APPLICATION

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Explore CRISPR Base Editing App

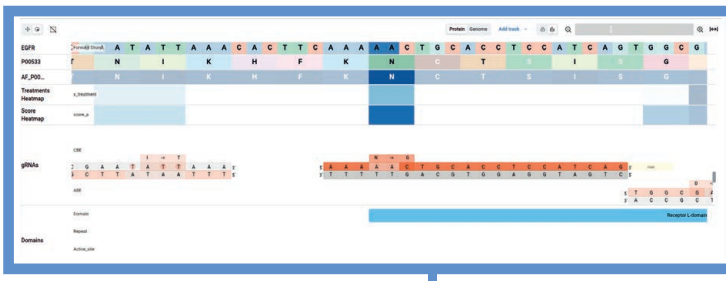
Analyze gRNAs in Genomic, Protein, and Structural Context

gRNA Candidates are Easy to List, but Hard to Interpret in Context

The CRISPR Base Editing App helps researchers map and interpret gRNA spacer regions and editing outcomes across genomic coordinates, protein sequences, and 3D protein structures.

The Challenge

A list of guide RNAs lacks context. Which protein/transcript region do they affect? Which domain are they targeting? Are there known variants in the region? The Base Editing App brings these layers together in one interactive workflow, combining your gRNA data with a wealth of public information from visynKB.



App Workflow

1. Load gRNA Candidates

Start from database-provided gRNA data or upload a CSV file containing spacer information, base editor type, editing outcomes, and related metadata.

2. Map Guides Across Biological Context

Map gRNAs onto genomic and protein coordinates, aligning them with transcripts, protein sequence, annotation tracks, variants, domains, and structure data.

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Advanced Use Case

Treatment-Response and Drug Binding Insight

Compare treatment effects across base edits at different positions to highlight regions that may contribute to drug response, resistance, binding-site behavior, or functional modulation.

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3. Explore Editing Outcomes

Use the heatmap and detail table to compare guide-level editing behavior, editor type, editing values, and candidate-specific effects across multiple base edits.

4. Prioritize Candidate Guides

Identify guides and edited regions that look most relevant based on position, annotation overlap, editing pattern, transcript context, or protein-level impact.

5. Interpret in 3D Structure

Explore whether edited positions localize near binding pockets, functional domains, known variants, or structurally important regions of the protein.

Questions the CRISPR app answers

- Where do my gRNAs map on the genome and protein sequence?
- Which transcripts or protein regions are affected?
- How do CBE and ABE candidates compare?
- Which edits show stronger or weaker treatment effects?
- Do treatment-associated edits cluster around a potential drug binding site?
- Are affected positions close to known variants, domains, pockets, or pathogenic regions?
- Which gRNAs or edited regions look most promising for deeper review?

Request a Demo

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Ready to Accelerate Your gRNA Analysis?

From raw gRNA candidates to interpretable base-editing insight.

Contact us

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