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 RecI (Rotates from APO to sgRNA bound) (white)

167-307 RecII (Rotates from APO to sgRNA bound) (yellow)

307-447 RecI (Rotates from APO to sgRNA bound) (silver)

447-718 RecIII (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'-*GGCGCATAAAGATGAGACGC*GTTTTAGAGCTATGCTGTTTTGAAAAAAACAGCATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGT
GGCACCGAGTCGGTGCTTCG-3'

1-20 guide

10-20 seed

1-41 crRNA

46-118 tracrRNA

DNA

30 dsDNA

5'-*GGCGCATAAAGATGAGACGC***TGG**CGATTAG-3'

3'-CCGCGTATTTCTACTCTGCGACCGCTAATC-5'

Details on the mechanism

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