

Structure

from PDB: 5f9r

Cas9

1380 aa

1-60 RuvCI nuclease	(Constant position) (iceblue)
60-94 Arginine rich helix	(Rotates from APO to sgRNA bound) (mauve)
94-167 Recl	(Rotates from APO to sgRNA bound) (white)
167-307 Recll	(Rotates from APO to sgRNA bound) (yellow)
307-447 Recl	(Rotates from APO to sgRNA bound) (silver)
447-718 Reclll	(Rotates from APO to sgRNA bound) (Conformational changes in 4zt0 4zt9 5xbl) (blue2)
718-765 RuvCII nuclease	(Constant position) (cyan2)
765-909 HNH endonuclease	(Two distinct conformations) (green)
909-1099 RuvCIII nuclease	(Constant position) (cyan3)
1099-1368 PAM-interacting domain (PI)	(Constant position) (red)

sgRNA

120 RNA

5'-GGCGCATAAAGATGAGACGCGTTTTAGAGCTATGCTGTTTTGAAAAAACAGCATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGACCGAGTCGGTGCTTCG-3'

1-20 guide

10-20 seed

1-41 crRNA

46-118 tracrRNA

DNA

30 dsDNA

5'-GGCGCATAAAGATGAGACGCT**TGG**CGATTAG-3'

3'-CCGCGTATTTCTACTCTGCGACCGCTAATC-5'

Details on the mechanism

<http://sites.tufts.edu/crispr/crispr-mechanism>