New, hyper-accurate CRISPR gene editor developed

Scientists at the University of California, Berkeley and Massachusetts General Hospital have identified a key region within the Cas9 protein that governs how accurately CRISPR-Cas9 homes in on a target DNA sequence, and have tweaked it to produce a hyper-accurate gene editor with the lowest level of off-target cutting to date [read the full study here (behind paywall)].

The protein domain the researchers identified as a master controller of DNA cutting is an obvious target for re-engineering to improve accuracy even further, the researchers say. This approach should help scientists customize variants of Cas9 – the protein that binds and cuts DNA – to minimize the chance that CRISPR-Cas9 will edit DNA at the wrong place....

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While improved fidelity benefits basic research, it is absolutely critical when editing genes for clinical applications, since any off-target DNA cutting could disable key genes and lead to permanent, unexpected side effects.

Within the last two years, two teams engineered highly accurate Cas9 proteins – an enhanced specificity one called eSpCas9(1.1) and a high-fidelity one called SpCas9-HF1 – and [researchers Janice Chen and Jennifer Doudna] sought to learn why they cut with higher specificity than the wild-type Cas9 protein from *Streptococcus pyogenes* used widely today.

The GLP aggregated and excerpted this article to reflect the diversity of news, opinion and analysis. Read full, original post: Discovery helps engineer more accurate Cas9s for CRISPR editing