# Article information:

Predicting base editing outcomes with an attention-based deep learning algorithm trained on high-throughput target library screens | Nature Communications  
<https://www.nature.com/articles/s41467-021-25375-z>

# Article summary:

1. Base editors are CRISPR-Cas-guided single-strand DNA deaminases that enable precise genome editing.

2. Variation in base editor efficiency across different target sequences can be influenced by several parameters, including the consensus sequence preference of the deaminase and the binding efficiency of the sgRNA to the protospacer.

3. This work developed a machine learning algorithm capable of predicting base editing outcomes of commonly used ABEs and CBEs on any given protospacer sequence in silico available via www.be-dict.org.

# Article rating:

May be slightly imbalanced: The article presents the information in a generally reliable way, but there are minor points of consideration that could be explored further or claims that are not fully backed by appropriate evidence. Some perspectives may also be omitted, and you are encouraged to use the research topics section to explore the topic further.

# Article analysis:

The article is generally reliable and trustworthy, as it provides a comprehensive overview of base editors and their potential applications in genome editing, as well as an introduction to a new machine learning algorithm for predicting base editing outcomes on any given protospacer sequence. The authors provide evidence for their claims, such as citing relevant studies and providing detailed descriptions of their experimental methods. Furthermore, they acknowledge potential limitations of their approach, such as the need for further optimization by experimental testing with alternative base editor constructs.

However, there are some points that could be improved upon in terms of trustworthiness and reliability. For example, while the authors discuss potential strategies for circumventing low editing rates on target loci containing single C or A bases (e.g., exchanging the sgRNA to shift Cas9 binding upstream or downstream), they do not provide any evidence or data to support these strategies or explain why they may be effective in improving editing rates. Additionally, while they mention possible risks associated with using base editors (e.g., undesired ‘bystander’ editing), they do not provide any details about how these risks can be minimized or avoided altogether when using this technology. Finally, while the authors cite relevant studies throughout the article, some sources are outdated (e.g., refs 7–10). Thus, it would be beneficial if more recent sources were included to ensure accuracy and up-to-date information is provided throughout the article.

# Topics for further research:

* Strategies for improving base editing efficiency
* Minimizing risks associated with base editing
* Recent advances in base editing technology
* Machine learning algorithms for base editing
* Bystander editing in base editing
* Optimizing base editor constructs

# Report location:

<https://www.fullpicture.app/item/6d4f9bffad50982b8fd108c69d40c446>