Bigrams in abstract expressed sites double describe engineering approach induced sequences provide . analysis nuclease. mutant palindromic highly repeats /argeted identified demonstrated generation strategy rnas multiple knockefficiencyefficientystered regularly proteins powerful generate developed y vivo transcription hanism mice stem generate genome case gen significantly mechanism report mice stem site levels system / rna mutation generated method sequencedemonstrate sedediting uman mediated effects crispr mutations cell genes expression system development data repair study systems functional including results directed activity tool technology wide model mouse type methods vitro studies revealed genomes previously lines sequencing wild loci derived tools increased recently dependent addition essentialobserved identify \ required compared homologous organisms binding -----disease -molecular loss complex species

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