

(A) DATA INPUT & CURATION

1. FASTA
2. NCBI ID
3. Manual DNA

(User uploads sequences
[recommended length < 20 Mb]
via web browser)

(B) PROCESSING

Z-Hunt Execution
(Raw Output)

(User supplies Z-Hunt parameters)

Z-GENIE CORE

1. Accepts raw Z-Hunt output (predicted Z-DNA).
2. Identifies isolated ZFS ("singletons") & clusters ("mountains").
3. Generates CSV & BED for downstream use.

(Z-GENIE processes
raw data)

(C) OUTPUT

Output Files
(CSV & BED)

Exports for additional
analysis/graphs

(D) VISUALIZATION

1. Plotly scatterplots
2. Interactive tables
3. Multiple sequence alignment