

User Documentation for Korean Nucleotide Archive (KoNA)

July 27, 2023

1. INTRODUCTION	1
1.1. About KoNA.....	1
1.2. Data model	1
2. DATA SUBMISSION	3
2.1. Submission overview	3
2.2. Create an account	3
2.3. Submit BioProject.....	5
2.4. Submit BioSample	6
2.5. Upload NGS raw data file with GBox.....	9
2.6. Submit NGS data.....	12
2.7. Manage my submission in MyPage.....	16
3. SEARCH AND DOWNLOAD.....	17
3.1. Search and browse.....	17
3.2. Download	18
4. FREQUENTLY ASKED QUESTIONS.....	23

1. INTRODUCTION

1.1. About KoNA

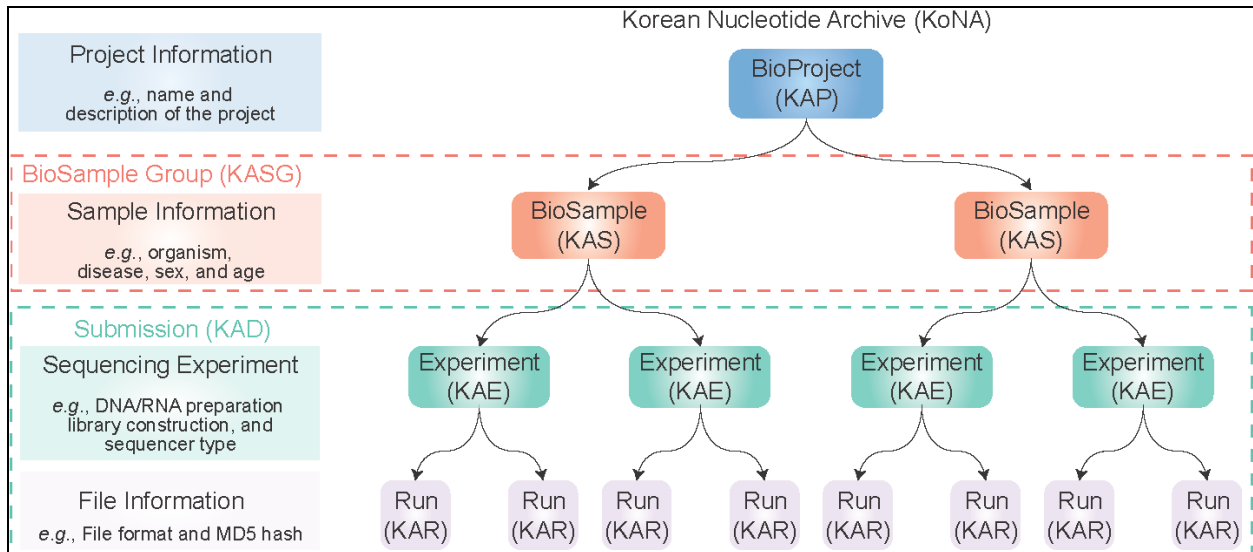
Korean Nucleotide Archive (KoNA) is a repository for NGS data. Its metadata model is equivalent to those established by the International Nucleotide Sequence Data Collaboration (INSDC), in which all the attributes are categorized into four objects: BioProject, BioSample, Experiment, and Run. To deposit data to KoNA, the metadata should be submitted to the KoNA website, whereas the raw sequence data should be submitted through a high-speed data transmission system called GBox.

When you cite your submitted data in your article, you can do so by citing the BioProject accession ID, for example:

“The data for this study have been deposited in the Korean Nucleotide Archive (KoNA) under accession number KAPxxxxxx.”

If you need help in using KoNA, please send your inquiry to data@kobic.kr.

1.2. Data model



In the data model of KoNA, attributes are categorized into four basic objects:

1. BioProject object with KAP prefix (e.g., KAP210001), which contains information of a study
2. BioSample object with KAS prefix (e.g., KAS21000001), which contains information of samples used in the sequencing experiment
3. Experiment object with KAE prefix (e.g., KAE21000001), which contains information of instrument and library
4. Run object with KAR prefix (e.g., KAR21000001), which is a manifest of data files

In addition, we denote a group of BioSamples as BioSample Group with KASG prefix (e.g., KASG210001) to manage and present relevant BioSamples in the system for user convenience. We issue an accession ID for a group of Experiments and Runs annotated in one submission batch (i.e., "Submission" object with KAD prefix; e.g., KAD2100001). Related BioProject entries can also be combined into an umbrella BioProject with KAU prefix (e.g., KAU200000).

2. DATA SUBMISSION

2.1. Submission overview

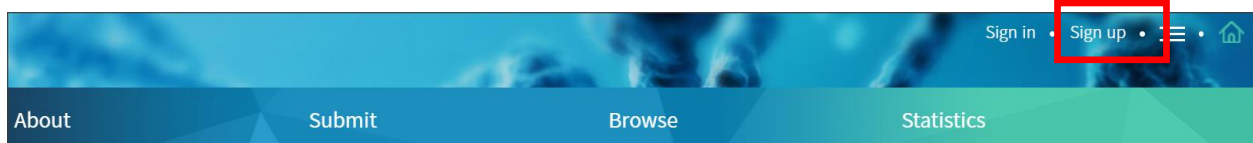
Submission is done in the following steps.

1. Log-in to your account. If you do not yet have an account, create one.
2. Input your data
 - Submit BioProject metadata on the KoNA website
 - Submit BioSample metadata on the KoNA website
 - Submit NGS raw data file with GBox
 - Submit NGS metadata on the KoNA website

Once the submission is complete, we will check the completeness of the submission. If the submission is found to be complete, we will issue accession IDs and release the data when the user-specified release date arrives. If the submission is found to be needing an edit, we will request what to update by e-mails.

2.2. Create an account


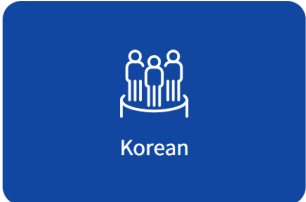
1. Click [Sign-up](#) at the top right of the main page.



2. Select the one on the right.

Select membership type

The registration process differs depending on the membership type.
Please select the membership type to join.



3. Fill out the form and click **Confirm**.

Sign up

01 Agree 02 Enter info 03 Done

(*Required)

Enter a personal information

Ⓞ 4-12 character-long. Only alphabets, numbers, special character _ are allowed.

Ⓞ 8-20 character-long. Uppercase and lowercase are distinguished. Must contain at least a number and a special character.

Select a country ▼

Ⓞ Please select your nationality.

4. Check your e-mail and activate your account. Then log-in.

Welcome and thank you for registering.
To activate your account, please click the below button within 24 hours.
If you experience any problems, please contact us at sso@kobic.re.kr.

2.3. Submit BioProject

On the top menu, select [Submit](#) → [Submit BioProject](#) and click [Create](#).

Submit BioProject

...

A BioProject is a collection of biological data related to a single initiative originating from a single organization or a consortium.
A BioProject record provides users a single place to find links to the diverse data types generated for that project.
The KoNA BioProject issues accession numbers with the prefix 'KAP' to the submitted projects.

Total: 1 / Page 1
[Submit 0](#) | [Return 0](#) | Approval 0

[Create](#)

NO	BioProject Accession ID	Project Title	Registration Date	Status	Operation
1	KAP230591	-	-	Writing	Edit Delete

On the resulting screen, fill out the form, which consists of four parts: [Submitter](#), [Project Design](#), [Hierarchy](#), and [Publications](#).

Fields in red font with asterisk (e.g., Name *) are mandatory whereas those in black font without asterisk (e.g., NTIS Number) are optional. Most of the fields should be straightforward from the fields name to see what to fill out. For several fields that need explanation, their descriptions are written in the form.

After filling out all necessary fields, click [Save](#) and [Submit](#) to complete your BioProject submission.

2.4. Submit BioSample

On the top menu, select [Submit](#) → [Submit BioSample](#) and click [Create](#).

Submit BioSample

...

BioSample is a sample repository where you can search, submit and curate sample metadata used in various projects. The BioSample is also being developed to capture descriptive information about the biological samples investigated in projects. BioProject and BioSample records link to corresponding data stored in KoNA. The KoNA BioSample issues accession numbers with the prefix 'KAS' to the submitted sample(s), and with the prefix "KASG" to the submitted sample group.

Total : 0 / Page 0
Submit 0 | Return 0 | Approval 0

[Create](#)

NO	Sample Group Accession ID	BioProject Accession ID	Sample Title	Organism	Release Date	Status	Operation
No Data							

In the resulting screen, you first need to import the BioProject that you submitted. To do so, click [Search](#) at the first field ([BioProject Accession ID](#)).

Submit BioSample

...

Please fill the below fields to describe your BioSamples.

Required * / Conditionally required *

Hierarchy

BioProject Accession ID * [Search](#)

In the resulting screen, tick the radio button of the BioProject and click [Select](#).

Project accession

Select	Project title	Registration date
<input type="radio"/>	Test	-

[Select](#)

Then, the BioProject ID should have been filled out in the form as shown below.

Hierarchy

BioProject Accession ID *

KAP230599

Search

Thereafter, most of the fields should be straightforward from the fields name to see what to fill out. For several fields that need explanation, their descriptions are written in the form.

For the **Sample Data Input Type** field, choose either **Direct Input** or **File Upload**.

Sample Data Input Type *

Direct Input

Direct Input

File Upload

- **Direct Input:** To fill out sample attribute information directly from the screen using the SpreadJS implementation. This option is recommended if you are not experienced in BioSample submission, or if you do not have many samples.
- **File Upload:** To download spreadsheet file, fill out sample attribute information on the file, then upload the file. This option is recommended if you have many samples.

In either case, whether an attribute field is mandatory or optional can be seen as colors in the corresponding column in the spreadsheet:

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	
1	1.Name / Designation								2.Sample history						3.
2	Sample name	Organism	Strain	Subgroup	Subtype	Culture collection	Specimen voucher	Biological replicate	Collected by	Collection date	Identified by	Passage history	Isolation source	Isolate	Gen
3	M	M	O	O	O	O	O	O	M	M	O	O	M	O	
10															
11															
12															
13															
14															
15															
16															
17															
18															
19															
20															
21															
22															
23															
24															

- **Green:** Mandatory field (M)
- **Yellow:** Optional field (O)

There are many attribute fields. Whether an attribute field is mandatory, optional, or not applicable depends on what you selected at the [Sample Type](#) field, which is called the “sample package” in NCBI and DDBJ, or “checklist” in EBI.

Sample Type *	Select appropriate types that best describes your samples : <input checked="" type="radio"/> Clinical or host-associated, pathogen <input type="radio"/> Environmental, food or other pathogen <input type="radio"/> Microbe : includes bacteria or other unicellular microbes that are not appropriate to Pathogen or Virus types. <input type="radio"/> Model organism or animal sample : includes multicellular samples or cell lines derived from common laboratory model organisms. <input type="radio"/> Human sample <input type="radio"/> Plant sample : includes any plant sample or cell line. <input type="radio"/> Virus sample
----------------------	--

Description of each attribute field is shown on the screen when you chose the [File Upload](#) option.

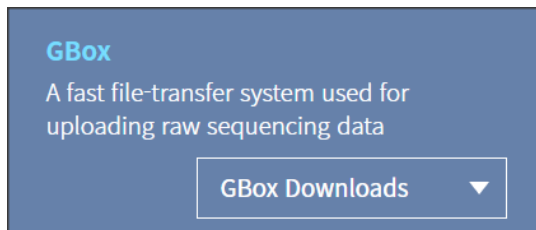
Fields	Description
Sample name *	A name that you choose for the sample. It can have any format, but we suggest that you make it concise, unique and consistent within your lab, and as informative as possible. Every Sample Name from a single Submitter must be unique.
Organism *	The most descriptive organism name for this sample (to the species, if relevant)
Strain	microbial or eukaryotic strain name, number or designation
Subgroup	Taxonomy below subspecies; sometimes used in viruses to denote subgroups taken from a single isolate
Subtype	Used as classifier in viruses (e.g. HIV type 1, Group M, Subtype A)

After filling out the spreadsheet form, click [Save](#) and [Submit](#) at the bottom of the web page.

2.5. Upload NGS raw data file with GBox

To upload NGS raw data file, you need to download GBox first, a high-speed file transfer system.

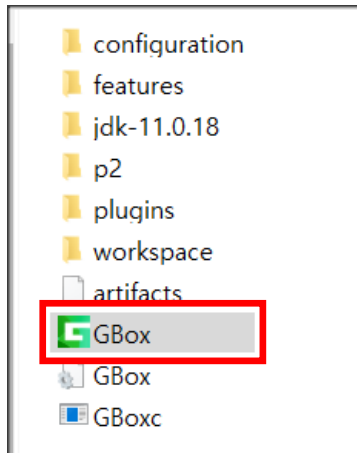
In the middle of the KoNA main page, there is a link [GBox Downloads](#).



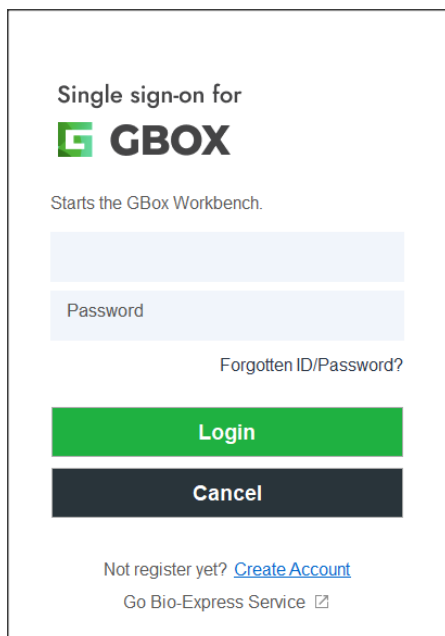
If you expand [GBox Downloads](#), there is a list of GBox implementations for Windows, Mac, and Linux. CLI stands for command line interface version. The entries without CLI are graphical user interface (GUI) versions.



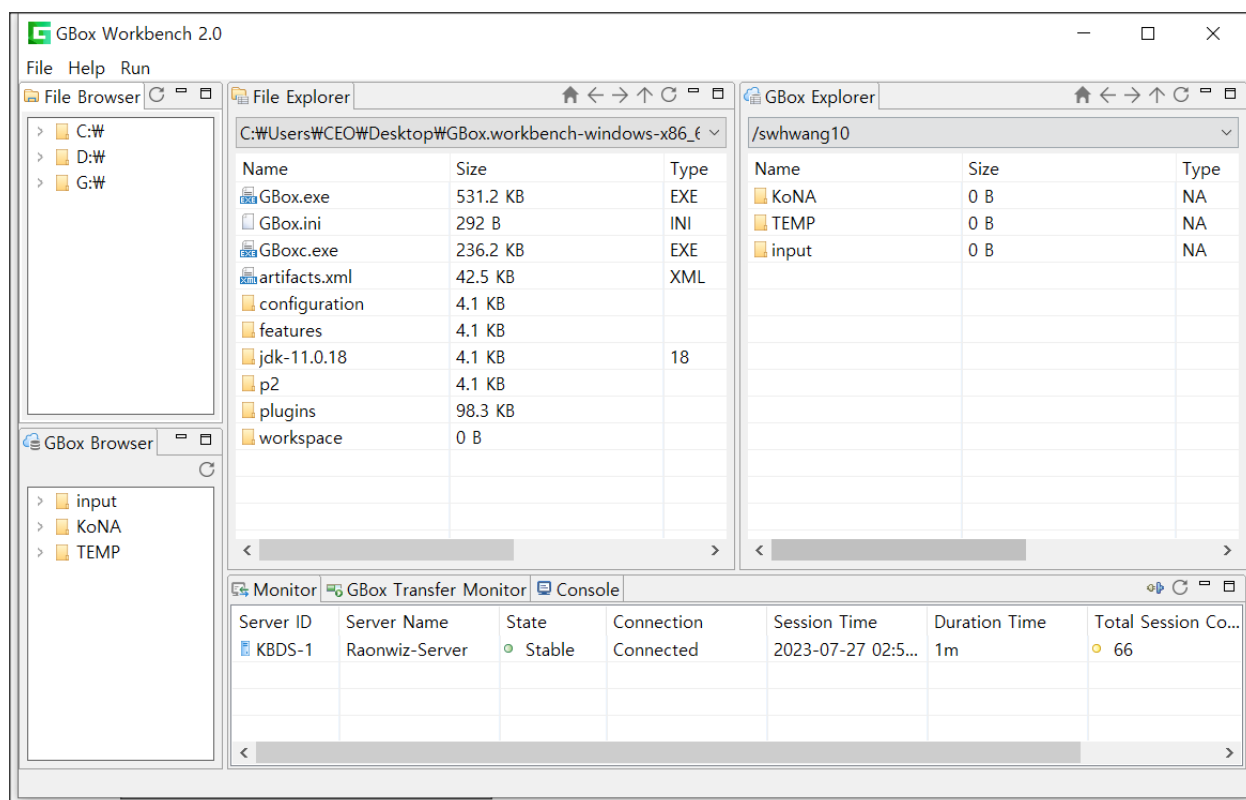
The following is based on Windows GUI version. When the GBox download is completed, unzip the download, find the executable and start it up.



A log-in windows will appear. Here, you log-in with the account information that you entered when you signed up for KoNA.



Upon log-in, the GBox interface comes up, and you can simply upload your NGS data file from your local PC to KoNA by dragging the file from the **File Explorer** pane to the **GBox Explorer** pane.



Important: There should be no space, special characters except underbar, and no non-English alphabet characters in the file name itself as well as in the path at your local PC. Otherwise, uploading to GBox will fail. For example, if your data file is named as `experiment 1.fq.gz`, uploading will fail because there is a space in the filename. You should rename it as `experiment_1.fq.gz`. Likewise, if the file `experiment_1.fq.gz` is in the folder name `C:\\My data\\`, uploading will fail because there is a space in the folder name. You should rename it as `C:\\My_data\\`.

2.6. Submit NGS data

On the top menu, select [Submit](#) → [Submit KAD](#) and click [Create](#).

Submit KAD

...

The Korean Read Archive (KAD) is a data repository for collecting, archiving, managing, and sharing raw NGS sequence data.
The KAD is the first repository of genome sequence data with international journal recognition in Korea.
Before creating a new KAD submission, you must create a BioProject and BioSample(s).
If you have any questions or would like to give us any suggestions/comments or report a bug, please feel free to contact us: data@kobic.re.kr

Total : 0 / Page 1
[Submit 0](#) | [Return 0](#) | Approval 0

[Create](#)

NO	BioProject Accession ID	Sample Group Accession ID	KAD Accession ID	Submission Date	Registration Date	Reviewer	Status	Operation
No Data								

In the resulting screen, you first need to import the BioProject and BioSample that you submitted. To do so, click [Search](#) at the first field ([BioProject Accession ID](#)) and at the first field ([BioSample Group Accession](#)).

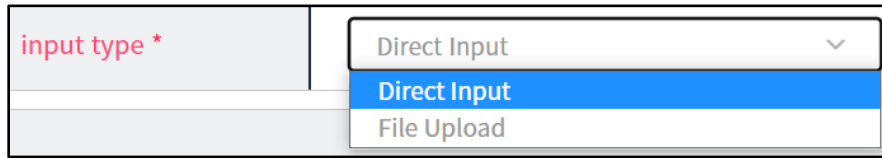
BioProject Accession ID *	<input type="text"/> <small>Select the Project ID related to the sample. Link data to BioProject that describes the research</small>
BioSample Group Accession *	<input type="text"/> <small>Enter a BioSample or KAD Sample Accession. BioSample accessions have 'KAS' prefix. KAD Sample Accessions have 'KRS' prefix. A BioSample describes the biological source material for your sequence library preparation.</small>

In the resulting screen, tick the radio button of the BioProject and click [Select](#), and the radio button of the BioProject and click [Select](#) as well.

Then, the two fields should have been filled out in the form as shown below.

BioProject Accession ID *	<input type="text" value="KAP230599"/> <small>Select the Project ID related to the sample. Link data to BioProject that describes the research</small>
BioSample Group Accession *	<input type="text" value="KASG231018"/> <small>Enter a BioSample or KAD Sample Accession. BioSample accessions have 'KAS' prefix. KAD Sample Accessions have 'KRS' prefix. A BioSample describes the biological source material for your sequence library preparation.</small>

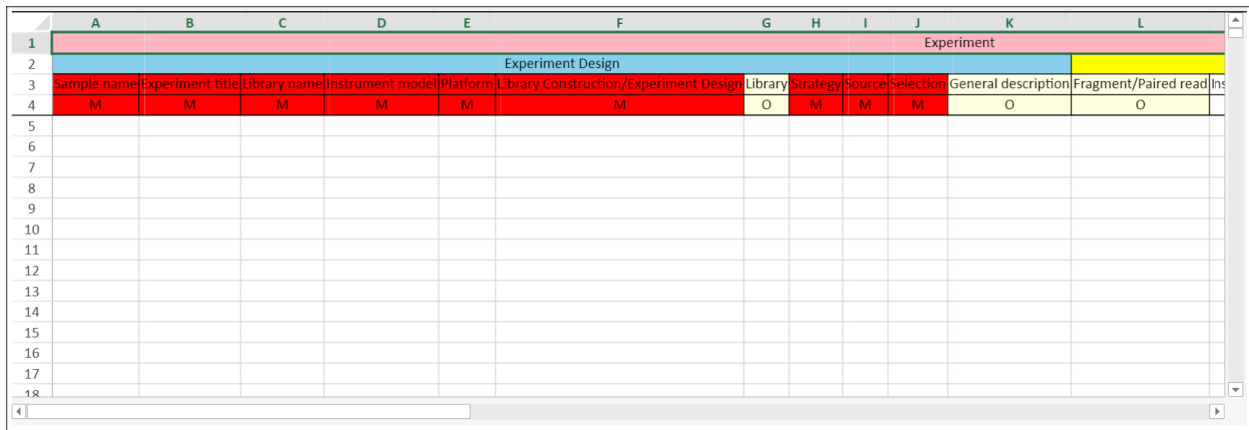
For the **input type** field, choose either **Direct Input** or **File Upload**.



The image shows a form field labeled "input type *". A dropdown menu is open, showing three options: "Direct Input" (selected and highlighted in blue), "Direct Input", and "File Upload".

- **Direct Input:** To fill out NGS metadata directly from the screen using the SpreadJS implementation. This option is recommended if you are not experienced in NGS data submission, or if you do not have many data files.
- **File Upload:** To download spreadsheet file, fill out NGS metadata on the file, then upload the file. This option is recommended if you have many data files.

In either case, whether a metadata field is mandatory or optional can be seen as colors in the corresponding column in the spreadsheet:



The image shows a spreadsheet with columns A through L. The rows are numbered 1 through 18. The spreadsheet is divided into sections: "Experiment" (rows 1-2), "Experiment Design" (rows 3-4), and "Library Construction/Experiment Design" (rows 5-18). The columns are: A (Sample name), B (Experiment title), C (Library name), D (Instrument model), E (Platform), F (Library Construction/Experiment Design), G (Library), H (Strategy), I (Source), J (Selection), K (General description), L (Fragment/Paired read), and M (Instrument). The mandatory fields (M) are highlighted in red, and the optional fields (O) are highlighted in ivory.

1	A	B	C	D	E	F	G	H	I	J	K	L
2	Experiment											
3	Experiment Design											
4	M	M	M	M	M	M	O	M	M	M	O	O
5												
6												
7												
8												
9												
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16												
17												
18												

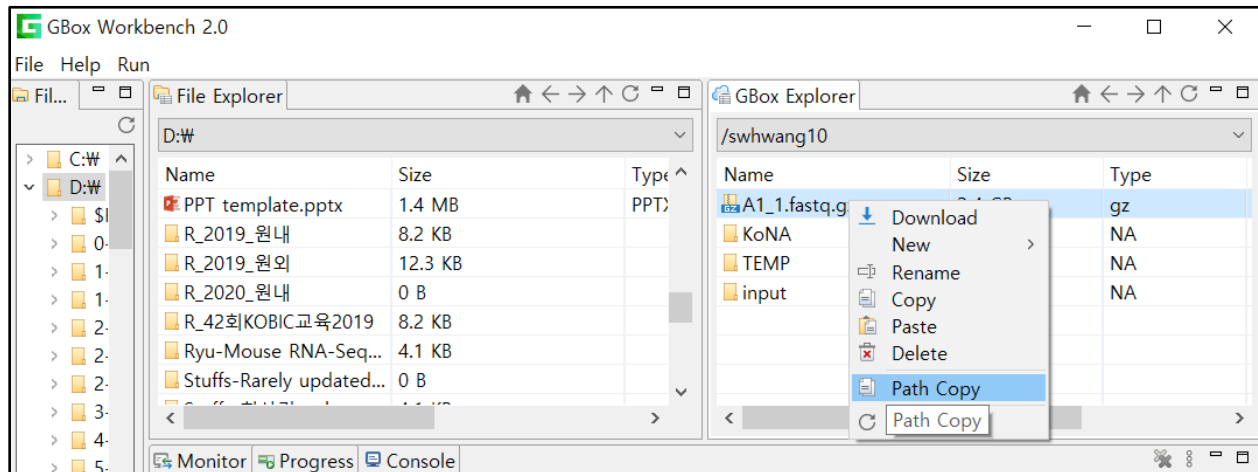
- **Red:** Mandatory field (M)
- **Ivory:** Optional field (O)

Description of each field is shown on the screen when you chose the [File Upload](#) option.

Field	Description
Sample name *	A name that you choose for the sample. It can have any format, but we suggest that you make it concise, unique and consistent within your lab, and as informative as possible. Every Sample Name from a single Submitter must be unique.
Experiment title (English) *	"Experiment title. Short description that will identify the dataset on public pages. A clear and concise formula for the title would be like: {methodology} of {organism}: {sample info} (e.g. "RNA-Seq of Mus musculus: adult female spleen")"
Experiment title (Korean) *	데이터베이스 공개 페이지에서 나타낼 실험 제목. 제목에 종을 포함한 샘플의 실험 정보와 사용한 시퀀싱 타입을 간략히 표현하는 것을 추천함. (예시: "성체 쥐의 비장에 대한 RNA-Seq")
Library name *	Short unique identifier for the sequencing library. Each library name MUST be unique! (Exception: libraries of the technical replicates are allowed to have the same library name)
Platform *	part of Instrument model of Sequencing Platform
Instrument model *	Sequencing platform 중 Instrument model 부분
Library Construction/Experiment Design *	Enter the details about your experimental design and molecular strategies including hybrid selection and affinity capture reagents; any detail that distinguishes your experiment from other similar experiments. This field should describe: <ul style="list-style-type: none"> - the protocols used to extract and prepare the material to be sequenced - the library construction protocol - name of the library preparation kit

To the last three fields in the spreadsheet ([READ 1](#), [READ 2](#), [OTHER](#)), fill out the path to the file that you uploaded by GBox. To get the path to the file, right click the file in the GBox and select [Path Copy](#). The path will look something like

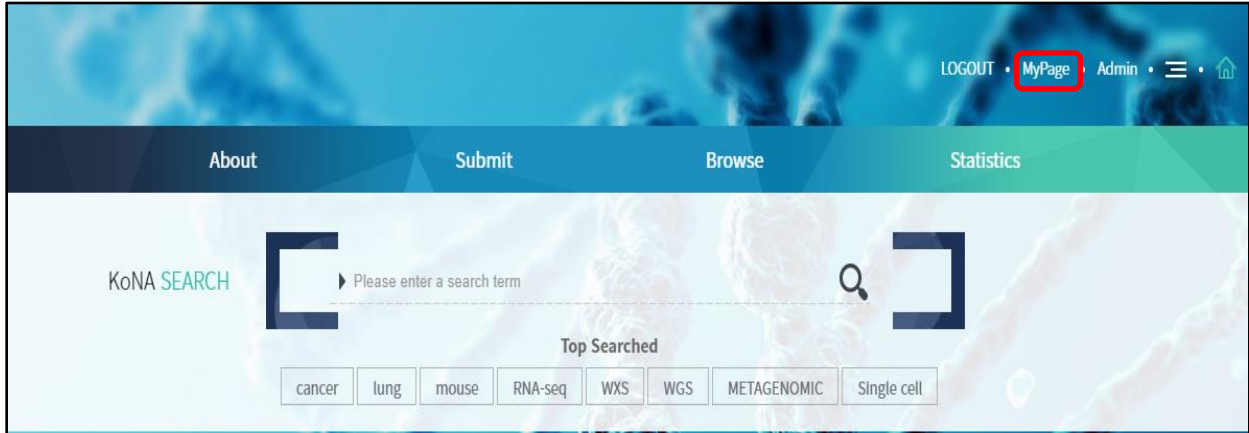
```
/john_smith/A1_1.fastq.gz.
```



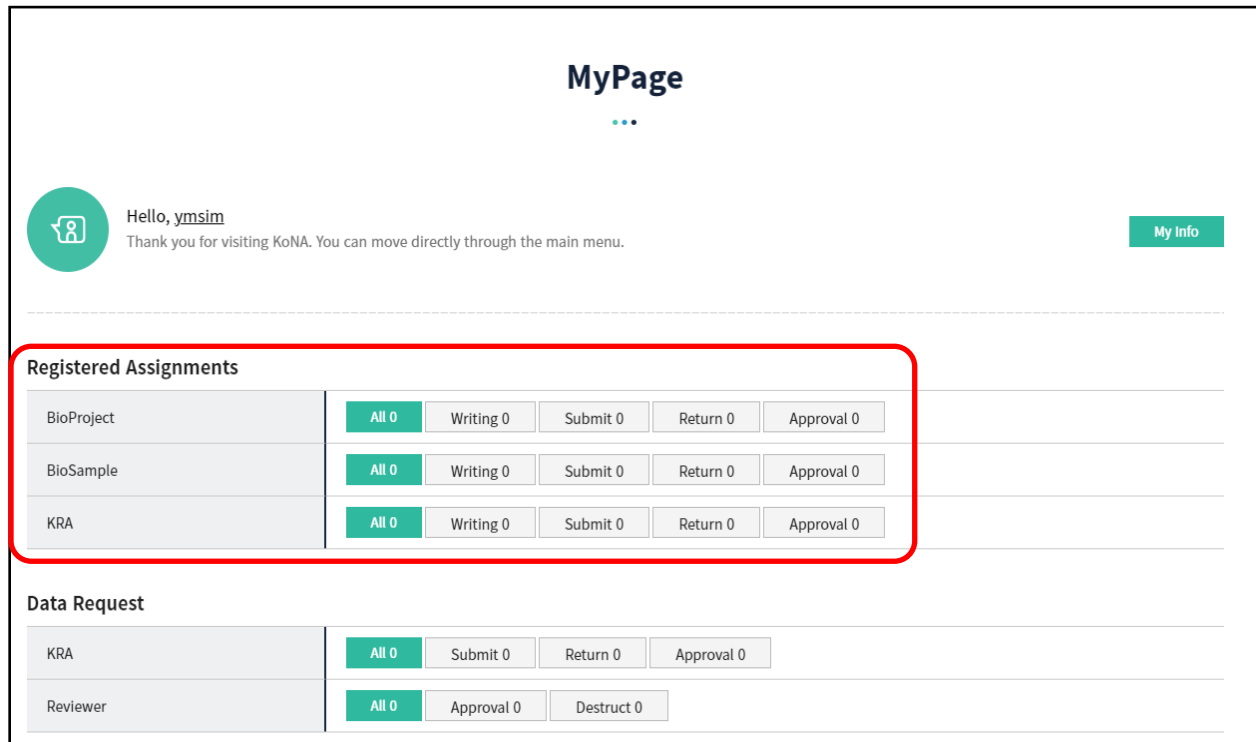
After filling out the spreadsheet form, click [Save](#) and [Submit](#) at the bottom of the web page.

2.7. Manage my submission at MyPage

You can check the status of your submission at [MyPage](#) in the top right.



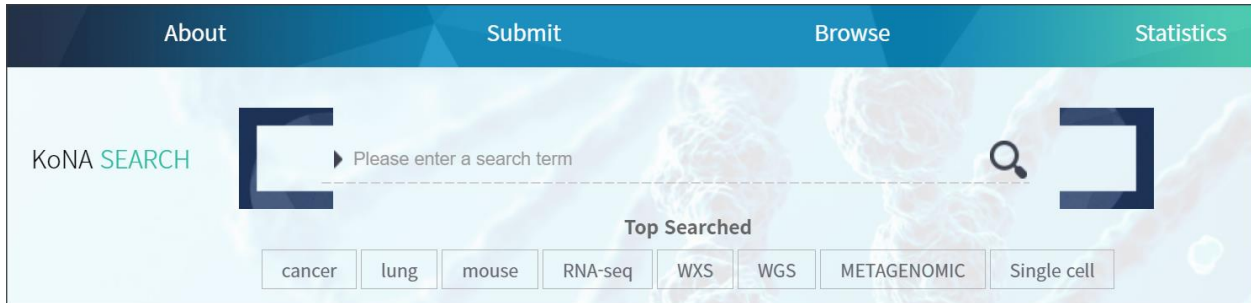
The status of your submission can be [Writing](#), [Submit](#), [Return](#), [Approval](#). The status right after submission would be [Submit](#). If we find the submission incomplete, the status will change to [Return](#), and you need to update your submission as written in the instruction that we will send you. If the submission is right, the status will change to [Approval](#).



3. SEARCH AND DOWNLOAD

3.1. Search and browse

You can search for keyword or accession ID at the search bar in the main page.



You can also search at the search bar in all other pages.



You can browse BioProject entries at Browse → BioProject menu.

Browse BioProject

...

A BioProject is a collection of biological data related to a single initiative originating from a single organization or a consortium.
A BioProject record provides users a single place to find links to the diverse data types generated for that project.
The KoNA BioProject issues accession numbers with the prefix 'KAP' to the submitted projects.

There are a total of 462 data registered in the "BioProject"

NO	BioProject Accession ID	Project Title	Sample Scope	Project Data Type	Registration Date
1	KAP210106	Construction of next generation sequencing system center	Monoisolate	Transcriptome or Gene Expression	2021-11-25
2	KAP230581	Multifaceted roles of retrotransposon-fusion RNAs	Multiisolate	Whole Genome sequencing,Epigenomics,Transcriptome	2023-05-09

3.2. Download

The following is an example of the accession ID KAD2200955, which is available at https://www.kobic.re.kr/kona/search_kra?bioproject_id=KAP220490&sample_group_id=KASG220880&kra_id=KAD2200955.

At the bottom of that page, there are links for download. By clicking the link Download Excel, you can download the metadata as a spreadsheet file. You do not need to log-in for this download.

Experiment												
Experiment Design												
Sample name	Experiment title	Library name	Instrument mode	Platform	Library Construction/Experiment Design	Library	Strategy	Source	Selection	General description	Fragment/ Paired read	
M	M	M	M	M	M	O	M	M	M	O	O	
TN1510R0435	Primate addictio	TN1510R043	HiSeq 30CILLUMIN	HiSeq 30CILLUMIN	TruSeq Stranded mRNA sample prep kit		RNA-Sec	TRANS	cDNA		Paired-end	
TN1510R0436	Primate addictio	TN1510R043	HiSeq 30CILLUMIN	HiSeq 30CILLUMIN	TruSeq Stranded mRNA sample prep kit		RNA-Sec	TRANS	cDNA		Paired-end	
TN1510R0437	Primate addictio	TN1510R043	HiSeq 30CILLUMIN	HiSeq 30CILLUMIN	TruSeq Stranded mRNA sample prep kit		RNA-Sec	TRANS	cDNA		Paired-end	
TN1510R0438	Primate addictio	TN1510R043	HiSeq 30CILLUMIN	HiSeq 30CILLUMIN	TruSeq Stranded mRNA sample prep kit		RNA-Sec	TRANS	cDNA		Paired-end	
TN1510R0439	Primate addictio	TN1510R043	HiSeq 30CILLUMIN	HiSeq 30CILLUMIN	TruSeq Stranded mRNA sample prep kit		RNA-Sec	TRANS	cDNA		Paired-end	
TN1510R0440	Primate addictio	TN1510R044	HiSeq 30CILLUMIN	HiSeq 30CILLUMIN	TruSeq Stranded mRNA sample prep kit		RNA-Sec	TRANS	cDNA		Paired-end	
TN1510R0441	Primate addictio	TN1510R044	HiSeq 30CILLUMIN	HiSeq 30CILLUMIN	TruSeq Stranded mRNA sample prep kit		RNA-Sec	TRANS	cDNA		Paired-end	
TN1510R0442	Primate addictio	TN1510R044	HiSeq 30CILLUMIN	HiSeq 30CILLUMIN	TruSeq Stranded mRNA sample prep kit		RNA-Sec	TRANS	cDNA		Paired-end	
TN1510R0443	Primate addictio	TN1510R044	HiSeq 30CILLUMIN	HiSeq 30CILLUMIN	TruSeq Stranded mRNA sample prep kit		RNA-Sec	TRANS	cDNA		Paired-end	
TN1510R0444	Primate addictio	TN1510R044	HiSeq 30CILLUMIN	HiSeq 30CILLUMIN	TruSeq Stranded mRNA sample prep kit		RNA-Sec	TRANS	cDNA		Paired-end	
TN1510R0445	Primate addictio	TN1510R044	HiSeq 30CILLUMIN	HiSeq 30CILLUMIN	TruSeq Stranded mRNA sample prep kit		RNA-Sec	TRANS	cDNA		Paired-end	
TN1510R0446	Primate addictio	TN1510R044	HiSeq 30CILLUMIN	HiSeq 30CILLUMIN	TruSeq Stranded mRNA sample prep kit		RNA-Sec	TRANS	cDNA		Paired-end	
TN1510R0447	Primate addictio	TN1510R044	HiSeq 30CILLUMIN	HiSeq 30CILLUMIN	TruSeq Stranded mRNA sample prep kit		RNA-Sec	TRANS	cDNA		Paired-end	
TN1510R0448	Primate addictio	TN1510R044	HiSeq 30CILLUMIN	HiSeq 30CILLUMIN	TruSeq Stranded mRNA sample prep kit		RNA-Sec	TRANS	cDNA		Paired-end	

Download Excel

GBOX Is GBox not installed?
GBox is a fast file-transfer system used for uploading raw sequencing data. Click the right button to go to the download page.

GBox Download **Direct Download**

By clicking the link Direct Download, you can download the raw data files. You do not need log-in for this download.

Experiment Design												
Sample name	Experiment title	Library name	Instrument mode	Platform	Library Construction/Experiment Design	Library	Strategy	Source	Selection	General description	Fragment/ Paired read	
M	M	M	M	M	M	O	M	M	M	O	O	
TN1510R0435	Primate addictio	TN1510R043	HiSeq 30CILLUMIN	TruSeq Stranded mRNA sample prep kit			RNA-SecTRANS	cDNA			Paired-end	
TN1510R0436	Primate addictio	TN1510R043	HiSeq 30CILLUMIN	TruSeq Stranded mRNA sample prep kit			RNA-SecTRANS	cDNA			Paired-end	
TN1510R0437	Primate addictio	TN1510R043	HiSeq 30CILLUMIN	TruSeq Stranded mRNA sample prep kit			RNA-SecTRANS	cDNA			Paired-end	
TN1510R0438	Primate addictio	TN1510R044	HiSeq 30CILLUMIN	TruSeq Stranded mRNA sample prep kit			RNA-SecTRANS	cDNA			Paired-end	
TN1510R0439	Primate addictio	TN1510R043	HiSeq 30CILLUMIN	TruSeq Stranded mRNA sample prep kit			RNA-SecTRANS	cDNA			Paired-end	
TN1510R0440	Primate addictio	TN1510R044	HiSeq 30CILLUMIN	TruSeq Stranded mRNA sample prep kit			RNA-SecTRANS	cDNA			Paired-end	
TN1510R0441	Primate addictio	TN1510R044	HiSeq 30CILLUMIN	TruSeq Stranded mRNA sample prep kit			RNA-SecTRANS	cDNA			Paired-end	
TN1510R0442	Primate addictio	TN1510R044	HiSeq 30CILLUMIN	TruSeq Stranded mRNA sample prep kit			RNA-SecTRANS	cDNA			Paired-end	
TN1510R0443	Primate addictio	TN1510R044	HiSeq 30CILLUMIN	TruSeq Stranded mRNA sample prep kit			RNA-SecTRANS	cDNA			Paired-end	
TN1510R0444	Primate addictio	TN1510R044	HiSeq 30CILLUMIN	TruSeq Stranded mRNA sample prep kit			RNA-SecTRANS	cDNA			Paired-end	
TN1510R0445	Primate addictio	TN1510R044	HiSeq 30CILLUMIN	TruSeq Stranded mRNA sample prep kit			RNA-SecTRANS	cDNA			Paired-end	
TN1510R0446	Primate addictio	TN1510R044	HiSeq 30CILLUMIN	TruSeq Stranded mRNA sample prep kit			RNA-SecTRANS	cDNA			Paired-end	
TN1510R0447	Primate addictio	TN1510R044	HiSeq 30CILLUMIN	TruSeq Stranded mRNA sample prep kit			RNA-SecTRANS	cDNA			Paired-end	
TN1510R0448	Primate addictio	TN1510R044	HiSeq 30CILLUMIN	TruSeq Stranded mRNA sample prep kit			RNA-SecTRANS	cDNA			Paired-end	

[Download Excel](#)

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Experiment												
Experiment Design												
Sample name	Experiment title	Library name	Instrument mode	Platform	Library Construction/Experiment Design	Library	Strategy	Source	Selection	General description	Fragment/ Paired read	
M	M	M	M	M	M	O	M	M	M	O	O	
TN1510R0435	Primate addictio	TN1510R043	HiSeq 30CILLUMIN	TruSeq Stranded mRNA sample prep kit			RNA-SecTRANS	cDNA			Paired-end	
TN1510R0436	Primate addictio	TN1510R043	HiSeq 30CILLUMIN	TruSeq Stranded mRNA sample prep kit			RNA-SecTRANS	cDNA			Paired-end	
TN1510R0437	Primate addictio	TN1510R043	HiSeq 30CILLUMIN	TruSeq Stranded mRNA sample prep kit			RNA-SecTRANS	cDNA			Paired-end	
TN1510R0438	Primate addictio	TN1510R043	HiSeq 30CILLUMIN	TruSeq Stranded mRNA sample prep kit			RNA-SecTRANS	cDNA			Paired-end	
TN1510R0439	Primate addictio	TN1510R043	HiSeq 30CILLUMIN	TruSeq Stranded mRNA sample prep kit			RNA-SecTRANS	cDNA			Paired-end	
TN1510R0440	Primate addictio	TN1510R044	HiSeq 30CILLUMIN	TruSeq Stranded mRNA sample prep kit			RNA-SecTRANS	cDNA			Paired-end	
TN1510R0441	Primate addictio	TN1510R044	HiSeq 30CILLUMIN	TruSeq Stranded mRNA sample prep kit			RNA-SecTRANS	cDNA			Paired-end	
TN1510R0442	Primate addictio	TN1510R044	HiSeq 30CILLUMIN	TruSeq Stranded mRNA sample prep kit			RNA-SecTRANS	cDNA			Paired-end	
TN1510R0443	Primate addictio	TN1510R044	HiSeq 30CILLUMIN	TruSeq Stranded mRNA sample prep kit			RNA-SecTRANS	cDNA			Paired-end	
TN1510R0444	Primate addictio	TN1510R044	HiSeq 30CILLUMIN	TruSeq Stranded mRNA sample prep kit			RNA-SecTRANS	cDNA			Paired-end	
TN1510R0445	Primate addictio	TN1510R044	HiSeq 30CILLUMIN	TruSeq Stranded mRNA sample prep kit			RNA-SecTRANS	cDNA			Paired-end	
TN1510R0446	Primate addictio	TN1510R044	HiSeq 30CILLUMIN	TruSeq Stranded mRNA sample prep kit			RNA-SecTRANS	cDNA			Paired-end	
TN1510R0447	Primate addictio	TN1510R044	HiSeq 30CILLUMIN	TruSeq Stranded mRNA sample prep kit			RNA-SecTRANS	cDNA			Paired-end	
TN1510R0448	Primate addictio	TN1510R044	HiSeq 30CILLUMIN	TruSeq Stranded mRNA sample prep kit			RNA-SecTRANS	cDNA			Paired-end	

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The download process proceeds in two steps:

1. The raw data files are copied to your GBox user space.
2. You can then download the copied raw data files to your local PC.

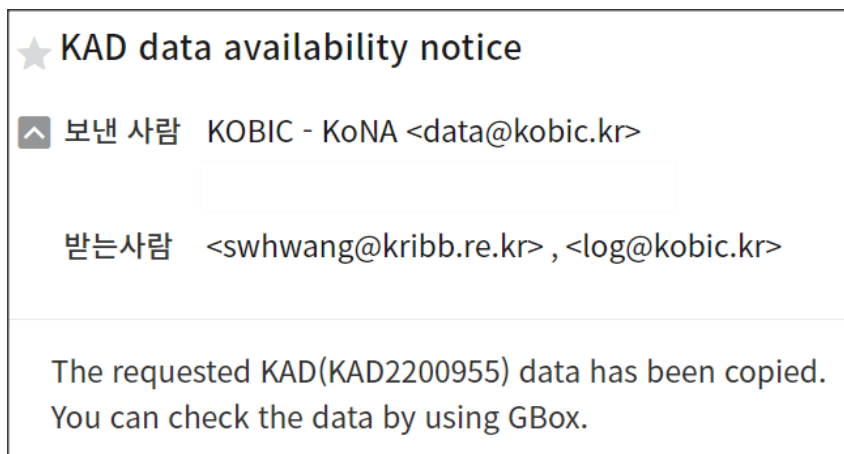
When you click **GBox Download**, a separate window appears. You just need to click **Confirm** here.



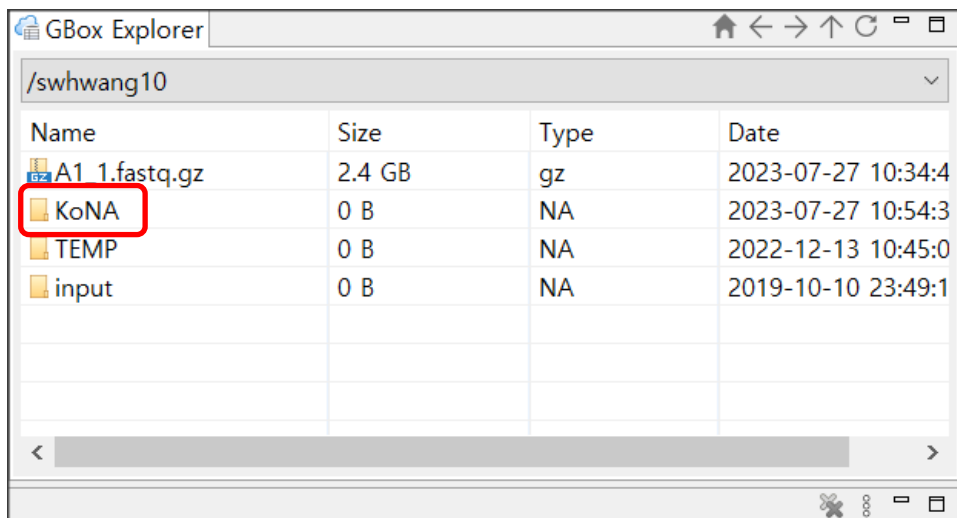
The operation can take from a few seconds to several tens of minutes depending on the size of the data.
 We will notify you by email when the work is complete.

Confirm

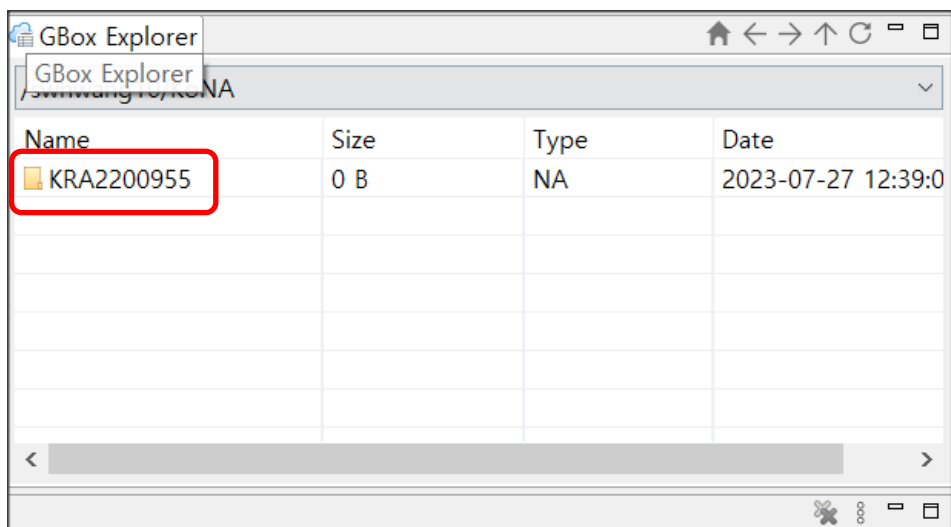
Shortly, you will receive an e-mail informing that the raw data files were copied to your GBox user space.



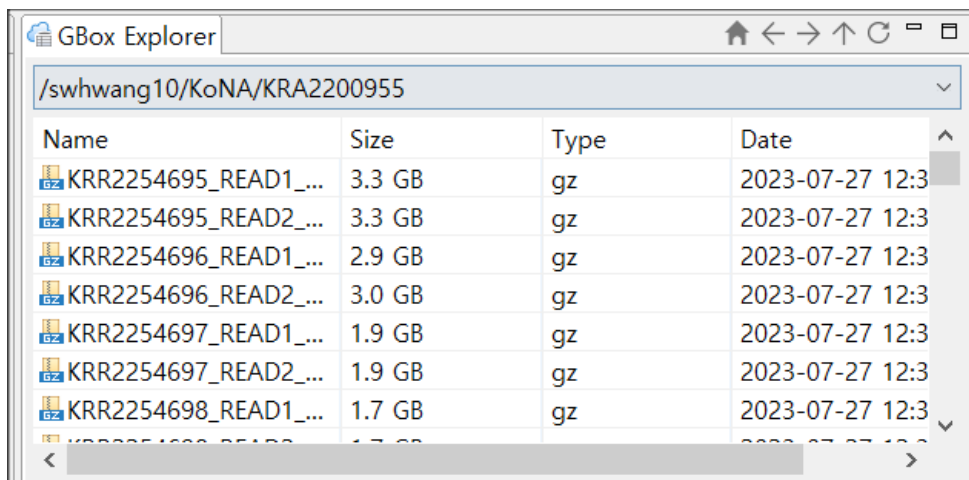
From GBox Explorer pane in GBox application, you will see a folder KoNA has been automatically created.



Inside the folder `KoNA`, you will find another automatically created folder whose name is the accession ID of the data you copied.



Inside that folder, you will find raw data files that you want to download.



You can just download them by dragging them from GBox Explorer pane to File Explorer pane.

4. FAQ

Q: How many samples and experiments do I need?

A: You may have more than one experiment per samples. SAMPLE is a record of biological isolate with unique physical properties. EXPERIMENT is a unique sequencing result for a specific sample. In the KoNA Metadata template, EXPERIMENT is represented by a combination of library + strategy + layout + instrument model and corresponds to one row in the table.

Q: What KoNA accession do I use for my publication and where can I find it?

A: We recommend using the BioProject accession (KAP#) in publications. A BioProject is an entry point for all data submitted for a given study. Each BioProject can be associated with more than one submission in KoNA. After you have successfully completed your submission, we will send an email notification with the BioProject accession.

Q: My manuscript reviewer is requesting a link to my submission. How do I get one?

A: Log in and go to the MyPage. Find the BioProject of interest and click "Reviewer link".

Q: How do I create more than one EXPERIMENT (library/replicate) per SAMPLE for the KAD submission ?

A: Each row in the KAD metadata template represents one EXPERIMENT. Simply use the same BioSample accession or name (depending on the template) in rows (EXPERIMENTs) that you want to associate with this sample.

Q: How do I create more than one RUN per EXPERIMENT?

A: Only one RUN per EXPERIMENT is allowed for KRA submission. When libraries are indeed identical (i.e., same combination of library + strategy + layout + instrument model), all files should be placed in the same RUN. To do this, simply enter the file names consecutively in the same row.

Q: How do I delete my submission?

A: To delete KoNA submissions, contact KoNA staff for assistance at data@kobic.kr and provide an ID and a reason.

Q: How do I add more samples to my KAD submission?

A: KAD Submission is a discrete act of depositing data (transaction). You cannot add data to a KAD after corresponding KAD accession ID has been issued. Instead, you need to add new samples and new KoNA data and/or new KoNA data to existing samples to a BioProject. BioProject serves as an entry point for all data submitted for a given research project. In order to update your BioProject with new samples and/or KoNA data you should create a new submission where you provide the BioProject accession (KAP#) of the project you want to update

Q: How do I change the release date of my KoNA submission?

A: Please contact KoNA staff for assistance at data@kobic.kr.

Q: How do I improve/correct my metadata after submitting?

A: Only KoNA staff can correct the metadata after an accession ID is issued. Please contact KoNA staff for assistance at data@kobic.kr.

Q: How do I rename my EXPERIMENT/RUN?

A: Name of EXPERIMENT and RUN cannot be changed.

Q: How do I change the PLATFORM in my EXPERIMENT?

A: Please contact KoNA staff for assistance at data@kobic.kr.

Q: How do I link an EXPERIMENT to a different SAMPLE?

A: Only KoNA staff can correct the metadata after an accession ID is issued. Please contact KoNA staff for assistance at data@kobic.kr.

Q: How do I link a RUN to a different EXPERIMENT?

A: Only KoNA staff can correct the metadata after an accession ID is issued. Please contact KoNA staff for assistance at data@kobic.kr.