Knight *et al.*, 2015) or binding of endogenous proteins such as transcription factors (Hilton *et al.*, 2015). Taking that notion into account target sites can be selected based on information regarding genome-bound proteins (e.g. using DNase-seq) (Maeder *et al.*, 2013b; Kearns *et al.*, 2014; Thakore *et al.*, 2015). Alternatively, DNA accessibility and off-target binding are determined *ad hoc* for every application. Off-target binding is related to flexibility in PAM sequence recognition and permitted mismatches in the PAM-distal part of the sgRNA (Kim *et al.*, 2015; Ran *et al.*, 2015; Tsai *et al.*, 2015; Wang *et al.*, 2015b; Leenay *et al.*, 2016). Efforts to reduce off-target binding include rational redesign of Cas9 for higher PAM specificity (Kleinstiver *et al.*, 2015), reduction of non-specific charge interactions between Cas9 and non-target DNA strand (Slaymaker *et al.*, 2016) or hydrogen bonding between Cas9 and the backbones of the target DNA strand and the sgRNA (Kleinstiver *et al.*, 2016), as well as use of truncated sgRNAs (Fu *et al.*, 2014). Although many of these strategies lead to a reduction of the DNA binding affinity of Cas9 or its activity, these efforts have contributed significantly to overcoming Cas9 off-target binding.

Another issue for applications of dCas9 is

its size. The coding sequence of the widely used SpyCas9 is around 4.2 kb, which is compatible with the ~4.5 kb maximum accommodated in common viral vectors used for delivery in mammalian cells. However, such a long dCas9 coding sequence does not leave 'space' for sgRNA sequences and regulatory elements to be co-delivered. This limits the application of some more complex design strategies such as extending the sgRNA with aptamers, adding effector domains to dCas9 or using pools of multiple sgRNAs. The relatively small Cas9 orthologue from *Staphylococcus aureus* (SaCas9) is 3.2 kb in size (Friedland *et al.*, 2015; Ran *et al.*, 2015). The use of such small orthologues reduces the size problem with no drawbacks on activity, as observed for a truncated SpyCas9 derivative in which a less-conserved, non-interacting portion of the recognition lobe had been removed (Nishimasu *et al.*, 2014). The split-dCas9 system also provides a solution to the size problem, but it requires two vectors for delivery (Truong *et al.*, 2015). Alternatively, cells stably expressing dCas9-effector proteins can be complemented by delivery of sgRNA, but stable expression is difficult to achieve when using primary cells or multicellular organisms. Another option is dCas9 delivery using *in vitro* assembled sgRNA-(d)Cas9 ribonucleoproteins (RNPs), an approach which was successful for dCas9-VP64 (Zuris *et al.*, 2015) and Cas9 genome editing applications (Cho *et al.*, 2013b; Kim *et al.*, 2014; Ramakrishna *et al.*, 2014; Sun *et al.*, 2015; Zuris *et al.*, 2015; D'Astolfo *et al.*, 2015). Finally, a potential hurdle for implementation in living organisms is the fact that the (d)Cas9 protein elicits an immunogenic responses due to its exogenous origin (Wang *et al.*, 2015a). Future dedicated studies will need to clarify the extent of this issue for possible clinical applications.

Conclusions and future perspectives

The importance of the epigenome is becoming increasingly clear in the light of developmental processes, cell differentiation status and diseases. In an attempt to draw causal relations rather than correlations to understand and control the interplay between the epigenome, chromatin structure and gene expression levels, targetable DNA-binding proteins have shown to be of great value. dCas9 has a more robust yet readily adjustable DNA-recognition

mechanism compared to ZFPs and TALEs; it has proven to be a flexible tool in recruiting effector domains to targeted DNA-sequences, in particular due to the numerous options arising from expanding the sgRNA even up to 5 kb long autonomous functional RNAs (Shechner *et al.*, 2015). The full value of dCas9 in the field of epigenetics has yet to be revealed with more functional studies at local scales and genome-wide level, providing detailed causal relations between epigenetic modifications, chromatin structure and gene expression. Future application in translational sciences such as medicine, synthetic biology or biotechnology, rely on advances in overcoming final hurdles provided by delivery problems due to its size, possible immunogenic response and off-target effects.

Alternatives for dCas9 emerge from the discovery and characterization of novel and known CRISPR systems involving protein complexes with different DNA-recognition mechanisms or different dimensions. Possible alternatives have recently become available in the form of the relatively small Cpf1 (~3.9 kb) (Zetsche *et al.*, 2015a; Yamano *et al.*, 2016), the C2c1 and C2c3 systems (Shmakov *et al.*, 2015) or even the multiprotein Cascade complex from the abundant Type I-E system native to *E. coli* K-12 (Luo *et al.*, 2015). These and future related systems add to a comprehensive CRISPR-based toolbox with distinct and orthogonal guiding crRNA, protospacer- or PAM-recognition, which is destined to occupy a permanent and prominent place in molecular biology.

Glossary

VP64: A strong transcriptional activation domain that recruits a variety of transcription factors and chromatin remodelling factors (Cress and Triezenberg, 1991). Tetrameric fusion of the acidic domain of herpes simplex viral protein 16 (VP16) (Beerli *et al.*, 1998).

p65: The 65 kDa subunit of the NF-κB transcription factor (Schmitz and Baeuerle, 1991). Often the principal transactivation domain (TA_1) is used as activation domain (p65AD).

KRAB: Krüppel-associated box (KRAB) is a common repression domain in eukaryotic transcription factors (Margolin *et al.*, 1994). It associates with KAP1, which forms a scaffold to recruit several proteins involved in inducing and spreading of heterochromatin over large distances (Groner *et al.*, 2010).

p300: Human transcriptional regulatory protein able to acetylate histone 3 at lysine residue 27 (Ogryzko *et al.*, 1996), a signal for active transcription. Often the isolated catalytic core of p300, containing the histone acetyltransferase (HAT) domain, is used as effector.

CBP: The CREB-binding protein (CBP) is able to bind many different transcription factors, acting as scaffold to co-activate transcription (Chan and La Thangue, 2001). Additionally, it has a histone acetyl transferase (HAT) domain, which can be used as epigenetic effector to acetylate lysine residues in histones.

LSD1: Lysine-specific demethylase 1 (LSD1) demethylates histone 3 at lysine residues 4 and 9, leading to silencing of enhancers (Shi *et al.*, 2004). LSD1 functionally interacts with other chromatin-modifying enzymes, including histone deacetylases that remove acetyl groups from histone 3 at lysine residue 27 (Lee *et al.*, 2006).

DNMT3A: DNA methyltransferase 3A (DNMT3A) catalyses *de novo* DNA methylation as well as methylation of hemimethylated DNA, preferentially at CpG sites (Okano *et al.*, 1998; Oka *et al.*, 2006). Methylated CpGs in promoters are associated with silenced transcription.

TET1: Ten-eleven translocation (TET) methylcytosine dioxygenase (TET1) is able to oxidate 5-methyl cytosines (5mC) to 5-hydroxymethylcytosines (5hmC), a step in the active removal of 5mC (Tahiliani *et al.*, 2009; Xu *et al.*, 2011). At promoters, this oxidation and removal is associated with activation of silenced genes.

Acknowledgements

References

Angermueller, C., Clark, S.J., Lee, H.J., Macaulay, I.C., Teng, M.J., Hu, T.X., Krueger, F., Smallwood, S.A., Ponting, C.P., Voet, T., *et al.* (2016). Parallel single-cell sequencing links transcriptional and epigenetic heterogeneity. Nat.

Methods *13*, 229–232. http://dx.doi.org/10.1038/nmeth.3728

Anton, T., Bultmann, S., Leonhardt, H., and Markaki, Y. (2014). Visualization of specific DNA sequences in living mouse embryonic stem cells with a programmable fluorescent CRISPR/Cas system. Nucleus *5*, 163–172. http://dx.doi.org/10.4161/nucl.28488

Banaszynski, L.A., Liu, C.W., and Wandless, T.J. (2005). Characterization of the FKBP.rapamycin.FRB ternary complex. JACS *127*, 4715–4721. http://dx.doi.org/10.1021/ja043277y

Barrangou, R., Fremaux, C., Deveau, H., Richards, M., Boyaval, P., Moineau, S., Romero, D.A., and Horvath, P. (2007). CRISPR provides acquired resistance against viruses in prokaryotes. Science *315*, 1709–1712.

Baylin, S.B., and Jones, P.A. (2011). A decade of exploring the cancer epigenome - biological and translational implications. Nat. Rev. Cancer. *11*, 726–734. http://dx.doi.org/10.1038/nrc3130

Beerli, R.R., Segal, D.J., Dreier, B., and Barbas III, C.F. (1998). Toward controlling gene expression at will: specific regulation of the erbB-2/HER-2 promoter by using polydactyl zinc finger proteins constructed from modular building blocks. Proc. Natl. Acad. Sci. U.S.A. *95*, 14628–14633.

Berger, S.L., Kouzarides, T., Shiekhattar, R., and Shilatifard, A. (2009). An operational definition of epigenetics. Genes. Dev. *23*, 781–783. http://dx.doi.org/10.1101/gad.1787609

Bernstein, B.E., Stamatoyannopoulos, J.A., Costello, J.F., Ren, B., Milosavljevic, A., Meissner, A., Kellis, M., Marra, M.A., Beaudet, A.L., Ecker, J.R., *et al.* (2010). The NIH Roadmap Epigenomics Mapping Consortium. Nat. Biotechnol. *28*, 1045–1048. http://dx.doi.org/10.1038/nbt1010-1045

Bhaya, D., Davison, M., and Barrangou, R. (2011). CRISPR-Cas systems in bacteria and archaea: versatile small RNAs for adaptive defense and regulation. Annu. Rev. Genet. *45*, 273–297. http://dx.doi.org/10.1146/annurev-genet-110410-132430

Bikard, D., Jiang, W., Samai, P., Hochschild, A., Zhang, F., and Marraffini, L.A. (2013). Programmable repression and activation of bacterial gene expression using an engineered CRISPR-Cas system. Nucleic Acids Res. *41*, 7429–7437. http://dx.doi.org/10.1093/nar/gkt520

Bird, A. (2002). DNA methylation patterns and epigenetic memory. Genes. Dev. *16*, 6–21. http://dx.doi.org/10.1101/gad.947102

Bird, A. (2007). Perceptions of epigenetics. Nature *447*, 396–398.

Boch, J., Scholze, H., Schornack, S., Landgraf, A., Hahn, S., Kay, S., Lahaye, T., Nickstadt, A., and Bonas, U. (2009). Breaking the code of DNA binding specificity of TAL-type III effectors. Science *326*, 1509–1512. http://dx.doi.org/10.1126/science.1178811

Bultmann, S., Morbitzer, R., Schmidt, C.S., Thanisch, K., Spada, F., Elsaesser, J., Lahaye, T., and Leonhardt, H. (2012). Targeted transcriptional activation of silent oct4 pluripotency gene by combining designer TALEs and inhibition of epigenetic modifiers. Nucleic Acids Res. *40*, 5368–5377. http://dx.doi.org/10.1093/nar/gks199

Chan, H.M., and La Thangue, N.B. (2001). p300/CBP proteins: HATs for transcriptional bridges and scaffolds. J. Cell Sci. *114*, 2363–2373.

Chavez, A., Scheiman, J., Vora, S., Pruitt, B.W., Tuttle, M., Iyer, E.P.R., Lin, S., Kiani, S., Guzman, C.D., Wiegand, D.J., *et al.* (2015). Highly efficient Cas9-mediated transcriptional programming. Nat. Methods *12*, 326–328. http://dx.doi.org/10.1038/nmeth.3312

Chen, B., Gilbert, L.A., Cimini, B.A., Schnitzbauer, J., Zhang, W., Li, G.-W., Park, J., Blackburn, E.H., Weissman, J.S., Qi, L.S., *et al.* (2013). Dynamic imaging of genomic loci in living human cells by an optimized CRISPR/Cas system. Cell *155*, 1479–1491. http://dx.doi.org/10.1016/j.cell.2013.12.001

Cheng, A.W., Jillette, N., Lee, P., Plaskon, D., Fujiwara, Y., Wang, W., Taghbalout, A., and Wang, H. (2016). Casilio: a versatile CRISPR-Cas9-Pumilio hybrid for gene regulation and genomic labeling. Cell Res. *26*, 254–257. http://dx.doi.org/10.1038/cr.2016.3

Cheng, A.W., Wang, H., Yang, H., Shi, L., Katz, Y., Theunissen, T.W., Rangarajan, S., Shivalila, C.S., Dadon, D.B., and Jaenisch, R. (2013). Multiplexed activation of endogenous genes by CRISPR-on, an RNA-guided transcriptional activator system. Cell Res. *23*, 1163–1171. http://dx.doi.org/10.1038/cr.2013.122

Cho, S.W., Kim, S., Kim, J.M., and Kim, J.-S. (2013a). Targeted genome engineering in human cells with the Cas9 RNA-guided endonuclease. Nat. Biotechnol. *31*, 230–232. http://dx.doi.org/10.1038/nbt.2507

Cho, S.W., Lee, J., Carroll, D., Kim, J.-S., and Lee, J. (2013b). Heritable gene knockout in Caenorhabditis elegans by direct injection of Cas9-sgRNA ribonucleoproteins. Genetics *195*, 1177–1180. http://dx.doi.org/10.1534/genetics.113.155853

Chong, S., and Whitelaw, E. (2004). Epigenetic germline inheritance. Curr. Opin. Genet. Dev. *14*, 692–696. http://dx.doi.org/10.1016/j.gde.2004.09.001

Choo, Y. (1998). Recognition of DNA methylation by zinc fingers. Nat. Struct. Biol. *5*, 264–265.

Choo, Y., Sánchez-García, I., and Klug, A. (1994). In vivo repression by a site-specific DNA-binding protein designed against an oncogenic sequence. Nature *372*, 642–645. http://dx.doi.org/10.1038/372642a0

Chylinski, K., Makarova, K.S., Charpentier, E., and Koonin, E.V. (2014). Classification and evolution of type II CRISPR-Cas systems. Nucleic Acids Res. *42*, 6091–6105. http://dx.doi.org/10.1093/nar/gku241

Cong, L., Ran, F.A., Cox, D., Lin, S., Barretto, R., Habib, N., Hsu, P.D., Wu, X., Jiang, W., Marraffini, L.A., *et al.* (2013). Multiplex genome engineering using CRISPR/Cas systems. Science *339*, 819–823. http://dx.doi.org/10.1126/science.1231143

Cress, W.D., and Triezenberg, S.J. (1991). Critical structural elements of the VP16 transcriptional activation domain. Science *251*, 87–90.

Cubas, P., Vincent, C., and Coen, E. (1999). An epigenetic mutation responsible for natural variation in floral symmetry. Nature *401*, 157–161. http://dx.doi.org/10.1038/43657

D'Astolfo, D.S., Pagliero, R.J., Pras, A., Karthaus, W.R., Clevers, H., Prasad, V., Lebbink, R.J., Rehmann, H., and Geijsen, N. (2015). Efficient intracellular delivery

of native proteins. Cell *161*, 674–690. http://dx.doi.org/10.1016/j.cell.2015.03.028

Daniel, J.M., Spring, C.M., Crawford, H.C., Reynolds, A.B., and Baig, A. (2002). The p120ctn-binding partner Kaiso is a bi-modal DNA-binding protein that recognizes both a sequence-specific consensus and methylated CpG dinucleotides. Nucleic Acids Res. *30*, 2911–2919.

Davis, K.M., Pattanayak, V., Thompson, D.B., Zuris, J.A., and Liu, D.R. (2015). Small molecule-triggered Cas9 protein with improved genome-editing specificity. Nat. Chem. Biol. *11*, 316–318. http://dx.doi.org/10.1038/nchembio.1793

de Groote, M.L., Verschure, P.J., and Rots, M.G. (2012). Epigenetic Editing: targeted rewriting of epigenetic marks to modulate expression of selected target genes. Nucleic Acids Res. *40*, 10596–10613. http://dx.doi.org/10.1093/nar/gks863

Delvecchio, M., Gaucher, J., Aguilar-Gurrieri, C., Ortega, E., and Panne, D. (2013). Structure of the p300 catalytic core and implications for chromatin targeting and HAT regulation. Nat. Struct. Mol. Biol. *20*, 1040–1046. http://dx.doi.org/10.1038/nsmb.2642

Deng, D., Yan, C., Pan, X., Mahfouz, M., Wang, J., Zhu, J.-K., Shi, Y., and Yan, N. (2012). Structural basis for sequence-specific recognition of DNA by TAL effectors. Science *335*, 720–723. http://dx.doi.org/10.1126/science.1215670

Doudna, J.A., and Charpentier, E. (2014). Genome editing. The new frontier of genome engineering with CRISPR-Cas9. Science *346*, 1258096. http://dx.doi.org/10.1126/science.1258096

Dow, L.E., Fisher, J., O'Rourke, K.P., Muley, A., Kastenhuber, E.R., Livshits, G., Tschaharganeh, D.F., Socci, N.D., and Lowe, S.W. (2015). Inducible in vivo genome editing with CRISPR-Cas9. Nat. Biotechnol. *33*, 390–394. http://dx.doi.org/10.1038/nbt.3155

ENCODE Project Consortium. (2012). An integrated encyclopedia of DNA elements in the human genome. Nature *489*, 57–74. http://dx.doi.org/10.1038/nature11247

Esvelt, K.M., Mali, P., Braff, J.L., Moosburner, M., Yaung, S.J., and Church, G.M. (2013). Orthogonal Cas9 proteins for RNA-guided gene regulation and editing. Nat. Methods *10*, 1116–1121. http://dx.doi.org/10.1038/nmeth.2681

Friedland, A.E., Baral, R., Singhal, P., Loveluck, K., Shen, S., Sanchez, M., Marco, E., Gotta, G.M., Maeder, M.L., Kennedy, E.M., *et al.* (2015). Characterization of Staphylococcus aureus Cas9: a smaller Cas9 for all-in-one adeno-associated virus delivery and paired nickase applications. Genome Biol. *16*. http://dx.doi.org/10.1186/s13059-015-0817-8

Fu, Y., Sander, J.D., Reyon, D., Cascio, V.M., and Joung, J.K. (2014). Improving CRISPR-Cas nuclease specificity using truncated guide RNAs. Nat. Biotechnol. *32*, 279–284. http://dx.doi.org/10.1038/nbt.2808

Gaj, T., Gersbach, C.A., and Barbas III, C.F. (2013). ZFN, TALEN, and CRISPR/Cas-based methods for genome engineering. Trends Biotechnol. *31*, 397–405. http://dx.doi.org/10.1016/j.tibtech.2013.04.004

Gardner, K.E., Allis, C.D., and Strahl, B.D. (2011). Operating on chromatin, a colorful language where context matters. J. Mol. Biol. *409*, 36–46. http://dx.doi.org/10.1016/j.jmb.2011.01.040

Gersbach, C.A., Gaj, T., and Barbas III, C.F. (2014). Synthetic zinc finger proteins: the advent of targeted gene regulation and genome modification technologies. Acc. Chem. Res. *47*, 2309–2318. http://dx.doi.org/10.1021/ar500039w

Gilbert, L.A., Horlbeck, M.A., Adamson, B., Villalta, J.E., Chen, Y., Whitehead, E.H., Guimaraes, C., Panning, B., Ploegh, H.L., Bassik, M.C., *et al.* (2014). Genome-scale CRISPR-mediated control of gene repression and activation. Cell *159*, 647–661. http://dx.doi.org/10.1016/j.cell.2014.09.029

Gilbert, L.A., Larson, M.H., Morsut, L., Liu, Z., Brar, G.A., Torres, S.E., Stern-Ginossar, N., Brandman, O., Whitehead, E.H., Doudna, J.A., *et al.* (2013). CRISPR-mediated modular RNA-guided regulation of transcription in eukaryotes. Cell *154*, 442–451. http://dx.doi.org/10.1016/j.cell.2013.06.044

González, F., Zhu, Z., Shi, Z.D., Lelli, K., Verma, N., Li, Q.V., and Huangfu, D. (2014). An iCRISPR platform for rapid, multiplexable, and inducible genome editing in human pluripotent stem cells. Cell Stem Cell *15*, 215–226. http://dx.doi.org/10.1016/j.stem.2014.05.018

Grau, J., Boch, J., and Posch, S. (2013). TALENoffer: genome-wide TALEN off-target prediction. Bioinformatics *29*, 2931–2932. http://dx.doi.org/10.1093/bioinformatics/btt501

Groner, A.C., Meylan, S., Ciuffi, A., Zangger, N., Ambrosini, G., Dénervaud, N., Bucher, P., and Trono, D. (2010). KRAB-zinc finger proteins and KAP1 can mediate long-range transcriptional repression through heterochromatin spreading. PLoS Genet. *6*, e1000869. http://dx.doi.org/10.1371/journal.pgen.1000869

Guilinger, J.P., Pattanayak, V., Reyon, D., Tsai, S.Q., Sander, J.D., Joung, J.K., and Liu, D.R. (2014). Broad specificity profiling of TALENs results in engineered nucleases with improved DNA-cleavage specificity. Nat. Methods *11*, 429–435. http://dx.doi.org/10.1038/nmeth.2845

Hemphill, J., Borchardt, E.K., Brown, K., Asokan, A., and Deiters, A. (2015). Optical control of CRISPR/Cas9 gene editing. JACS *137*, 5642–5645. http://dx.doi.org/10.1021/ja512664v

Henikoff, S., and Shilatifard, A. (2011). Histone modification: cause or cog? Trends Genet. *27*, 389–396. http://dx.doi.org/10.1016/j.tig.2011.06.006

Hilton, I.B., D'Ippolito, A.M., Vockley, C.M., Thakore, P.I., Crawford, G.E., Reddy, T.E., and Gersbach, C.A. (2015). Epigenome editing by a CRISPR-Cas9-based acetyltransferase activates genes from promoters and enhancers. Nat. Biotechnol. *33*, 510–517. http://dx.doi.org/10.1038/nbt.3199

Hirano, H., Gootenberg, J.S., Horii, T., Abudayyeh, O.O., Kimura, M., Hsu, P.D., Nakane, T., Ishitani, R., Hatada, I., Zhang, F., *et al.* (2016). Structure and engineering of *Francisella novicida* Cas9. Cell *164*, 950–961. http://dx.doi.org/10.1016/j.cell.2016.01.039

Holliday, R. (1987). The inheritance of epigenetic defects. Science *238*, 163–170.

Holliday, R. (2006). Epigenetics: a historical overview. Epigenetics *1*, 76–80. http://dx.doi.org/10.4161/epi.1.2.2762

Hwang, W.Y., Fu, Y., Reyon, D., Maeder, M.L., Tsai, S.Q., Sander, J.D., Peterson, R.T., Yeh, J.R., and Joung, J.K. (2013). Efficient genome editing in zebrafish using a CRISPR-Cas system. Nat. Biotechnol. *31*, 227–229. http://dx.doi.org/10.1038/nbt.2501

Jinek, M., Chylinski, K., Fonfara, I., Hauer, M., Doudna, J.A., and Charpentier, E. (2012). A programmable dual-RNA-guided DNA endonuclease in adaptive bacterial immunity. Science *337*, 816–821. http://dx.doi.org/10.1126/science.1225829

Jinek, M., East, A., Cheng, A., Lin, S., Ma, E., and Doudna, J. (2013). RNA-programmed genome editing in human cells. Elife *2*, e00471. http://dx.doi.org/10.7554/eLife.00471

Kawano, F., Suzuki, H., Furuya, A., and Sato, M. (2015). Engineered pairs of distinct photoswitches for optogenetic control of cellular proteins. Nat. Commun. *6*, 6256. http://dx.doi.org/10.1038/ncomms7256

Kearns, N.A., Genga, R.M.J., Enuameh, M.S., Garber, M., Wolfe, S.A., and Maehr, R. (2014). Cas9 effector-mediated regulation of transcription and differentiation in human pluripotent stem cells. Development *141*, 219–223. http://dx.doi.org/10.1242/dev.103341

Kearns, N.A., Pham, H., Tabak, B., Genga, R.M., Silverstein, N.J., Garber, M., and Maehr, R. (2015). Functional annotation of native enhancers with a Cas9-histone demethylase fusion. Nat. Methods *12*, 401–403. http://dx.doi.org/10.1038/nmeth.3325

Kelly, T.K., De Carvalho, D.D., and Jones, P.A. (2010). Epigenetic modifications as therapeutic targets. Nat. Biotechnol. *28*, 1069–1078. http://dx.doi.org/10.1038/nbt.1678

Kim, D., Bae, S., Park, J., Kim, E., Kim, S., Yu, H.R., Hwang, J., Kim, J.-I., and Kim, J.-S. (2015). Digenome-seq: genome-wide profiling of CRISPR-Cas9 off-target effects in human cells. Nat. Methods *12*, 237–243. http://dx.doi.org/10.1038/nmeth.3284

Kim, S., Kim, D., Cho, S.W., Kim, J., and Kim, J.-S. (2014). Highly efficient RNA-guided genome editing in human cells via delivery of purified Cas9 ribonucleoproteins. Genome Res. *24*, 1012–1019. http://dx.doi.org/10.1101/gr.171322.113

Kleinstiver, B.P., Pattanayak, V., Prew, M.S., Tsai, S.Q., Nguyen, N.T., Zheng, Z., and Joung, J.K. (2016). High-fidelity CRISPR-Cas9 nucleases with no detectable genome-wide off-target effects. Nature *529*, 490–495. http://dx.doi.org/10.1038/nature16526

Kleinstiver, B.P., Prew, M.S., Tsai, S.Q., Topkar, V.V., Nguyen, N.T., Zheng, Z., Gonzales, A.P.W., Li, Z., Peterson, R.T., Yeh, J.R., *et al.* (2015). Engineered CRISPR-Cas9 nucleases with altered PAM specificities. Nature *523*, 481–485. http://dx.doi.org/10.1038/nature14592

Klug, A. (2010). The discovery of zinc fingers and their applications in gene regulation and genome manipulation. Annu. Rev. Biochem. *79*, 213–231. http://dx.doi.org/10.1146/annurev-biochem-010909-095056

Knight, S.C., Xie, L., Deng, W., Guglielmi, B., Witkowsky, L.B., Bosanac, L., Zhang, E.T., El Beheiry, M., Masson, J.B., Dahan, M., *et al.* (2015). Dynamics of CRISPR-Cas9 genome interrogation in living cells. Science *350*, 823–826. http://dx.doi.org/10.1126/science.aac6572

Konermann, S., Brigham, M.D., Trevino, A.E., Hsu, P.D., Heidenreich, M., Cong, L., Platt, R.J., Scott, D.A., Church, G.M., and Zhang, F. (2013). Optical control of mammalian endogenous transcription and epigenetic states. Nature *500*, 472–476. http://dx.doi.org/10.1038/nature12466

Konermann, S., Brigham, M.D., Trevino, A.E., Joung, J., Abudayyeh, O.O., Barcena, C., Hsu, P.D., Habib, N., Gootenberg, J.S., Nishimasu, H., *et al.* (2015). Genome-scale transcriptional activation by an engineered CRISPR-Cas9 complex. Nature *517*, 583–588. http://dx.doi.org/10.1038/nature14136

Kouzarides, T. (2007). Chromatin modifications and their function. Cell *128*, 693–705.

Kuscu, C., Arslan, S., Singh, R., Thorpe, J., and Adli, M. (2014). Genome-wide analysis reveals characteristics of off-target sites bound by the Cas9 endonuclease. Nat. Biotechnol. *32*, 677–683. http://dx.doi.org/10.1038/nbt.2916

Lawhorn, I.E.B., Ferreira, J.P., and Wang, C.L. (2014). Evaluation of sgRNA target sites for CRISPR-mediated repression of TP53. PLoS One *9*, e113232. http://dx.doi.org/10.1371/journal.pone.0113232

Lee, M.G., Wynder, C., Bochar, D.A., Hakimi, M.-A., Cooch, N., and Shiekhattar, R. (2006). Functional interplay between histone demethylase and deacetylase enzymes. Mol. Cell. Biol. *26*, 6395–6402. http://dx.doi.org/10.1128/MCB.00723-06

Leenay, R.T., Maksimchuk, K.R., Slotkowski, R.A., Agrawal, R.N., Gomaa, A.A., Briner, A.E., Barrangou, R., and Beisel, C.L. (2016). Identifying and visualizing functional PAM diversity across CRISPR-Cas systems. Mol. Cell *62*, 137–147. http://dx.doi.org/10.1016/j.molcel.2016.02.031

Luo, M.L., Mullis, A.S., Leenay, R.T., and Beisel, C.L. (2015). Repurposing endogenous type I CRISPR-Cas systems for programmable gene repression. Nucleic Acids Res. *43*, 674–681. http://dx.doi.org/10.1093/nar/gku971

Lyko, F., and Brown, R. (2005). DNA methyltransferase inhibitors and the development of epigenetic cancer therapies. J. Natl. Cancer Inst. *97*, 1498–1506. http://dx.doi.org/10.1093/jnci/dji311

Ma, H., Naseri, A., Reyes-Gutierrez, P., Wolfe, S.A., Zhang, S., and Pederson, T. (2015). Multicolor CRISPR labeling of chromosomal loci in human cells. Proc. Natl. Acad. Sci. U.S.A. *112*, 3002–3007. http://dx.doi.org/10.1073/pnas.1420024112

Maeder, M.L., Angstman, J.F., Richardson, M.E., Linder, S.J., Cascio, V.M., Tsai, S.Q., Ho, Q.H., Sander, J.D., Reyon, D., Bernstein, B.E., *et al.* (2013a). Targeted DNA demethylation and activation of endogenous genes using programmable TALE-TET1 fusion proteins. Nat. Biotechnol. *31*, 1137–1142. http://dx.doi.org/10.1038/nbt.2726

Maeder, M.L., Linder, S.J., Cascio, V.M., Fu, Y., Ho, Q.H., and Joung, J.K. (2013b). CRISPR RNA-guided activation of endogenous human genes. Nat. Methods *10*, 977–979. http://dx.doi.org/10.1038/nmeth.2598

Mali, P., Aach, J., Stranges, P.B., Esvelt, K.M., Moosburner, M., Kosuri, S., Yang, L., and Church, G.M. (2013a). CAS9 transcriptional activators for target specificity screening and paired nickases for cooperative genome engineering. Nat. Biotechnol. *31*, 833–838. http://dx.doi.org/10.1038/nbt.2675

Mali, P., Yang, L., Esvelt, K.M., Aach, J., Guell, M., DiCarlo, J.E., Norville, J.E., and Church, G.M. (2013b). RNA-guided human genome engineering via Cas9. Science *339*, 823–826. http://dx.doi.org/10.1126/science.1232033

Margolin, J.F., Friedman, J.R., Meyer, W.K.-H., Vissing, H., Thiesen, H.-J., and Rauscher III, F.J. (1994). Krüppel-associated boxes are potent transcriptional repression domains. Proc. Natl. Acad. Sci. U.S.A. *91*, 4509–4513.

McDonald, J.I., Celik, H., Rois, L.E., Fishberger, G., Fowler, T., Rees, R., Kramer, A., Martens, A., Edwards, J.R., and Challen, G.A. (2016). Reprogrammable CRISPR/Cas9-based system for inducing site-specific DNA methylation. Biol. Open. *5*, 866–874. http://dx.doi.org/10.1242/bio.019067

Memedula, S., and Belmont, A.S. (2003). Sequential recruitment of HAT and SWI/SNF components to condensed chromatin by VP16. Curr. Biol. *13*, 241–246. http://dx.doi.org/10.1016/S0960-9822(03)00048-4

Mendenhall, E.M., Williamson, K.E., Reyon, D., Zou, J.Y., Ram, O., Joung, J.K., and Bernstein, B.E. (2013). Locus-specific editing of histone modifications at endogenous enhancers. Nat. Biotechnol. *31*, 1133–1136. http://dx.doi.org/10.1038/nbt.2701

Mittler, G., Stühler, T., Santolin, L., Uhlmann, T., Kremmer, E., Lottspeich, F., Berti, L., and Meisterernst, M. (2003). A novel docking site on Mediator is critical for activation by VP16 in mammalian cells. EMBO J. *22*, 6494–6504. http://dx.doi.org/10.1093/emboj/cdg619

Morbitzer, R., Römer, P., Boch, J., and Lahaye, T. (2010). Regulation of selected genome loci using de novo-engineered transcription activator-like effector (TALE)-type transcription factors. Proc. Natl. Acad. Sci. U.S.A. *107*, 21617–21622. http://dx.doi.org/10.1073/pnas.1013133107

Moscou, M.J., and Bogdanove, A.J. (2009). A simple cipher governs DNA recognition by TAL effectors. Science *326*, 1501. http://dx.doi.org/10.1126/science.1178817

Mussolino, C., and Cathomen, T. (2012). TALE nucleases: tailored genome engineering made easy. Curr. Opin. Biotechnol. *23*, 644–650. http://dx.doi.org/10.1016/j.copbio.2012.01.013

Nihongaki, Y., Kawano, F., Nakajima, T., and Sato, M. (2015a). Photoactivatable CRISPR-Cas9 for optogenetic genome editing. Nat. Biotechnol. *33*, 755–760. http://dx.doi.org/10.1038/nbt.3245

Nihongaki, Y., Yamamoto, S., Kawano, F., Suzuki, H., and Sato, M. (2015b). CRISPR-Cas9-based photoactivatable transcription system. Chem. Biol. *22*, 169–174. http://dx.doi.org/10.1016/j.chembiol.2014.12.011

Nishimasu, H., Ran, F.A., Hsu, P.D., Konermann, S., Shehata, S.I., Dohmae, N., Ishitani, R., Zhang, F., and Nureki, O. (2014). Crystal structure of Cas9 in complex with guide RNA and target DNA. Cell *156*, 935–949. http://dx.doi.org/10.1016/j.cell.2014.02.001

Ogryzko, V.V., Schiltz, R.L., Russanova, V., Howard, B.H., and Nakatani, Y. (1996). The transcriptional coactivators p300 and CBP are histone acetyltransferases. Cell *87*, 953–959.

Oka, M., Rodić, N., Graddy, J., Chang, L.-J., and Terada, N. (2006). CpG sites preferentially methylated by Dnmt3a

in vivo. J. Biol. Chem. *281*, 9901–9908. http://dx.doi.org/10.1074/jbc.M511100200

Okano, M., Xie, S., and Li, E. (1998). Cloning and characterization of a family of novel mammalian DNA (cytosine-5) methyltransferases. Nat. Genet. *19*, 219–220. http://dx.doi.org/10.1038/890

Pavletich, N.P., and Pabo, C.O. (1991). Zinc finger-DNA recognition: crystal structure of a Zif268-DNA complex at 2.1 Å. Science *252*, 809–817. http://dx.doi.org/10.1126/science.2028256

Perez-Pinera, P., Kocak, D.D., Vockley, C.M., Adler, A.F., Kabadi, A.M., Polstein, L.R., Thakore, P.I., Glass, K.A., Ousterout, D.G., Leong, K.W., *et al.* (2013). RNA-guided gene activation by CRISPR-Cas9-based transcription factors. Nat. Methods *10*, 973–976. http://dx.doi.org/10.1038/nmeth.2600

Plass, C., Pfister, S.M., Lindroth, A.M., Bogatyrova, O., Claus, R., and Lichter, P. (2013). Mutations in regulators of the epigenome and their connections to global chromatin patterns in cancer. Nat. Rev. Genet. *14*, 765–780. http://dx.doi.org/10.1038/nrg3554

Polstein, L.R., and Gersbach, C.A. (2015). A light-inducible CRISPR-Cas9 system for control of endogenous gene activation. Nat. Chem. Biol. *11*, 198–200. http://dx.doi.org/10.1038/nchembio.1753

Qi, L.S., Larson, M.H., Gilbert, L.A., Doudna, J.A., Weissman, J.S., Arkin, A.P., and Lim, W.A. (2013). Repurposing CRISPR as an RNA-guided platform for sequence-specific control of gene expression. Cell *152*, 1173–1183. http://dx.doi.org/10.1016/j.cell.2013.02.022

Ramakrishna, S., Abu-Bonsrah, K.D., Beloor, J., Gopalappa, R., Lee, S.-K., and Kim, H. (2014). Gene disruption by cell-penetrating peptide-mediated delivery of Cas9 protein and guide RNA. Genome Res. *24*, 1020–1027. http://dx.doi.org/10.1101/gr.171264.113

Ramani, V., Shendure, J., and Duan, Z. (2016). Understanding spatial genome organization: methods and insights. Genomics Proteomics Bioinformatics *14*, 7–20. http://dx.doi.org/10.1016/j.gpb.2016.01.002

Ran, F.A., Cong, L., Yan, W.X., Scott, D.A., Gootenberg, J.S., Kriz, A.J., Zetsche, B., Shalem, O., Wu, X., Makarova, K.S., *et al.* (2015). In vivo genome editing using *Staphylococcus aureus* Cas9. Nature *520*, 186–191. http://dx.doi.org/10.1038/nature14299

Reyon, D., Tsai, S.Q., Khayter, C., Foden, J.A., Sander, J.D., and Joung, J.K. (2012). FLASH assembly of TALENs for high-throughput genome editing. Nat. Biotechnol. *30*, 460–465. http://dx.doi.org/10.1038/nbt.2170

Riggsbee, C.W., and Deiters, A. (2010). Recent advances in the photochemical control of protein function. Trends Biotechnol. *28*, 468–475. http://dx.doi.org/10.1016/j.tibtech.2010.06.001

Rivera, C.M., and Ren, B. (2013). Mapping human epigenomes. Cell *155*, 39–55. http://dx.doi.org/10.1016/j.cell.2013.09.011

Roadmaps Epigenomics Consortium, Kundaje, A., Meuleman, W., Ernst, J., Bilenky, M., Yen, A., Heravi-Moussavi, A., Kheradpour, P., Zhang, Z., Wang, J., *et al.* (2015). Integrative analysis of 111 reference human epigenomes. Nature *518*, 317–330. http://dx.doi.org/10.1038/nature14248

Rogers, J.M., Barrera, L.A., Reyon, D., Sander, J.D., Kellis, M., Joung, J.K., and Bulyk, M.L. (2015). Context influences on TALE-DNA binding revealed by quantitative profiling. Nat. Commun. *6*, 7440. http://dx.doi.org/10.1038/ncomms8440

Sanjana, N.E., Cong, L., Zhou, Y., Cunniff, M.M., Feng, G., and Zhang, F. (2012). A transcription activator-like effector toolbox for genome engineering. Nat. Protoc. 7, 171–192. http://dx.doi.org/10.1038/nprot.2011.431

Schmitz, M.L., and Baeuerle, P.A. (1991). The p65 subunit is responsible for the strong transcription activating potential of NF-kappaB. EMBO J. *10*, 3805–3817.

Schübeler, D. (2015). Function and information content of DNA methylation. Nature *517*, 321–326. http://dx.doi.org/10.1038/nature14192

Shechner, D.M., Hacisuleyman, E., Younger, S.T., and Rinn, J.L. (2015). Multiplexable, locus-specific targeting of long RNAs with CRISPR-Display. Nat. Methods *12*, 664–670. http://dx.doi.org/10.1038/nmeth.3433

Shi, Y., Lan, F., Matson, C., Mulligan, P., Whetstine, J.R., Cole, P.A., Casero, R.A., and Shi, Y. (2004). Histone demethylation mediated by the nuclear amine oxidase homolog LSD1. Cell *119*, 941–953. http://dx.doi.org/10.1016/j.cell.2004.12.012

Shmakov, S., Abudayyeh, O.O., Makarova, K.S., Wolf, Y.I., Gootenberg, J.S., Semenova, E., Minakhin, L., Joung, J., Konermann, S., Severinov, K., *et al.* (2015). Discovery and functional characterization of diverse Class 2 CRISPR-Cas SYSTEMS. Mol. Cell *60*, 385–397. http://dx.doi.org/10.1016/j.molcel.2015.10.008

Slaymaker, I.M., Gao, L., Zetsche, B., Scott, D.A., Yan, W.X., and Zhang, F. (2016). Rationally engineered Cas9 nucleases with improved specificity. Science *351*, 84–88. http://dx.doi.org/10.1126/science.aad5227

Smith, Z.D., and Meissner, A. (2013). DNA methylation: roles in mammalian development. Nat. Rev. Genet. *14*, 204–220. http://dx.doi.org/10.1038/nrg3354

Snowden, A.W., Gregory, P.D., Case, C.C., and Pabo, C.O. (2002). Gene-specific targeting of H3K9 methylation is sufficient for initiating repression in vivo. Curr. Biol. *12*, 2159–2166. http://dx.doi.org/10.1016/S0960-9822(02)01391-X

Song, C.-X., Diao, J., Brunger, A.T., and Quake, S.R. (2016). Simultaneous single-molecule epigenetic imaging of DNA methylation and hydroxymethylation. Proc. Natl. Acad. Sci. U.S.A. *113*, 4338–4343. http://dx.doi.org/10.1073/pnas.1600223113

Stancheva, I., and Meehan, R.R. (2000). Transient depletion of xDnmt1 leads to premature gene activation in *Xenopus* embryos. Genes Dev. *14*, 313–327.

Sun, W., Ji, W., Hall, J.M., Hu, Q., Wang, C., Beisel, C.L., and Gu, Z. (2015). Self-assembled DNA nanoclews for the efficient delivery of CRISPR-Cas9 for genome editing. Angew. Chem. Int. Ed. Engl. *54*, 12029–12033. http://dx.doi.org/10.1002/anie.201506030

Tahiliani, M., Koh, K.P., Shen, Y., Pastor, W.A., Bandukwala, H., Brudno, Y., Agarwal, S., Iyer, L.M., Liu, D.R., Aravind, L., *et al.* (2009). Conversion of 5-methylcytosine to 5-hydroxymethylcytosine in mammalian DNA by MLL partner TET1. Science *324*, 930–935. http://dx.doi.org/10.1126/science.1170116

Tanenbaum, M.E., Gilbert, L.A., Qi, L.S., Weissman, J.S., and Vale, R.D. (2014). A protein-tagging system for signal amplification in gene expression and fluorescence imaging. Cell *159*, 635–646. http://dx.doi.org/10.1016/j.cell.2014.09.039

Thakore, P.I., Black, J.B., Hilton, I.B., and Gersbach, C.A. (2016). Editing the epigenome: technologies for programmable transcription and epigenetic modulation. Nat. Methods *13*, 127–137. http://dx.doi.org/10.1038/nmeth.3733

Thakore, P.I., D'Ippolito, A.M., Song, L., Safi, A., Shivakumar, N.K., Kabadi, A.M., Reddy, T.E., Crawford, G.E., and Gersbach, C.A. (2015). Highly specific epigenome editing by CRISPR-Cas9 repressors for silencing of distal regulatory elements. Nat. Methods *12*, 1143–1149. http://dx.doi.org/10.1038/nmeth.3630

Thurman, R.E., Rynes, E., Humbert, R., Vierstra, J., Maurano, M.T., Haugen, E., Sheffield, N.C., Stergachis, A.B., Wang, H., Vernot, B., *et al.* (2012). The accessible chromatin landscape of the human genome. Nature *489*, 75–82. http://dx.doi.org/10.1038/nature11232

Truong, D.-J., Kühner, K., Kühn, R., Werfel, S., Engelhardt, S., Wurst, W., and Ortiz, O. (2015). Development of an intein-mediated split-Cas9 system for gene therapy. Nucleic Acids Res. *43*, 6450–6458. http://dx.doi.org/10.1093/nar/gkv601

Tsai, S.Q., Zheng, Z., Nguyen, N.T., Liebers, M., Topkar, V.V., Thapar, V., Wyvekens, N., Khayter, C., Iafrate, A.J., Le, L.P., *et al.* (2015). GUIDE-seq enables genome-wide profiling of off-target cleavage by CRISPR-Cas nucleases. Nat. Biotechnol. *33*, 187–197. http://dx.doi.org/10.1038/nbt.3117

Turner, B.M. (2012). The adjustable nucleosome: an epigenetic signaling module. Trends Genet. *28*, 436–444. http://dx.doi.org/10.1016/j.tig.2012.04.003

Urnov, F.D., Rebar, E.J., Holmes, M.C., Zhang, H.S., and Gregory, P.D. (2010). Genome editing with engineered zinc finger nucleases. Nat. Rev. Genet. *11*, 636–646. http://dx.doi.org/10.1038/nrg2842

van Essen, D., Engist, B., Natoli, G., and Saccani, S. (2009). Two modes of transcriptional activation at native promoters by NF-kappaB p65. PLoS Biol. 7, e73. http://dx.doi.org/10.1371/journal.pbio.1000073

Vandevenne, M., Jacques, D.A., Artuz, C., Nguyen, C.D., Kwan, A.H.Y., Segal, D.J., Matthews, J.M., Crossley, M., Guss, J.M., and Mackay, J.P. (2013). New insights into DNA recognition by zinc fingers revealed by structural analysis of the oncoprotein ZNF217. J. Biol. Chem. *288*, 10616–10627. http://dx.doi.org/10.1074/jbc.M112.441451

Vardimon, L., Kressmann, A., Cedar, H., Maechler, M., and Doerfler, W. (1982). Expression of a cloned adenovirus gene is inhibited by in vitro methylation. Proc. Natl. Acad. Sci. U.S.A. *79*, 1073–1077.

Vojta, A., Dobrinić, P., Tadić, V., Bočkor, L., Korać, P., Julg, B., Klasić, M., and Zoldoš, V. (2016). Repurposing the CRISPR-Cas9 system for targeted DNA methylation. Nucleic Acids Res. *44*, 5615–5628. http://dx.doi.org/10.1093/nar/gkw159

Wang, D., Mou, H., Li, S., Li, Y., Hough, S., Tran, K., Li, J., Yin, H., Anderson, D.G., Sontheimer, E.J., *et al.* (2015a). Adenovirus-mediated somatic genome editing of Pten by CRISPR/Cas9 in mouse liver in spite of Cas9-specific immune responses. Hum. Gene Ther. *26*, 432–442. http://dx.doi.org/10.1089/hum.2015.087

Wang, L., Grossman, S.R., and Kieff, E. (2000). Epstein–Barr virus nuclear protein 2 interacts with p300, CBP, and PCAF histone acetyltransferases in activation of the LMP1 promoter. Proc. Natl. Acad. Sci. U.S.A. *97*, 430–435.

Wang, T., Wei, J.J., Sabatini, D.M., and Lander, E.S. (2014). Genetic screens in human cells using the CRISPR-Cas9 system. Science *343*, 80–84. http://dx.doi.org/10.1126/science.1246981

Wang, X., Wang, Y., Wu, X., Wang, J., Wang, Y., Qiu, Z., Chang, T., Huang, H., Lin, R.-J., and Yee, J.-K. (2015b). Unbiased detection of off-target cleavage by CRISPR-Cas9 and TALENs using integrase-defective lentiviral vectors. Nat. Biotechnol. *33*, 175–178. http://dx.doi.org/10.1038/nbt.3127

Webster, K.E., O'Bryan, M.K., Fletcher, S., Crewther, P.E., Aapola, U., Craig, J., Harrison, D.K., Aung, H., Phutikanit, N., Lyle, R., *et al*. (2005). Meiotic and epigenetic defects in Dnmt3L-knockout mouse spermatogenesis. Proc. Natl. Acad. Sci. U.S.A. *102*, 4068–4073. http://dx.doi.org/10.1073/pnas.0500702102

Wolfe, S.A., Grant, R.A., Elrod-Erickson, M., and Pabo, C.O. (2001). Beyond the "recognition code": structures of two Cys2His2 zinc finger/TATA box complexes. Structure *9*, 717–723. http://dx.doi.org/10.1016/S0969-2126(01)00632-3

Wolfe, S.A., Nekludova, L., and Pabo, C.O. (2000). DNA recognition by Cys2His2 zinc finger proteins. Annu. Rev. Biophys. Biomol. Struct. *29*, 183–212. http://dx.doi.org/10.1146/annurev.biophys.29.1.183

Wright, A.V., Sternberg, S.H., Taylor, D.W., Staahl, B.T., Bardales, J.A., Kornfeld, J.E., and Doudna, J.A. (2015). Rational design of a split-Cas9 enzyme complex. Proc. Natl. Acad. Sci. U.S.A. *112*, 2984–2989. http://dx.doi.org/10.1073/pnas.1501698112

Xu, X., Tao, Y., Gao, X., Zhang, L., Li, X., Zou, W., Ruan, K., Wang, F., Xu, G.-L., and Hu, R. (2016). A CRISPR-based approach for targeted DNA demethylation. Cell Discov. *2*, 16009. http://dx.doi.org/10.1038/celldisc.2016.9

Xu, Y., Wu, F., Tan, L., Kong, L., Xiong, L., Deng, J., Barbera, A.J., Zheng, L., Zhang, H., Huang, S., *et al*. (2011). Genome-wide regulation of 5hmC, 5mC, and gene expression by Tet1 hydroxylase in mouse embryonic stem cells. Mol. Cell *42*, 451–464. http://dx.doi.org/10.1016/j.molcel.2011.04.005

Yamano, T., Nishimasu, H., Zetsche, B., Hirano, H., Slaymaker, I.M., Li, Y., Fedorova, I., Nakane, T., Makarova, K.S., Koonin, E.V., *et al*. (2016). Crystal structure of Cpf1 in complex with guide RNA and target DNA. Cell *165*, 949–962. http://dx.doi.org/10.1016/j.cell.2016.04.003

Youngson, N.A., and Whitelaw, E. (2008). Transgenerational epigenetic effects. Annu. Rev. Genomics. Hum. Genet. *9*, 233–257. http://dx.doi.org/10.1146/annurev.genom.9.081307.164445

Zalatan, J.G., Lee, M.E., Almeida, R., Gilbert, L.A., Whitehead, E.H., La Russa, M., Tsai, J.C., Weissman, J.S., Dueber, J.E., Qi, L.S., *et al*. (2015). Engineering complex synthetic transcriptional programs with CRISPR RNA scaffolds. Cell *160*, 339–350. http://dx.doi.org/10.1016/j.cell.2014.11.052

Zentner, G.E., and Henikoff, S. (2014). High-resolution digital profiling of the epigenome. Nat. Rev. Genet. *15*, 814–827. http://dx.doi.org/10.1038/nrg3798

Zetsche, B., Gootenberg, J.S., Abudayyeh, O.O., Slaymaker, I.M., Makarova, K.S., Essletzbichler, P., Volz, S.E., Joung, J., van der Oost, J., Regev, A., *et al*. (2015a). Cpf1 is a single RNA-guided endonuclease of a class 2 CRISPR-Cas system. Cell *163*, 759–771. http://dx.doi.org/10.1016/j.cell.2015.09.038

Zetsche, B., Volz, S.E., and Zhang, F. (2015b). A split-Cas9 architecture for inducible genome editing and transcription modulation. Nat. Biotechnol. *33*, 139–142. http://dx.doi.org/10.1038/nbt.3149

Zhang, F., Cong, L., Lodato, S., Kosuri, S., Church, G.M., and Arlotta, P. (2011). Efficient construction of sequence-specific TAL effectors for modulating mammalian transcription. Nat. Biotechnol. *29*, 149–154. http://dx.doi.org/10.1038/nbt.1775

Zhou, V.W., Goren, A., and Bernstein, B.E. (2011). Charting histone modifications and the functional organization of mammalian genomes. Nat. Rev. Genet. *12*, 7–18. http://dx.doi.org/10.1038/nrg2905

Zuris, J.A., Thompson, D.B., Shu, Y., Guilinger, J.P., Bessen, J.L., Hu, J.H., Maeder, M.L., Joung, J.K., Chen, Z.-Y., and Liu, D.R. (2015). Cationic lipid-mediated delivery of proteins enables efficient protein-based genome editing in vitro and in vivo. Nat. Biotechnol. *33*, 73–80. http://dx.doi.org/10.1038/nbt.3081