

HOMING ENDONUCLEASES%0A

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[Evolution of I-SecI homing endonucleases with increased ...](#)

Homing endonucleases genes are found associated with self-splicing RNA introns, as part of inteins that self-splice at the protein level, or as free-standing elements. They are pervasive in nature, occurring in organisms from all phyla. Several families of HEGs have evolved, the largest being the LAGLIDADG family that is defined on the basis of conserved sequence and structural motifs.

[The Structure of a Bacterial DUF199/WhiA Protein ...](#)

Similarly, the folds found within homing endonucleases (proteins that promote the genetic mobility of microbial introns and inteins) are also found in an impressive array of enzymes.

[Ironing out the kinks: splicing and translation in bacteria](#)

The endonucleases trigger homing, or site-specific movement of the intron sequences to intronless alleles.

Self-splicing requires that the intron RNA fold into a unique secondary and tertiary structure (Cech and Herschlag 1996).

[Identification of conserved features of LAGLIDADG homing ...](#)

LAGLIDADG family of homing endonucleases are rare-cutting enzymes which recognize long target sequences and are of great interest in genome engineering.

[doi:10.1093/nar/gkm183 The C-terminal loop of the homing ...](#)

Directed by homing endonucleases (HEs), a family of endonucleases encoded by mobile genetic elements, whose function is to initiate DSB-induced recombination events in a process referred to as homing (8). Several hundreds of HEs have been identified in bacteria, eukaryotes and archaea (8); however, the probability of finding a HE cleavage site in a chosen gene is low. Thus, the making of

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LETTERS

The homing endonucleases provide an excellent model system for understanding protein-DNA interaction specificity, as well as starting points for engineering of novel specificities for targeted genomics applications, including gene therapy^{4,5}. Crystal structures of the enzymes bound to their recognition sites reveal a rich assortment of side-chain-nucleotide contacts within the DNA major