



# Storage-D: a user-friendly platform that enables practical and personalized DNA data storage

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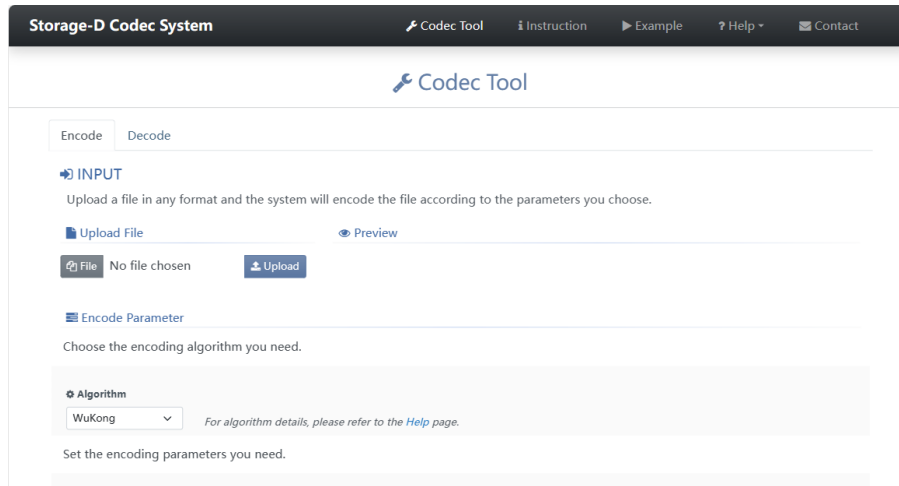
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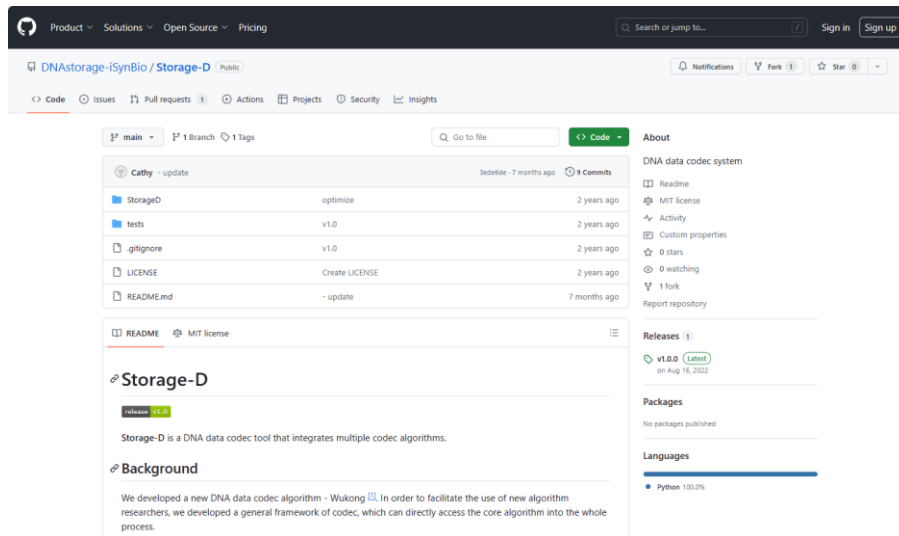
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# Introduction



**website:** <http://storage.dailab.xyz:16666/>

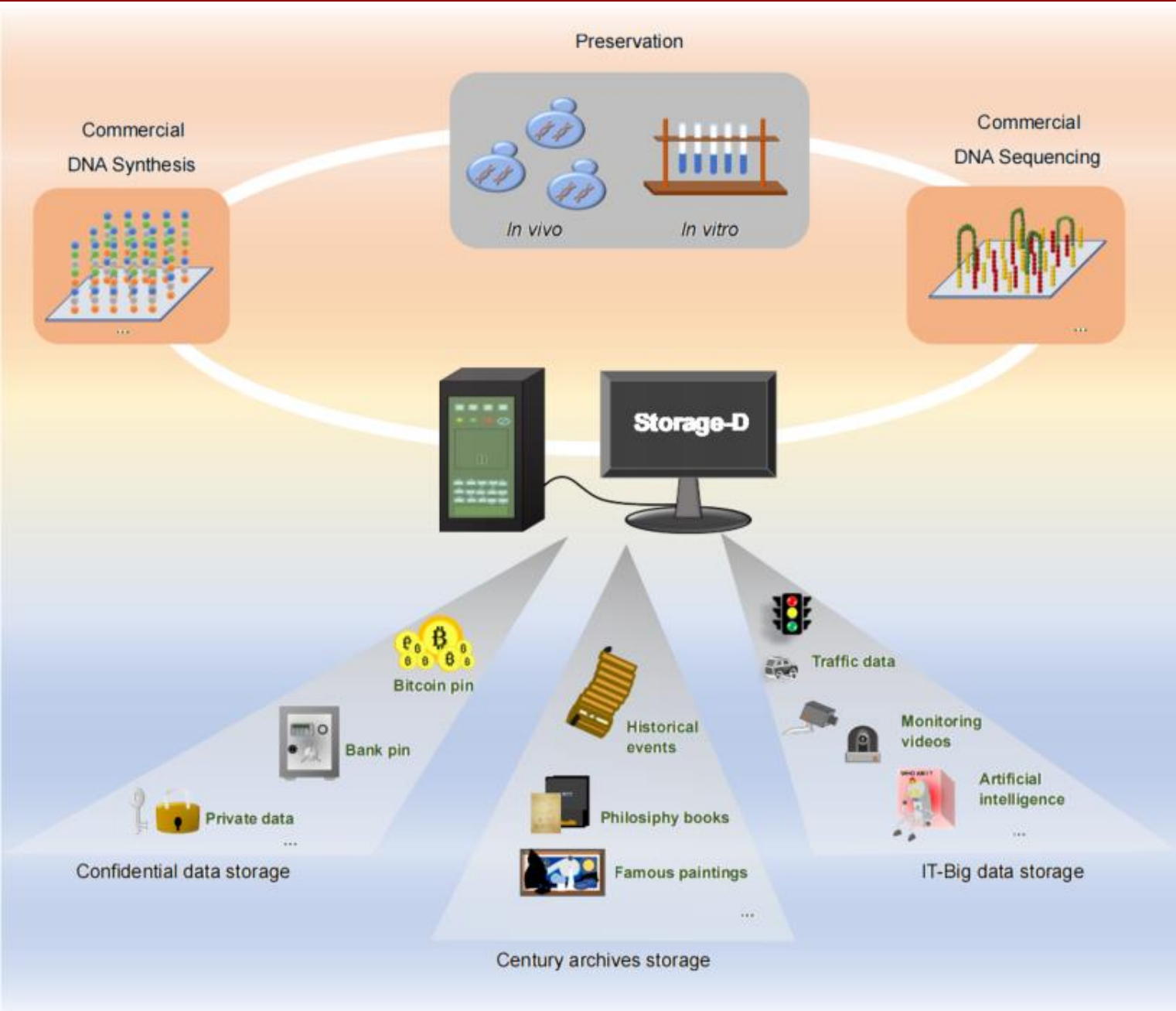


**code:** <https://github.com/DNASTorage-iSynBio/Storage-D/>

Deoxyribonucleic acid (DNA) is suggested as a promising data storage medium, but its practical use lacks a user-friendly platform. We developed the “Storage-D” web-based codec platform, which modularized key codec functions and provided a customizable choice for practical data storage use. A novel algorithm called “Wukong” was developed and integrated into the platform, which employed a flexible encoding logic and was able to generate a large number of encoding rules that can be employed for various DNA data storage demands. We verified the algorithm through in vitro and in vivo experiments, and provided the website service and source code.

The web server and codes of the platform are available at <http://storage.dailab.xyz:16666/> and <https://github.com/DNASTorage-iSynBio/Storage-D/>, respectively.

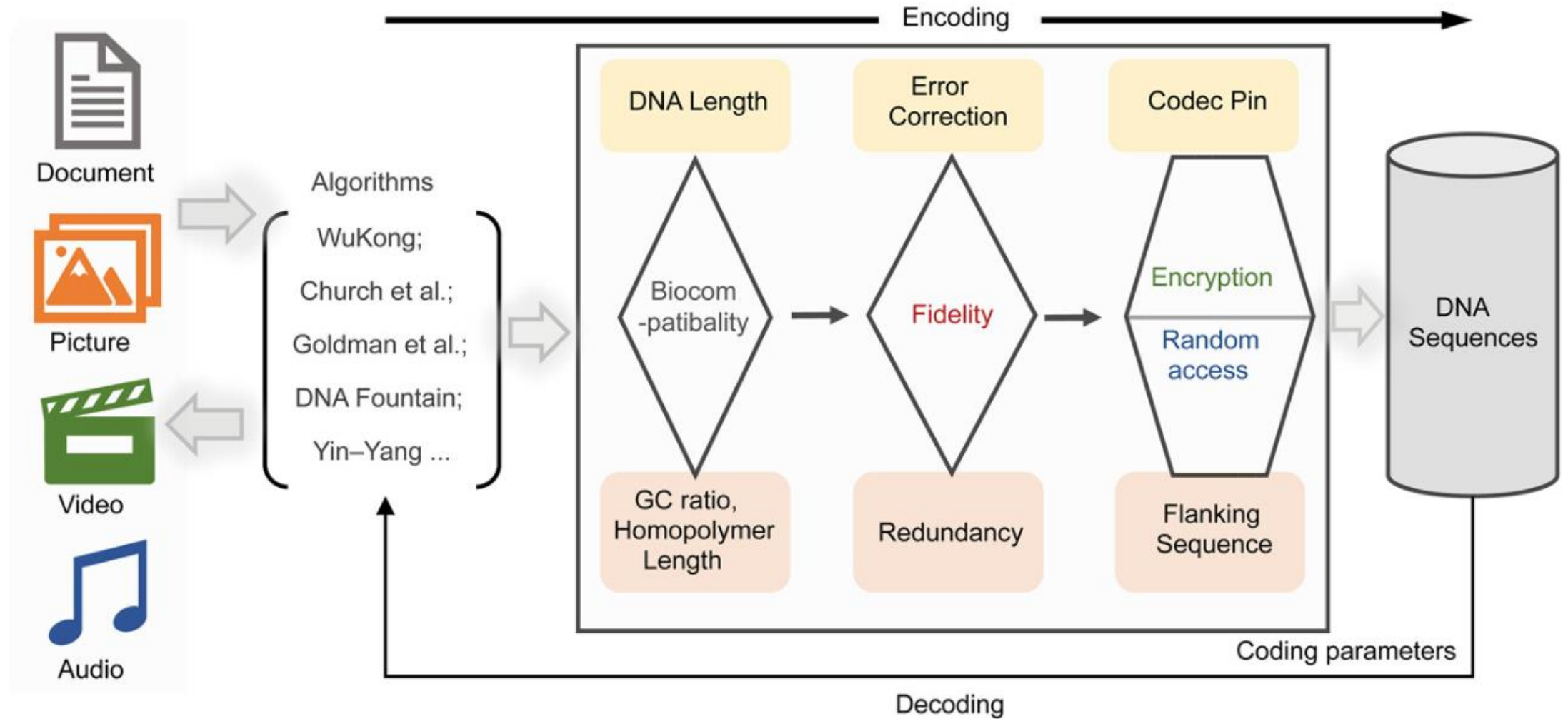
# Highlights



- Deoxyribonucleic acid (DNA) data storage exhibits remarkable advantages, such as high density and long lifespan, and is suggested to be one of the most promising media for coping with future data storage crises.
- A user-friendly platform, “Storage-D” was developed, which enables users to store any format of practical data with personalized choice.
- Specifically, a new algorithm, named “Wukong” was developed, which contains a sizeable collection of codec pins that enables encoding data into any DNA sequence with considerable privacy.
- The “Wukong” algorithm shows overall better performance than earlier algorithms in encoding a suitable length of DNA sequence matching downstream biochemical working flow for in vitro and in vivo storage.
- The tool provides an open-frame for integrating other codec algorithms and can be easily connected to commercial DNA synthesis and sequencing platform for building a complete pipeline for practical data storage into DNA. The web server and codes of the platform are available at <http://storage.dailab.xyz:16666/> and <https://github.com/DNAstorage-iSynBio/Storage-D/>, respectively.

# Results

## The working flow of Storage-D





# Results

## The interface of Storage-D

### Encode Parameter

Choose the encoding algorithm you need.

**Algorithm**  
WuKong ▼ *For algorithm details, please refer to the [Help](#) page.*

Set the encoding parameters you need.

<b>Encoded Length</b>	<b>Homopolymer</b>	<b>Min GC%</b>	<b>Max GC%</b>
<input type="text" value="200"/>	<input type="text" value="6"/>	<input type="text" value="40"/>	<input type="text" value="60"/>

**Codec Pin**  
 ▼

*\*If the Codec Pin is set to User Defined, remember your Pin value, because the same value needs to be entered when decoding.*

*For parameter details, please refer to the [Help](#) page.*

Set the additional parameters you need.

<b>ECC (RS)</b>	<b>Flanking Sequence</b>	<input type="checkbox"/> <b>Redundancy</b>
<input type="text" value="0"/>	<input type="text" value="No"/> <span>▼</span>	

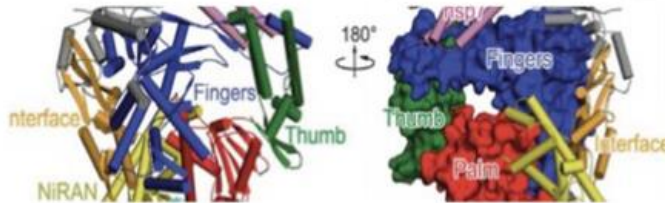
*\*ECC (RS) : The number of RS Code bytes in each maximum 256 bytes. For details, please refer to [reed-solo](#).*

*For parameter details, please refer to the [Help](#) page.*

You can fill in an email to receive the encoded result file.

### Preview

Ribbon diagram of COVID-19 Virus RNA-dependent RNA polymerase.jpg



### OUTPUT

The coding results will be shown here.

**Result Preview**

Ribbon diagram of COVID-19 Virus RNA-dependent RNA polymerase\_wukong.fasta

```
>totalBit:676816,binSegLen:187,leftPrimer:,rightPrimer:,fileExtension:.jpg,br
>seq_1
CGCGTCGGCCAAGTGCCAGTGAGTAGTGAATGCTCAGCAGGTTGGCAACGGCGGCTTTGAGCATTGATTATAAG
>seq_2
```

**Result Information**

**Input**

File Name : Ribbon diagram of COVID-19 Virus RNA-dependent RNA polymerase.jpg  
File size : 676816 (bit)

**Result**

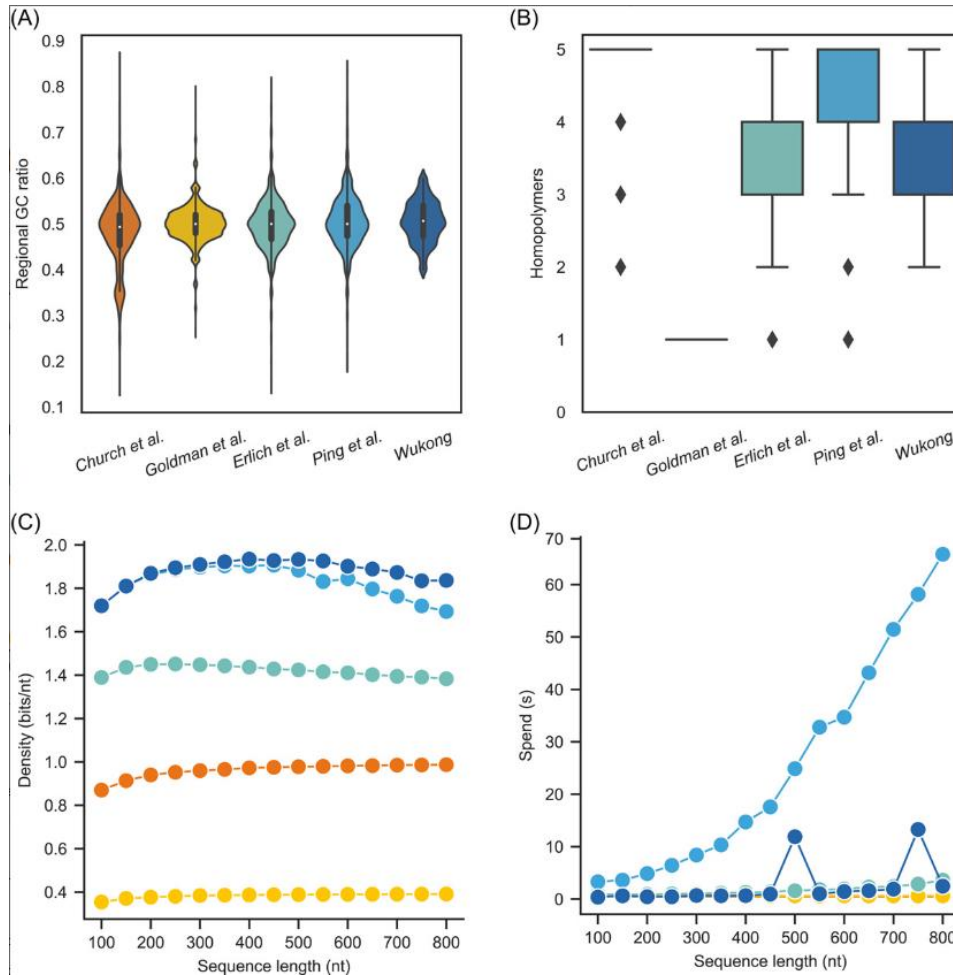
Run Time : 0:00:00.298942  
Total Base : 362000 (nt)

[Download](#)

# Results

## The “Wukong” codec algorithm implemented in Storage-D

### ➤ Encoding with different algorithms

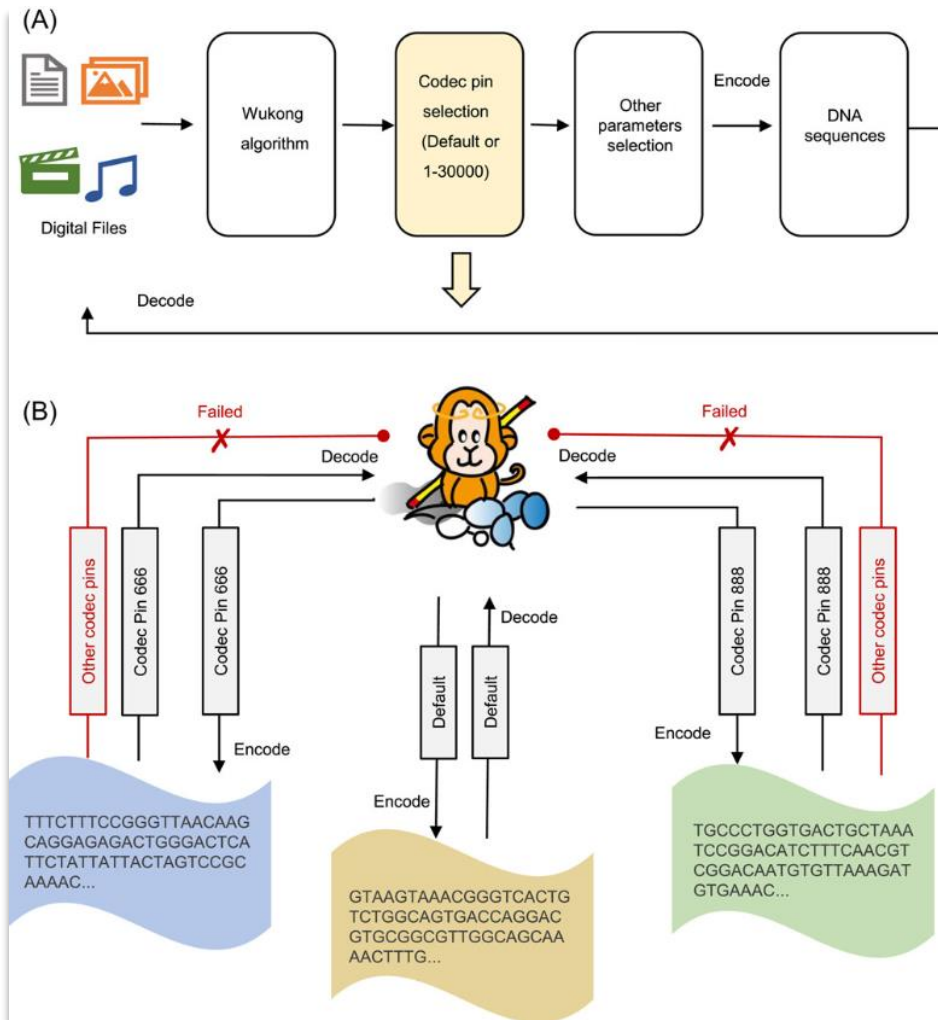


### ➤ Comparison between “Wukong” and other codec algorithms.

General features	Details	Church <i>et al.</i>	Goldman <i>et al.</i>	Erlich <i>et al.</i>	Ping <i>et al.</i>	Wukong
Density	Coding potential*	1	1.58	1.98	1.95	1.98
Biochemical Compatibility	Regional GC (%)	15–85	26–79	15–80	20–84	40–60 or defined
	Homopolymer	4	1	4	4	4 or defined
Data Fidelity	Error correction	NO	NO	Yes	Yes	Yes or defined
	Redundancy	NO	Yes	Yes	Yes	Yes or defined
Encryption	Codec Pin	--	--	--	1536 <sup>#</sup>	> 20 Trillion
Random-Access	Primer Design	--	--	--	--	Yes or defined

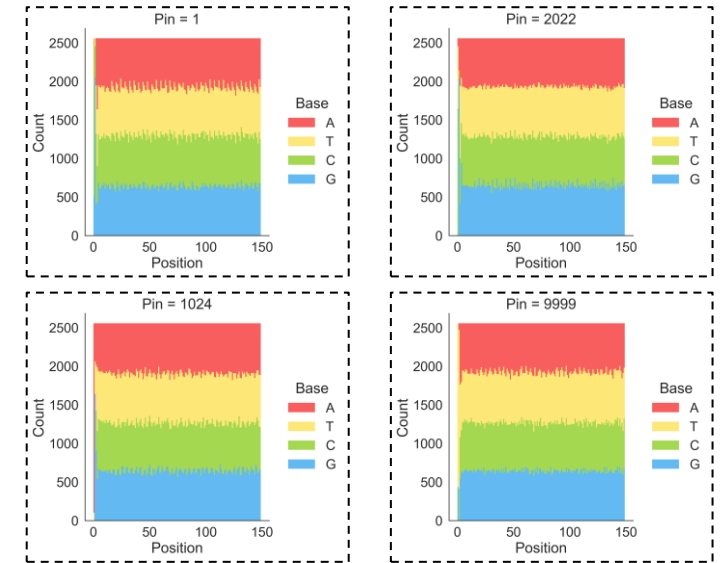
# Results

## Encode data with different codec pins



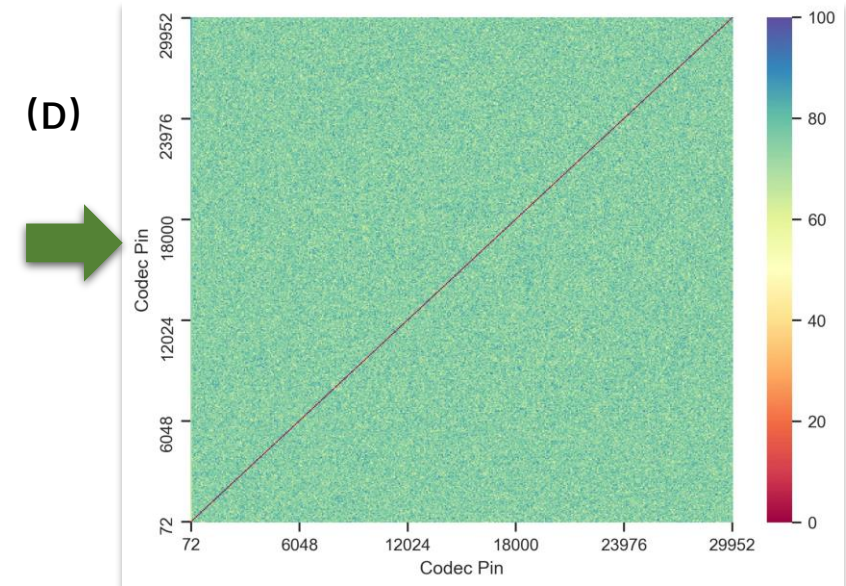
Encode data with different codec pins

(C)



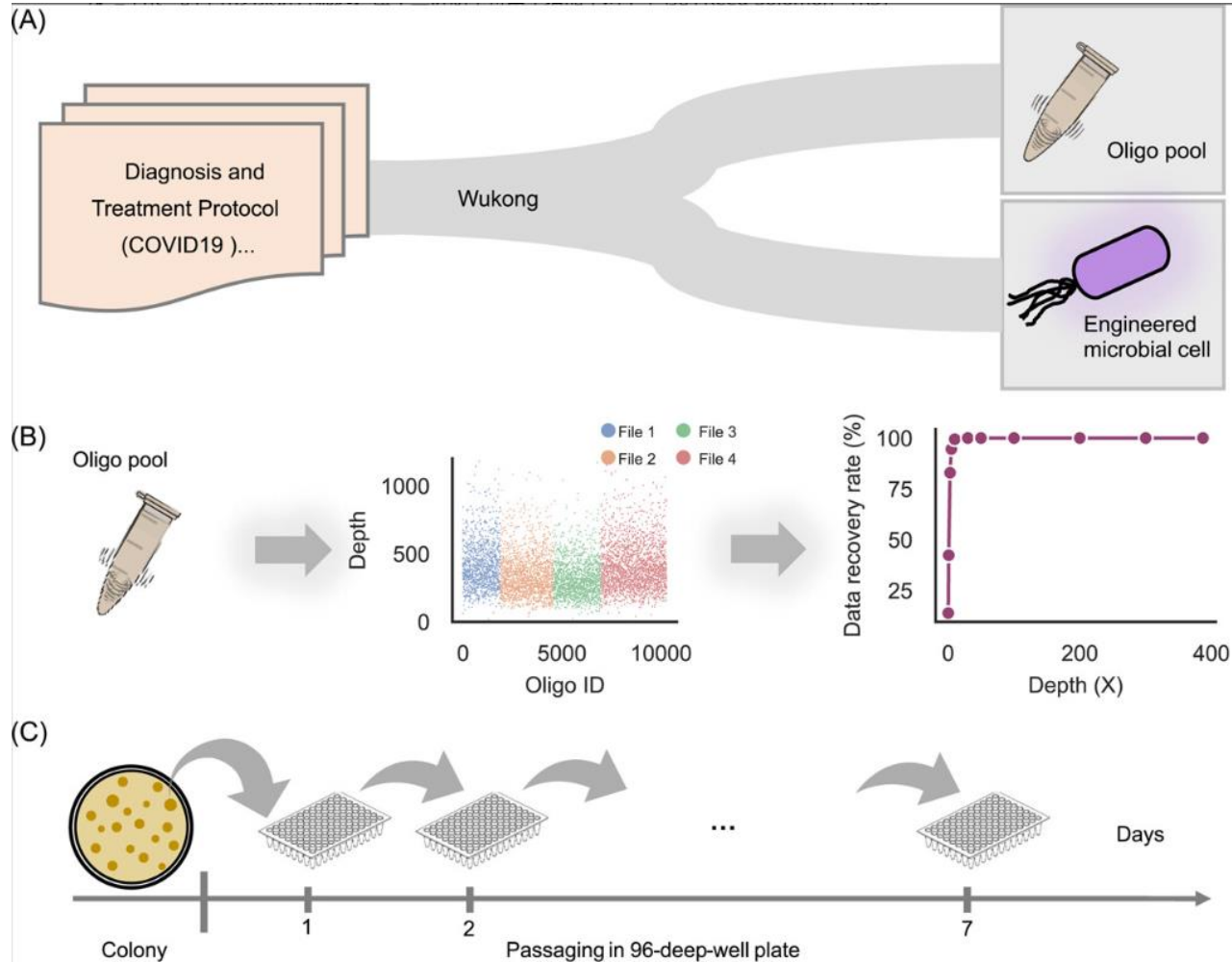
Heatmap of hamming distance between encoded DNA sequences by different codec Pins

(D)

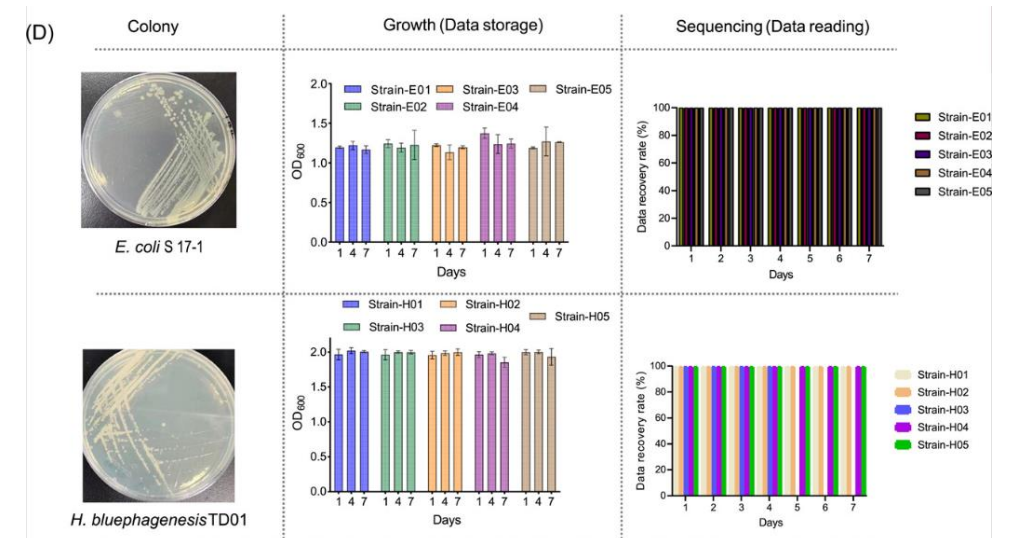


# Results

## Validation of "Storage-D" by practical data storage



- (A) Illustration of data storage in vitro and in vivo by "Wukong" algorithm
- (B) The oligo-pool is read by sequencing
- (C) Illustration of data passage in vivo.
- (D) The growth state and data recovery rate obtained through sequencing







# Summary

- ❑ “Storage-D” modularizes the basic functions of DNA data storage, such as encoding and decoding, error correction, and random access, and integrates four existing algorithms.
- ❑ The "Wukong" algorithm is capable of encoding DNA into diverse lengths with controlled homopolymer runs and regional even GC content while maintaining a high coding potential and offering a unique codec pin library. The feasibility of the "Wukong" algorithm was verified through computational simulations and in vitro and in vivo experiments.
- ❑ A user-friendly online web service and source code available for local download and integration are provided.




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