CRISPRcruncher: A tool for engineering restriction sites into coding regions

Samuel F. Fay1*, David S. Fay2§* and Vikram E. Chhatre2,1
1Wyoming INBRE Bioinformatics Core
2Department of Molecular Biology, University of Wyoming, Laramie, WY USA
§To whom correspondence should be addressed: davidfay@uwyo.edu
*These authors contributed equally.

Abstract

CRISPR/Cas9 genome editing strategies often rely on the placement of an introduced restriction endonuclease (RE) site adjacent to the genomic edit of interest. This allows for rapid initial PCR-based detection of cells and organisms containing the edit of interest and may also be used for subsequent genotyping. Nevertheless, engineering RE sites at optimal locations within coding regions can be difficult due to the many hundreds of potential endonuclease options and the strict requirement to maintain the correct amino acid sequence. Here we report CRISPRcruncher, a computational tool that analyzes an input coding sequence and produces a complete list of all possible changes that could be made that will create new RE sites while preserving the original peptide sequence. Notably, for sequences tested, CRISPRcruncher identified approximately one new RE site per input nucleotide when mining for 4-bp or longer RE motifs and 0.5 new RE sites per input nucleotide when mining for 6-bp or longer motifs. Therefore, CRISPRcruncher represents a powerful new computational tool in the CRISPR arsenal.
### A

#### 65 RESULTS FOR ATGGAGTGTCACACTGTCTCCTCGTCTA

<table>
<thead>
<tr>
<th>Enzyme</th>
<th>Enzyme Sequence</th>
<th>Modified Input Sequence</th>
<th>Strand</th>
</tr>
</thead>
<tbody>
<tr>
<td>BsmI</td>
<td>GAATGC</td>
<td>ATGGAGTGTCACACTGTCTCCTCGTCTAAGCT</td>
<td>Top</td>
</tr>
<tr>
<td>Mva1269I</td>
<td>GAATGC</td>
<td>ATGGAGTGTCACACTGTCTCCTCGTCTAAGCT</td>
<td>Top</td>
</tr>
<tr>
<td>Nb.BsmI</td>
<td>GAATGC</td>
<td>ATGGAGTGTCACACTGTCTCCTCGTCTAAGCT</td>
<td>Top</td>
</tr>
<tr>
<td>Nb.Mva1269I</td>
<td>GAATGC</td>
<td>ATGGAGTGTCACACTGTCTCCTCGTCTAAGCT</td>
<td>Top</td>
</tr>
<tr>
<td>Pci</td>
<td>GAATGC</td>
<td>ATGGAGTGTCACACTGTCTCCTCGTCTAAGCT</td>
<td>Top</td>
</tr>
<tr>
<td>BaeGI</td>
<td>GGGCCMC</td>
<td>ATGGAGTGTCACACTGTCTCCTCGTCTAAGCT</td>
<td>Both</td>
</tr>
<tr>
<td>BseSI</td>
<td>GGGCCMC</td>
<td>ATGGAGTGTCACACTGTCTCCTCGTCTAAGCT</td>
<td>Both</td>
</tr>
<tr>
<td>Bsp1286I</td>
<td>GGGCCMC</td>
<td>ATGGAGTGTCACACTGTCTCCTCGTCTAAGCT</td>
<td>Both</td>
</tr>
<tr>
<td>BstS1I</td>
<td>GGGCCMC</td>
<td>ATGGAGTGTCACACTGTCTCCTCGTCTAAGCT</td>
<td>Both</td>
</tr>
<tr>
<td>MseI</td>
<td>GGGCCMC</td>
<td>ATGGAGTGTCACACTGTCTCCTCGTCTAAGCT</td>
<td>Both</td>
</tr>
<tr>
<td>Ssal</td>
<td>GGGCCMC</td>
<td>ATGGAGTGTCACACTGTCTCCTCGTCTAAGCT</td>
<td>Both</td>
</tr>
<tr>
<td>Mmel</td>
<td>TCCACAC</td>
<td>ATGGAGTGTCACACTGTCTCCTCGTCTAAGCT</td>
<td>Top</td>
</tr>
<tr>
<td>BgGI</td>
<td>CGAGNNNNNTTGC</td>
<td>ATGGAGTGTCACACTGTCTCCTCGTCTAAGCT</td>
<td>Top</td>
</tr>
<tr>
<td>Bfml</td>
<td>CRAGYAG</td>
<td>ATGGAGTGTCACACTGTCTCCTCGTCTAAGCT</td>
<td>Both</td>
</tr>
<tr>
<td>Bsh1285I</td>
<td>CRYCG</td>
<td>ATGGAGTGTCACACTGTCTCCTCGTCTAAGCT</td>
<td>Both</td>
</tr>
<tr>
<td>BsiEI</td>
<td>CRYCG</td>
<td>ATGGAGTGTCACACTGTCTCCTCGTCTAAGCT</td>
<td>Both</td>
</tr>
<tr>
<td>BstDSI</td>
<td>CRYCG</td>
<td>ATGGAGTGTCACACTGTCTCCTCGTCTAAGCT</td>
<td>Both</td>
</tr>
</tbody>
</table>

### B

#### Distinct Sequences (99 bp)

- (Cutter ≥4)
- (Cutter ≥6)

### C

#### Total Reported REs (99 bp)

- (Cutter ≥4)
- (Cutter ≥6)

### D

#### Distinct Sequences (33 bp)

- (Cutter ≥4)
- (Cutter ≥6)

### E

#### Total Reported REs (33 bp)

- (Cutter ≥4)
- (Cutter ≥6)

### F

#### Distinct Sequences

- ≥4 Cutters (33 bp)

### G

#### Distinct Sequences

- ≥6 Cutters (33 bp)

### H

#### Identified Sites

- (Cutter 24, 26)

#### Percent Palindromic

- (99 bp)
CRISPRcruncher scans coding regions in a 5′ to 3′ direction using a series of 15-bp sliding windows, each offset by 3 bp (the reading frame). The end user, in addition to entering the DNA sequence, can also choose a minimum cutoff length for the reported RE sites (e.g., ≥6 bp). We define ≥6 bp cutters as REs that recognize motifs containing six or more bp as part of their core recognition sequence. As such, both HindIII (5′-AAGCTT-3′) and the 8-bp cutter, NotI (5′-GCGGCCGC-3′), are ≥6 bp cutters. Likewise ≥4 bp cutters include 4-bp cutters, such as AluI (5′-AGCT-3′), as well as REs with longer recognition motifs, such as HindIII and NotI (also see discussion below). The output lists the identified REs together with their corresponding sites in a 5′ to 3′ order (Figure 1A). The output indicates the altered nucleotides and strand location (top, bottom, or both) and places isoschizomers, distinct enzymes with identical recognition motifs, on separate lines (Figure 1A).

To get a sense for how many potential new RE sites can be identified by CRISPRcruncher, we examined the first 99 coding nucleotides within the first exon of five randomly chosen genes on the X chromosome of *Caenorhabditis elegans* (Extended Data). In searches for 4-bp or longer RE recognition sites (≥4 cutters), we obtained an average of 128 distinct 99-bp sequences (range, 70–182), that correspond to an average total of 652 total reported REs (range, 508–945) (Figure 1B,C; Extended Data). In searches for 6-bp or longer RE recognition sites (≥6 cutters), we obtained an average of 56 distinct 99-bp sequences (range, 41–80), that correspond to an average total of 213 total reported REs (range, 168–291) (Figure 1B,C; Extended Data). The difference between the numbers obtained for ‘distinct sequences’ and ‘total reported REs’ is due in part to isoschizomers and also to enzymes with related but divergent consensus motifs that can recognize the same distinctly altered sequence (Extended Data). For example, by changing 5′-CCTGGG-3′, which encodes Pro-Gly, to 5′-CCCCGGG-3′, which also encodes Pro-Gly, sites for XmAL (5′-CCCCGGG-3′), BsoBI (5′-CYCGRG-3′), and HpaII (5′-CCGG-3′) are simultaneously created.

As expected, using a 6-bp cutoff for recognition motifs (≥6 cutters) we observed fewer ‘distinct sequences’ and ‘total reported REs’ than when using a ≥4-bp cutoff (Figure 1B,C; Extended Data). Notably, these data indicate that on average more than one distinct sequence can be identified per 2 bp of coding sequence for ≥6 cutters and more than one distinct sequence can be identified per each base pair for ≥4 cutters. With respect to the availability of enzymes, a quick survey of ≥6 cutter sites identified within the first 33 bp of *CELE* _F54B11.2_ indicated that a very high proportion (21/21) can be cleaved using enzymes that are commercially available through at least one major vendor in the United States (Extended Data). Thus, the RE sites identified by CRISPRcruncher are both abundant and useful.
We also examined distinct sequences and total reported enzymes for 15 non-overlapping 33-bp DNA segments derived from the five 99-bp regions (Figure 1D,E). For ≥4 cutters we observed averages of 36 ‘distinct sequences’ (range, 16–51) and 175 ‘total reported REs’ (range, 79–253), whereas for 6 cutters we observed averages of 16 ‘distinct sequences’ (range, 5–22) and 58 ‘total reported REs’ (range, 13–80). A further breakdown of these parameters for each of the five genes is shown in Figure 1F,G. These numbers are consistent with those reported for the 99-bp segments but are slightly lower due to the absence of RE sites spanning the sequence breaks at 33 bp and 66 bp. Overall, CRISPRcruncher identified about one distinct change per 2 bp for ≥4 cutters and one distinct change per each base pair for ≥4 cutters. Nevertheless, as can be seen (Figure 1F,G; Extended Data), the distribution of RE sites can vary considerably between regions due to factors including DNA sequence composition and codon flexibility.

Several additional points are worth noting. (1) CRISPRcruncher ‘counts’ degenerate base symbols, such as R (A or G) and Y (C or T), the same as it does G, A, T, and C. Thus, BanII (5'-GRGNCYC-3') and BaeGI (5'-GKGCYC-3') are both considered 6-bp cutters, even though their genomic site frequencies will be greater than that of Apal (5'-GGGCCN-3'). In contrast, the non-specific designation (N) is not factored into motif size. Thus, NlaIV (5'-GGNNCC-3') is considered a 4-bp cutter. (2) Because of codon redundancy and RE motif degeneracy, there will be cases when multiple different substitutions at the same nucleotide position can produce a consensus match for a given RE while preserving the original amino acid sequence. For example, changing 5'-ACCTGG-3', which encodes Thr-Trp, to either 5'-ACATGG-3' or 5'-ACGTGG-3' will preserve the amino acid sequence, and both substitutions will create a consensus site for AffIII (5'-ACRYGT-3'). CRISPRcruncher will report only one of these changes; however, it may be advisable to consider both options if, for example, codon bias is an issue. This can easily be done by checking codon usage tables along with the relevant RE consensus motif to see if the ‘non-reported’ alternative nucleotide is preferable. (3) Some changes may be made outside RE consensus motifs. For example, the sequence 5'-GATCTTCGT-3', which encodes Asp-Leu-Arg, can be changed to 5'-GACTTAAAGA-3', creating a new site for AffIII (5'-CCTAAG-3') while preserving the amino acid sequence. In this case, the 3'-most substitution occurs outside the consensus motif for AffIII (i.e., both CGT and AGA encode Arg). As can be appreciated, this type of RE site creation would be difficult to accomplish without the use of a computational tool. (4) Stop codons are treated identically to amino acids. Thus, 5'-TA-3' may be changed to either 5'-TA-3' or 5'-TG-3'. (5) An analysis of RE sites identified by CRISPRcruncher indicates that whereas ~70% are palindromic (a.k.a., inverted repeats), ~30% are not (Figure 1H). Because non-palindromic motifs are generally more difficult to design without computational tools, this subclass represents an additional benefit of using CRISPRcruncher.

We also note that CRISPRcruncher is not designed to take into account codon bias, guide-RNA preferences, or other relevant repair-template design considerations, all of which will be important in achieving success with CRISPR editing. Many other tools and resources address these concerns and can be easily used in conjunction with CRISPRcruncher. In addition, although CRISPRcruncher reports RE sites that are already present within the input sequence, it does not make suggestions for ablating these sites. In most cases, such sites will either be too abundant for screening purposes (e.g., many 4-cutters) or will be located at non-optimal positions when taking into account repair design principles. In rare cases where they may prove useful, disruption of such RE sites is easily accomplished ‘by hand’.

In summary, CRISPRcruncher is a powerful new design tool for introducing useful RE sites into repair templates. CRISPRcruncher should be used in combination with (i) current tools for predicting the efficiency and specificity of guide-RNAs, (ii) species-specific codon usage tables, and (iii) validated repair-template design principles. In some cases, choice of the engineered RE site may come down to which enzymes are already available to the lab, thereby reducing costs.

Methods
Request a detailed protocol

CRISPRcruncher is available as a web-based tool at https://crisprcruncher.io. The Python source code (release v1.0) is available on CaltechData (10.22002/D1.1861). Future updates to the code will be maintained at https://github.com/samuelfay/CRISPRcruncher.git. The standalone script may be implemented locally on Windows, Mac OSX and Unix platforms to achieve greater computational efficiency. A user manual and interpretation guide are available.

Extended data are archived and available on Caltech Data (10.22002/D1.1862).

Information regarding RE motifs and other properties was obtained primarily from (https://www.neb.com). Analyses associated with Figure 1 were done in GraphPad Prism 9.

Acknowledgments: We thank Amy Fluet for editing the manuscript and for giving birth to S.F.F. We thank Bobby Farboud, Daniel Dickinson, Mike Boxem, and Jordan Ward for valuable input. This publication was made possible by an Institutional Development Award (IDeA) from the National Institute of General Medical Sciences of the National Institutes of Health under Grant # 2P20GM103432.
Funding: This work was funded by R35 GM136236-01 (to D.S.F.) and P20 GM103432.

Author Contributions: Samuel F. Fay: Investigation, Methodology, Validation, Software, Resources, Formal analysis. David S. Fay: Conceptualization, Data curation, Formal analysis, Funding acquisition, Investigation, Methodology, Project administration, Resources, Supervision, Validation, Visualization, Writing - original draft. Vikram E. Chhatre: Conceptualization, Writing - review and editing, Methodology, Project administration, Supervision, Data curation.

Reviewed By: Anonymous

History: Received December 5, 2020 Revision received January 8, 2021 Accepted January 12, 2021 Published January 18, 2021

Copyright: © 2021 by the authors. This is an open-access article distributed under the terms of the Creative Commons Attribution 4.0 International (CC BY 4.0) License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

Citation: Fay, SF; Fay, DS; Chhatre, VE (2021). CRISPRcruncher: A tool for engineering restriction sites into coding regions. microPublication Biology. https://doi.org/10.17912/micropub.biology.000343