Korean Nucleotide Archive (KoNA)

사 용 매 뉴 얼

I INTRODUCTION

1-1. About KoNA

Korean Nucleotide Archive(KoNA)는 차세대유전체기술(NGS, Next Generation Sequencing) 기반으로 생산된 대용량(high-throughput) 유전체 서열(read)의 저장 및 공유를 목적으로 국가생명연구자원정보센터(KOBIC, Korea Bioinformation Center)에서 개발하여 운영하는 데이터 저장소(repository)입니다.

KoNA의 게놈 데이터의 표준 형식은 Nucleotide Sequence collaboration (INSDC)에 의해 규정된 형식을 따릅니다. 따라서, KoNA에 등록된 데이터는 National Center for Biotechnology Information(NCBI)의 Sequence Read Archive(SRA) 및 European Bioinformatics Institute(EBI)의 European Nucleotide Archive (ENA)의 데이터와 호환됩니다.

또한, KoNA에 저장된 모든 데이터는 큐레이션되고 품질 관리됩니다. 그런 다음, 이 모든 검증된 데이터가 연구원들에게 공개됩니다. KoNA에서 제공하는 모든 공개 데이터는 인체에서 생성된 데이터를 제외하고 제한 없이 사용할 수 있습니다.

2020년 9월 보건복지부 개인정보보호위원회가 마련한 '생명윤리 및 안전에 관한 법률 시행규칙(생명윤리법)'과 '국내 보건의료데이터 활용지침'에 따라 인체소재의 게놈 데이터를 공유·활용해야 합니다. 본 법률 및 지침에 따라 모든 데이터를 수집하고 공유할 수 있습니다. 향후, KoNA는 최첨단 single-cell 기술과 같은 여러 게놈 플랫폼에서 생성된 모든 데이터의 저장, 관리 및 공유를 위해 확장해 나갈 것입니다.

1-2. Structure of KoNA

◎ KoNA data format

KoNA 는 INSDC 의 데이터 형식 및 구조 모델을 기반으로 구축되었습니다. 주요 국가와 유사한 genome 데이터 저장 서비스를 국내 및 전 세계 연구자에게 제공합니다. 미국 SRA, 유럽 ENA 등 INSDC 데이터베이스에 데이터를 제출했거나 검색 서비스를 이용한 경험이 있는 연구자는 KoNA 의 데이터 구조를 빠르게 이해할 수 있습니다

KoNA 에 저장된 게놈 데이터는 주로 raw 데이터와 메타데이터로 나뉩니다. raw 데이터는 FASTQ 파일을 포함한 시퀀싱 장치를 통해 생성된 genome read 입니다. 메타데이터는 raw 데이터를 설명하는 정보이며 주로 프로젝트, 샘플, 실험 및 Run 으로 구성됩니다. 이 형식은 INSDC 데이터베이스의 형식과 동일합니다.

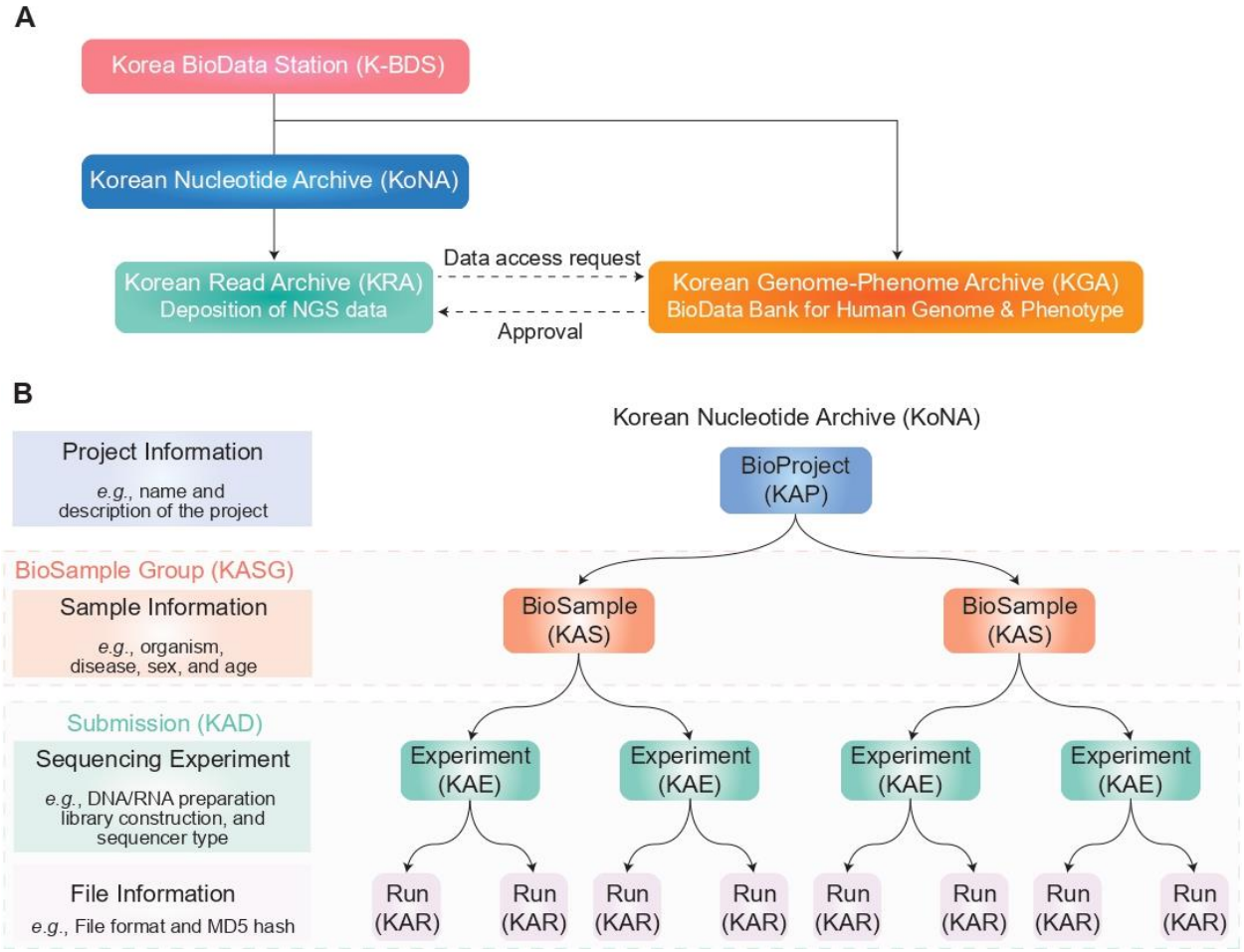
◎ Metadata format

메타데이터는 주로 관련된 프로젝트, 샘플, 실험 및 Run 으로 구성됩니다. 즉, raw 데이터를 제출하려면 프로젝트-표본-실험-Run 정보가 존재하고 서로 연결되어야 합니다. 프로젝트 정보는 프로젝트에 대한 설명과 genome 생성을 위한 연구 정보를 포함한 바이오 프로젝트 데이터베이스로 구현됩니다. BioProject 에는 제출자, 날짜, 프로젝트 설계 및 발행과 같은 정보가 포함됩니다. 바이오 프로젝트는 독립적으로 운용되며 다른 데이터와 연결되지 않지만 포괄적인 프로젝트와 연결될 수 있습니다. 또한 대규모 프로젝트 또는 컨소시엄(예: 한국 포스트 게놈 프로젝트)에 포함될 수 있는 바이오 프로젝트가 있는 경우, 바이오 프로젝트에는 그들의 포괄적인 프로젝트에 대한 정보가 포함됩니다. 바이오 프로젝트 가입 ID 는 "KAP"로 시작합니다

샘플 정보는 BioSample 데이터베이스로 구현되며, 데이터 생성에 사용되는 생물학적 소스 재료 또는 샘플에 대한 정보를 포함합니다. BioSample 은 BioProject 와 구조적으로 연결되어야 합니다. 따라서 BioSample 에 샘플 정보를 제출하기 전에 BioProject 에서 프로젝트 정보를 제출하고 KoNA 관리자의 승인을 받아야 합니다(즉, BioSample 을 제출하려면 '상위' BioProject 가입 ID 가 필요함). 동일한 유형의 여러 바이오 검체(예: 여러 폐암 환자의 검체)를 제출하려면 바이오 검체 그룹이 필요합니다. 제출자는 스프레드시트를 사용하여 바이오샘플에 대한 정보를 설명할 수 있습니다. 스프레드시트의 각 행은 각 바이오샘플을 나타내며 스프레드시트 자체는 바이오샘플 그룹을 나타냅니다. BioSample Group 의 등록 ID 는 "KASG"로 시작하며, 각 BioSample 의 등록 ID 는 "KAS"로 시작합니다

각 실험은 특정 샘플에 대한 고유한 시퀀싱 라이브러리를 나타내며, 실험 및 Run 은 KAD(Korea Read Archive)로 그룹화됩니다.

▶ 4 가지유형의 메타데이터 객체



< BioProject, BioSample 및 KAR 의 관계 >

BioProject, BioSample Group 및 KAD 데이터는 위와 같이 연결되어 있습니다. BioProject 의 메타데이터 개체에는 umbrella 프로젝트를 제외한 다른 데이터와의 연결 정보가 포함되어 있지 않습니다. 따라서 바이오 프로젝트는 독립적입니다. 바이오샘플 데이터에는 바이오프로젝트와의 연결 정보가 있어야 하며 샘플이 생성된 프로젝트 정보를 얻을 수 있습니다. KAD 에는 연결된 바이오샘플 그룹에 대한 정보가 있어야 합니다. 이와 같이 BioProject, BioSample Group, KAD 는 서로 연계되어 있습니다.

1-3. How to cite

귀하의 논문에서 바이오 프로젝트, 바이오 샘플 그룹 또는 KAD 제출을 인용하려면:
"본 출판물에서 논의된 raw 염기서열 데이터는 KAP20xxxxx 의 등록 번호로 KoNA(Korean Nucleotide Archive)에 보관되었습니다." 제출자는 KAP20xxxx(바이오 프로젝트) 대신 KASG20xxxx(바이오 샘플 그룹) 또는 KAD20xxxx(KAD 제출)를 사용할 수도 있습니다."
KoNA 데이터베이스 인용하기:
"우리는 이제 peer reviewed journal 에 대한 기사를 준비합니다. 출판 절차가 완료될 때까지 URL 주소(https://kobic.re.kr/kona) 를 인용해 주시기 바랍니다.

◎ KoNA 구조

KoNA 의 모든 표준 및 구조가 INSDC 표준을 따르므로 KoNA 가 발행하는 등록 ID 시스템은 INSDC 에서 일반적으로 사용되는 형식을 따릅니다. 앞서 설명한 바와 같이, KoNA 의 모든 메타데이터는 다음과 같은 네 가지 객체로 구성됩니다: 바이오 프로젝트, 바이오 샘플, 실험 및 Run. 바이오샘플 그룹과 KAD 는 각각 여러 바이오샘플과 실험 및 Run 을 그룹화하는 데 사용됩니다. 각 개체에는 고유한 등록 ID 가 있습니다. 모든 등록 ID 는 대문자와 숫자로 구성됩니다. 문자는 객체를 나타내고 숫자는 승인 연도와 순서를 나타냅니다. 국가를 나타내는 문자의 경우 "K"가 포함되어 Korea 을 나타냅니다(다른 국가의 경우 "S", "E", "D" 및 "C"는 각각 U.S.A., Europe, Japan, China 를 나타냅니다).
먼저, 바이오 프로젝트의 가입 ID 는 "KAP"로 시작하고 그 뒤에 숫자가 나옵니다. "KA"는 Korean Archive 를 의미하고 "P"는 프로젝트를 의미합니다. umbrella 프로젝트의 가입 ID 는 "KAU"로 시작하며 "U"는 umbrella 를 나타냅니다.
BioSample 의 등록 ID 는 "KAS"로 시작하고 그 뒤에 숫자가 나옵니다. "S"는 Sample, "KA"는 Korean Archive 를 나타냅니다. 동일한 유형의 여러 샘플 그룹의 경우, 등록 ID 는 "KASG"로 시작하고 "G"는 그룹을 나타냅니다.
Experiment 및 Run 의 등록 ID 는 각각 "KAE" 및 "KAR"로 시작합니다. 첫 글자 "K"는 Korea 를 나타냅니다.

Object Name	KoNA Accession
Umbrella Project	KAU + 6 digits of number
BioProject	KAP+ 6 digits of number
BioSample Group	KASG + 6 digits of number
BioSample	KAS + 8 digits of number
KAD	KAD + 7 digits of number
Experiment	KAE + 8 digits of number
Run	KAR + 8 digits of number

1-4. Contact Us

데이터 작성/등록 문의 시 작성 중 또는 제출한 데이터의 임시 ID나 문제의 페이지를 캡쳐하여 보내주시면 더 빠르고 정확한 답변을 받을 수 있음

◎ EMAIL 문의

▶data@kobic.kr

◎ 유선 및 팩스 문의

▶ Tel : +82-42-879-8549

▶ Fax : +82-42-879-8519

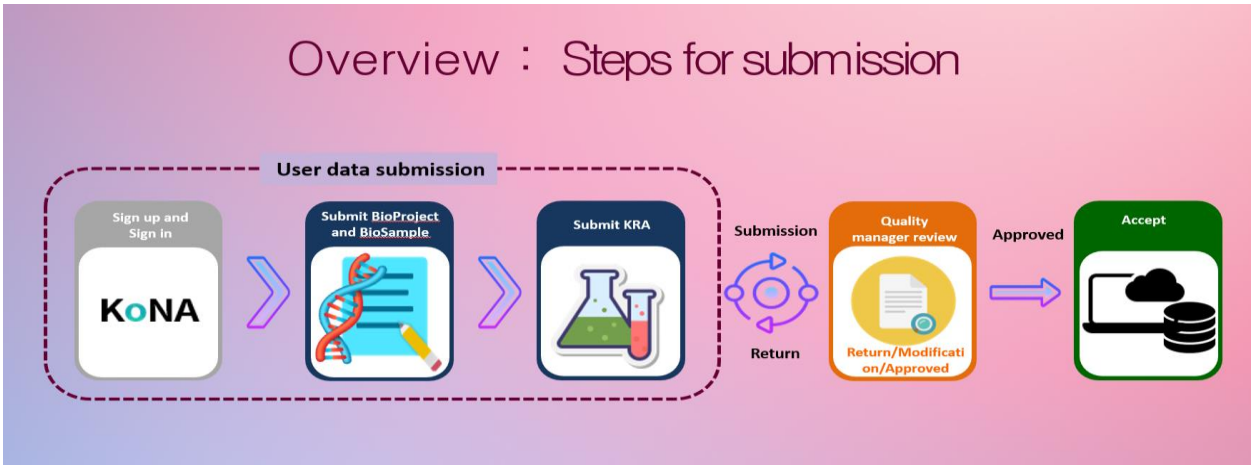
◎ 주소

▶ Address : Korean Bioinformation Center (KOBIC), Korea Research Institute of Bioscience & Biotechnology (KRIBB), Daejeon 34141, Republic of Korea

II DATA SUBMITTION

2-1. Submission overview

◎ 데이터 등록 절차



① 계정 생성 및 로그인

▶ KoNA에 기존 계정이 없는 경우 계정 생성 필수

▶ 데이터 작성 전 로그인 필수

② 데이터 작성 단계

▶ 기본 연구 과제 정보(BioProject)와 샘플(BioSample) 작성*

* 항목에 대해서 빠짐없이 모두 입력해야 제출 가능

▶ 실데이터(raw data) 업로드 및 메타데이터 작성

▶ 필요시 (제출 전) 데이터 추가, 수정, 삭제 가능*

* 제출 완료 이후 관리자 요청을 통한 수정 가능

③ 데이터 검토 단계

▶ 제출된 데이터에 대해 품질관리자가 검토

▶ 검토 반려 시 제출자가 데이터 추가/수정하여 재제출

④ 데이터 등록단계

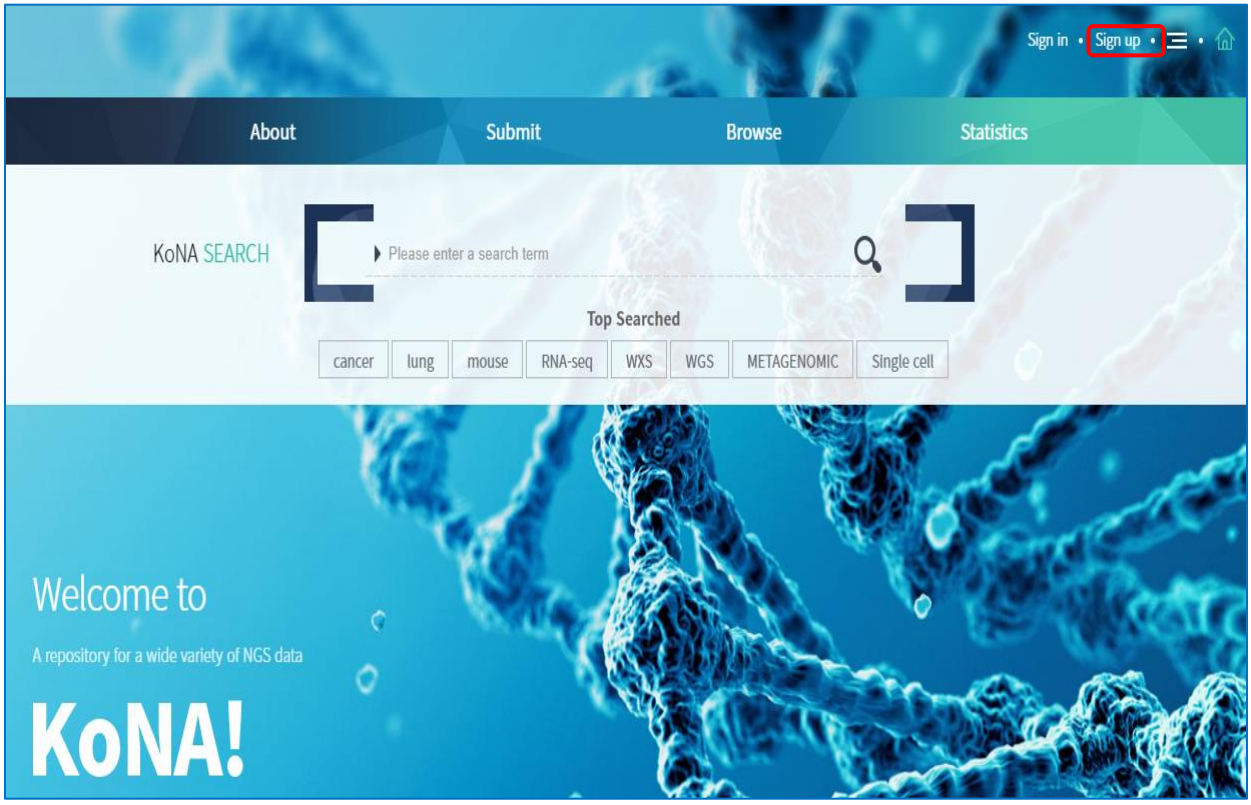
▶ 검수 완료된 데이터에 대해 등록 완료 및 공개

2-2. Create account

◎ 회원가입 및 로그인

▶ 회원가입은 [개인정보입력 》 가입완료] 절차 순으로 진행

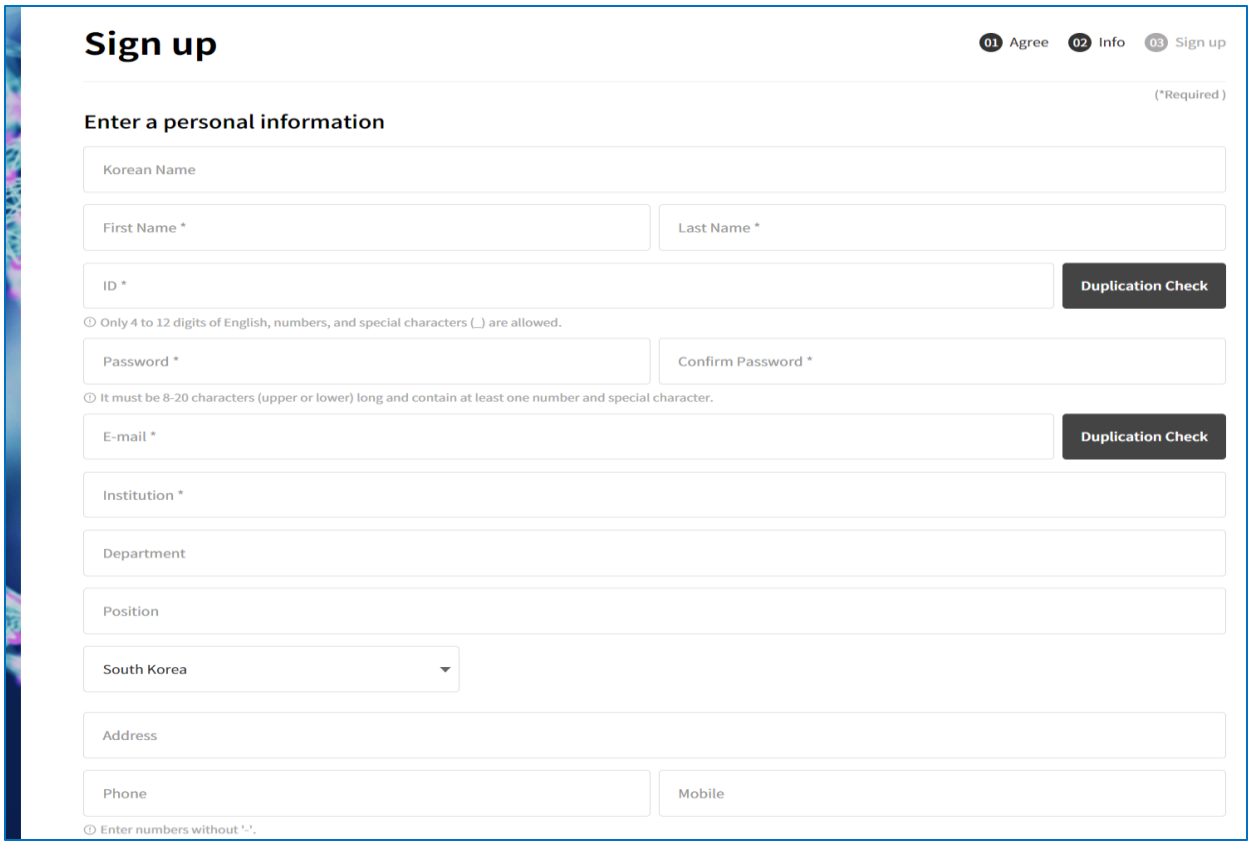
① 메인페이지 우측 상단에서 [Sign up]을 클릭하여 페이지 이동

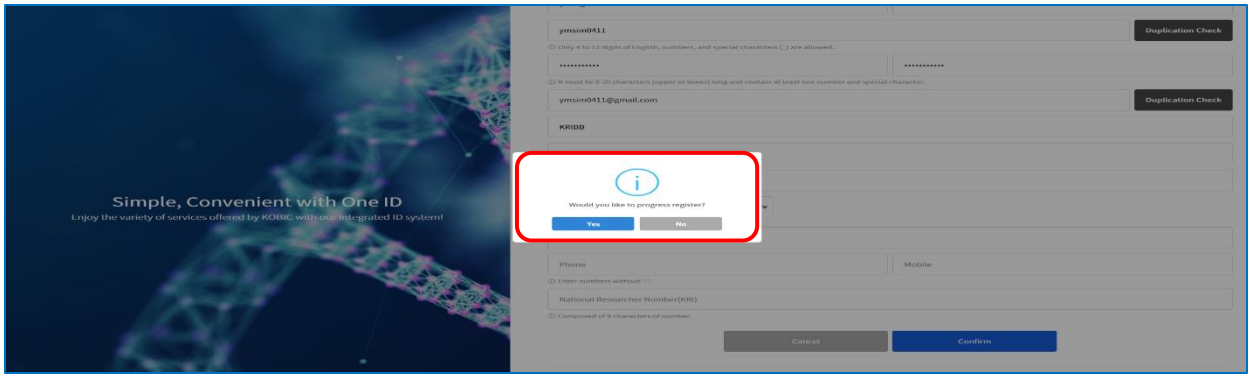


② “회원유형 선택”에서 [내국인] 또는 [외국인] 선택

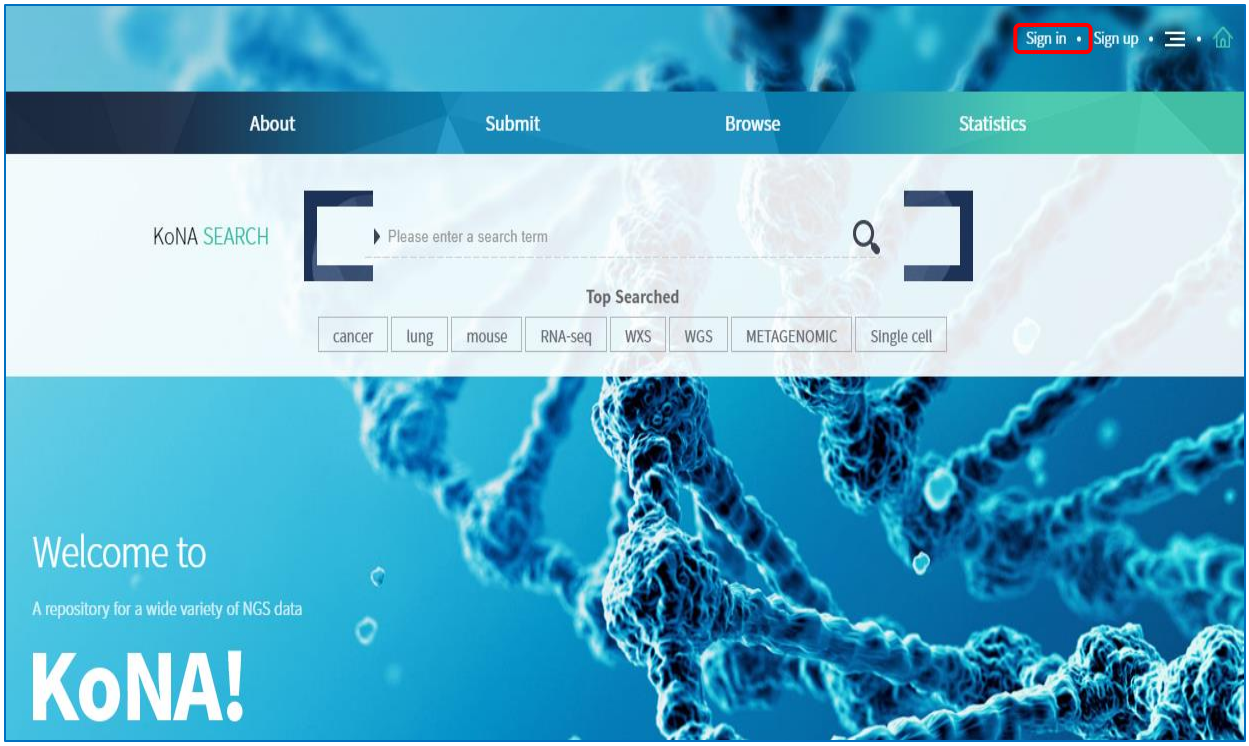
③ 회원정보를 빠짐없이 입력 후 [Confirm]를 클릭 하여 제출한다.

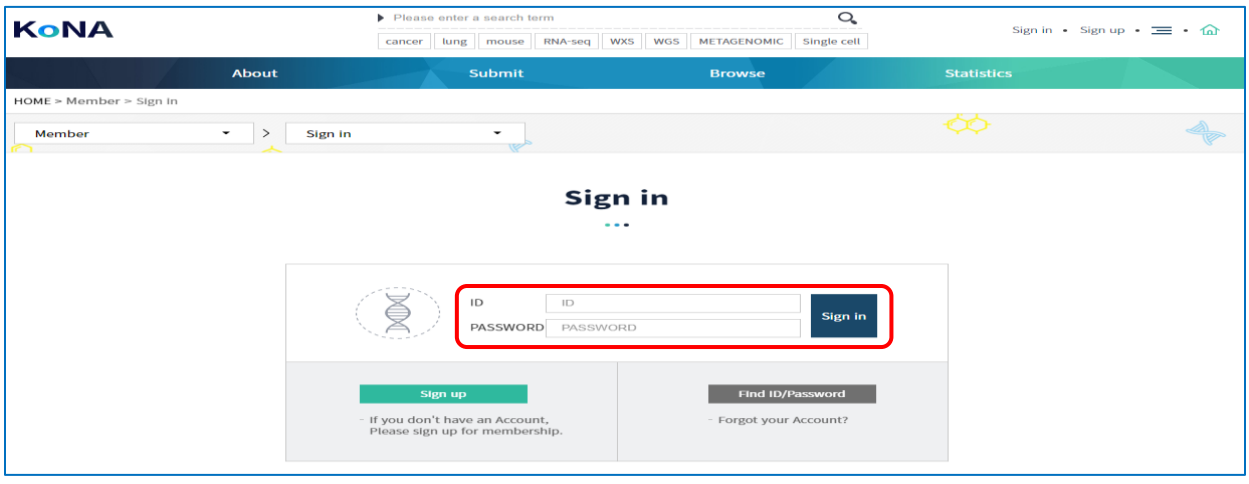
*회원가입에 문제가 발생 했을 경우 , kbds.help@kobic.kr로 문의





④ 계정 생성 후 우측 상단의 [Sign in]을 클릭하여 로그인





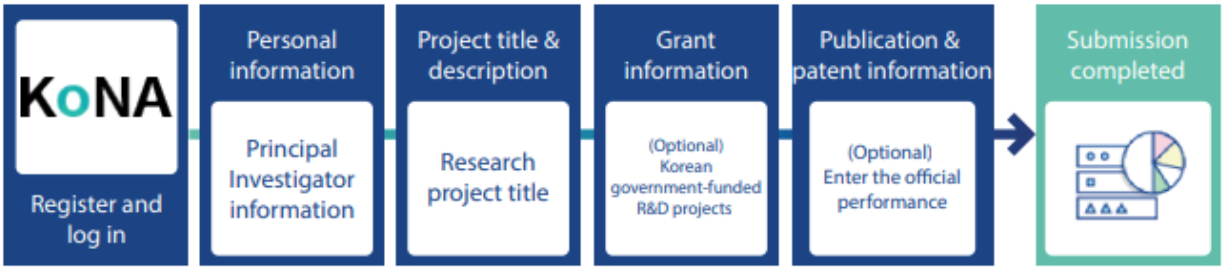
2-3. Submit study information (BioProject)

◎ 기본 연구 정보 작성 및 등록

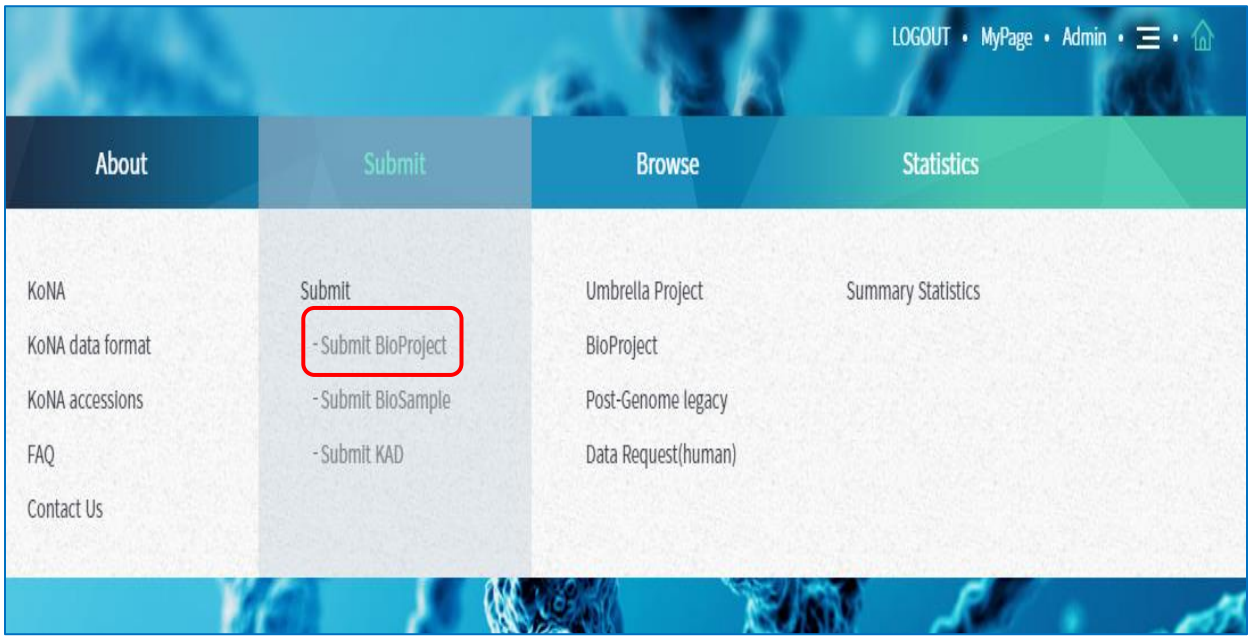
기본 연구 정보 작성 및 등록 기본 연구 정보 등록을 위해 BioProject를 작성 및 제출

- **BioProject**
  - ▶ 연구 프로젝트에 대한 개괄적인 정보를 작성
  - ▶ KoNA내 등록되는 모든 데이터 타입에 대해 필수적으로 작성되어야 함
  - ▶ 제출자의 정보, 과제정보, 연구성과 등의 정보를 작성
  - ▶ 제출된 BioProject는 관리자 검토를 통해 승인 후 등록 완료

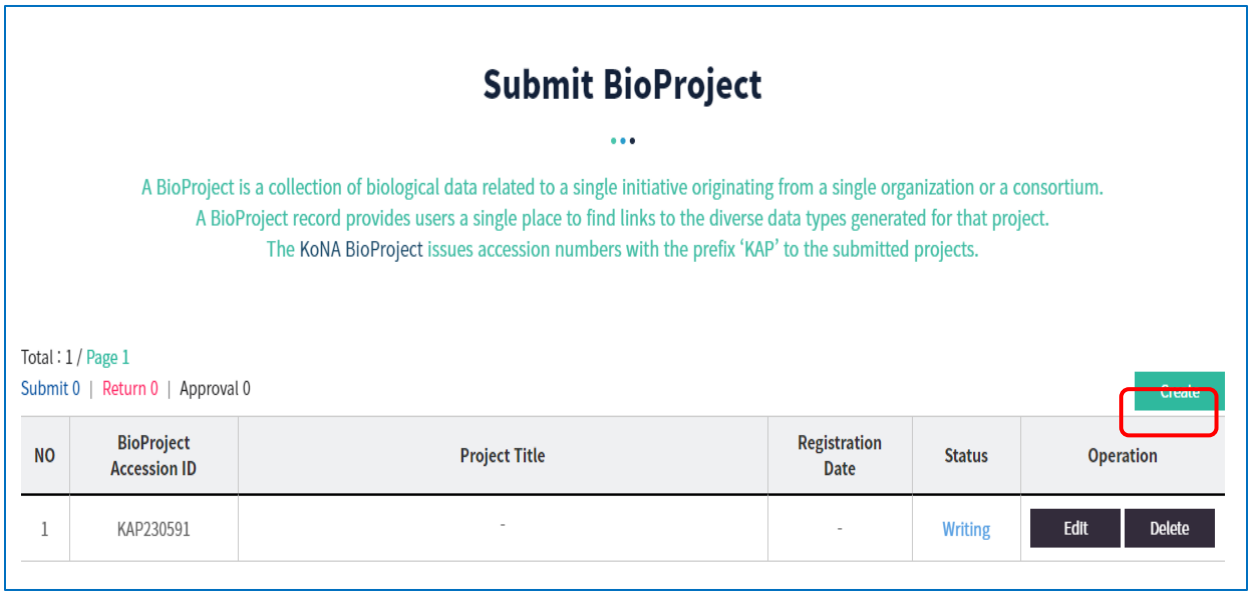
• BioProject 작성단계



1. 데이터 등록을 위하여 KoNA 메인페이지(https://www.kobic.re.kr/kona/) 상단 메뉴의 [Submit 》 Submit BioProject] 페이지로 이동



2. Create 메뉴를 눌러 새로운 BioProject 페이지를 활성화 한다.

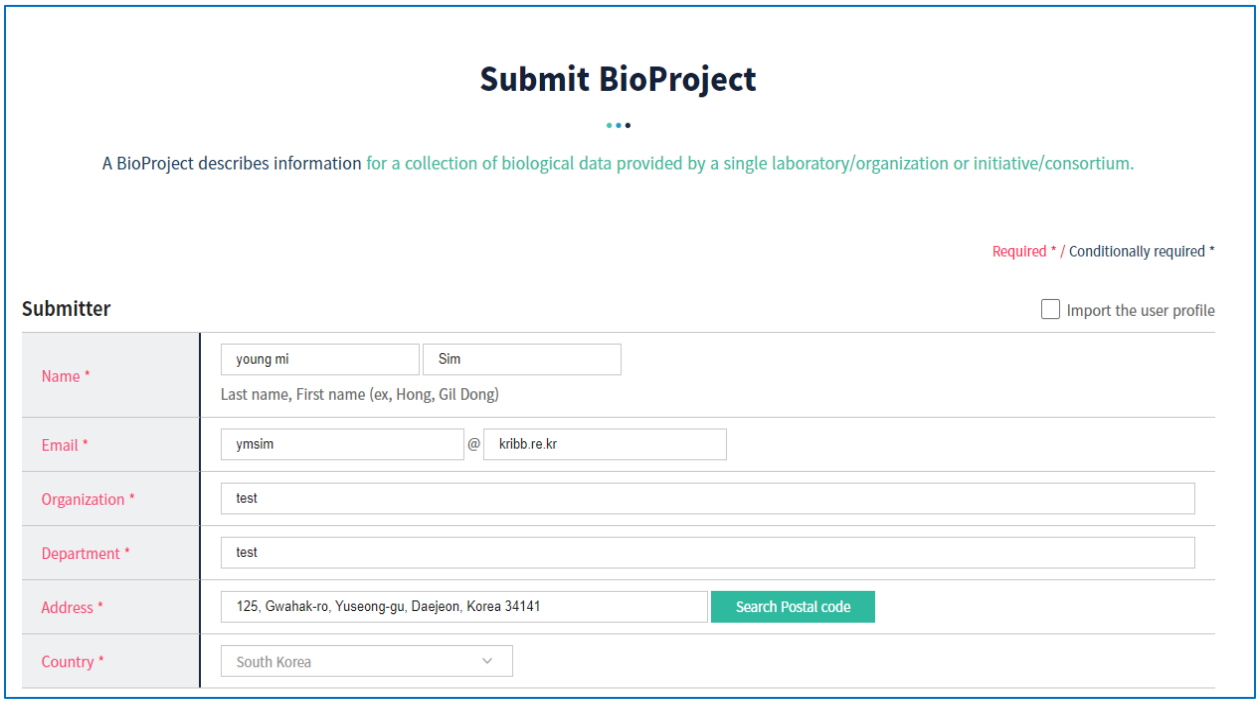


3. 등록자의 인적사항

① 등록자 인적사항을 빠짐없이 입력

* BioProject 등록 시 PI (Principal Investigator; 연구책임자) 인적사항 기입을 권장

② 등록자 인적사항은 회원가입 시의 정보가 자동 입력되며, 등록자 인적사항에 변동이 있는 경우, 웹페이지 내에서 수정 가능



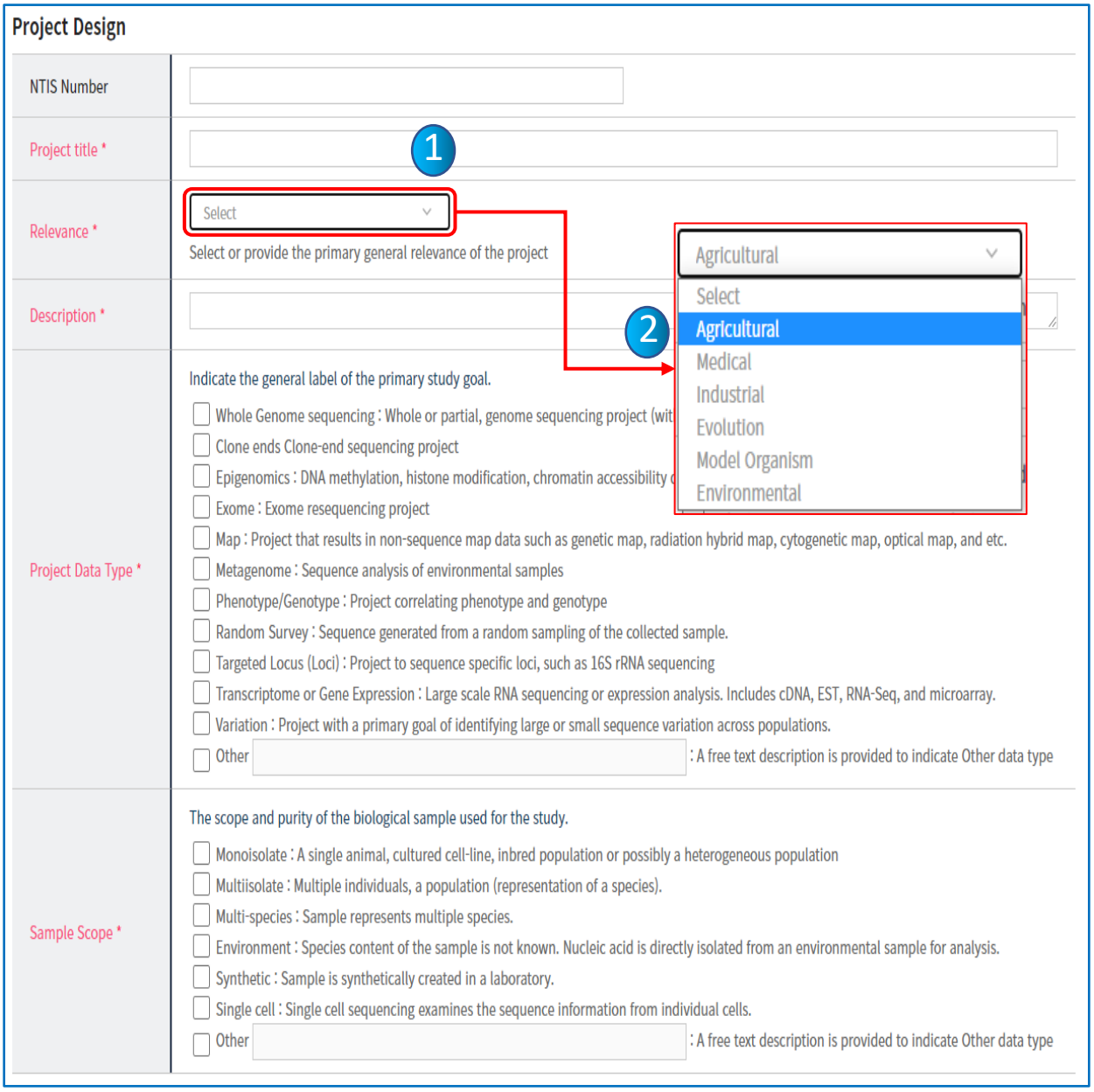
4. 연구 과제 정보 기입 및 프로젝트의 제목 및 설명

① NTIS 과제 정보 입력 (해당 사항 없으면 공란 처리)

② 프로젝트의 영문 제목 : 연구 과제 정보의 '주요 연구과제의 제목'이 아닌 등록자가 BioProject에 포함할 시료/기기 정보와 실험 데이터의 특성을 고려한 연구 프로젝트의 제목을 명명하여 입력

③ 프로젝트의 영문 설명 : 프로젝트에 대한 상세 설명을 영문으로 입력

④ Propject Data type 및 sample Scope 입력



5. Umbrella Project 정보[선택사항]

① 연구 과제 정보는 오른쪽 상단의 [Search]을 클릭하여 검색조건으로 해당과제를 찾아 선택하면 자동으로 입력됨

6. 논문 및 성과 정보[선택사항]

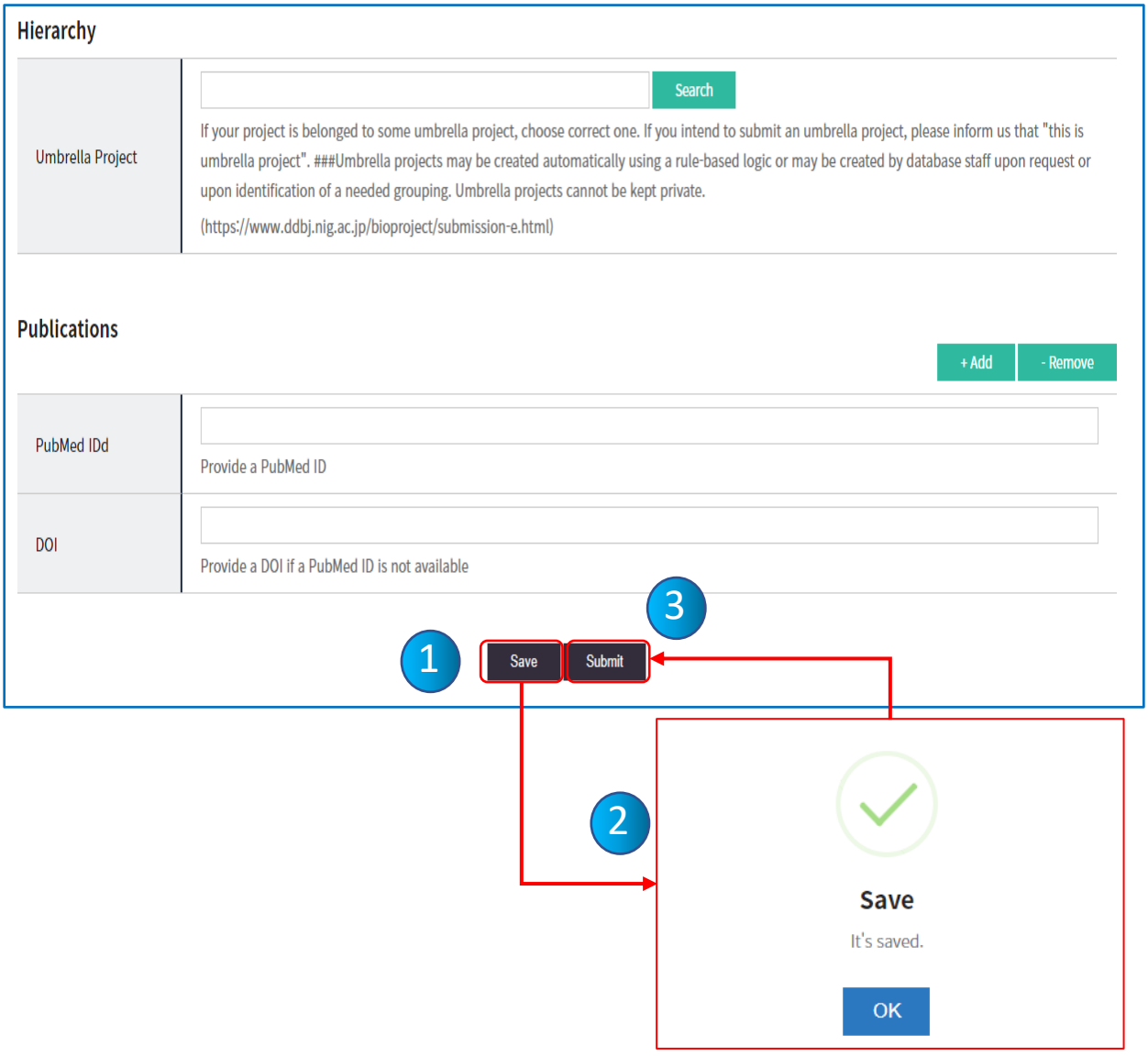
① 논문의 PubMed ID: 해당 프로젝트의 수행 결과로 산출된 논문의 PubMed ID 입력

② 논문의 DOI: 논문의 PubMed ID가 없을 경우 DOI (Digital Object Identifier) 입력

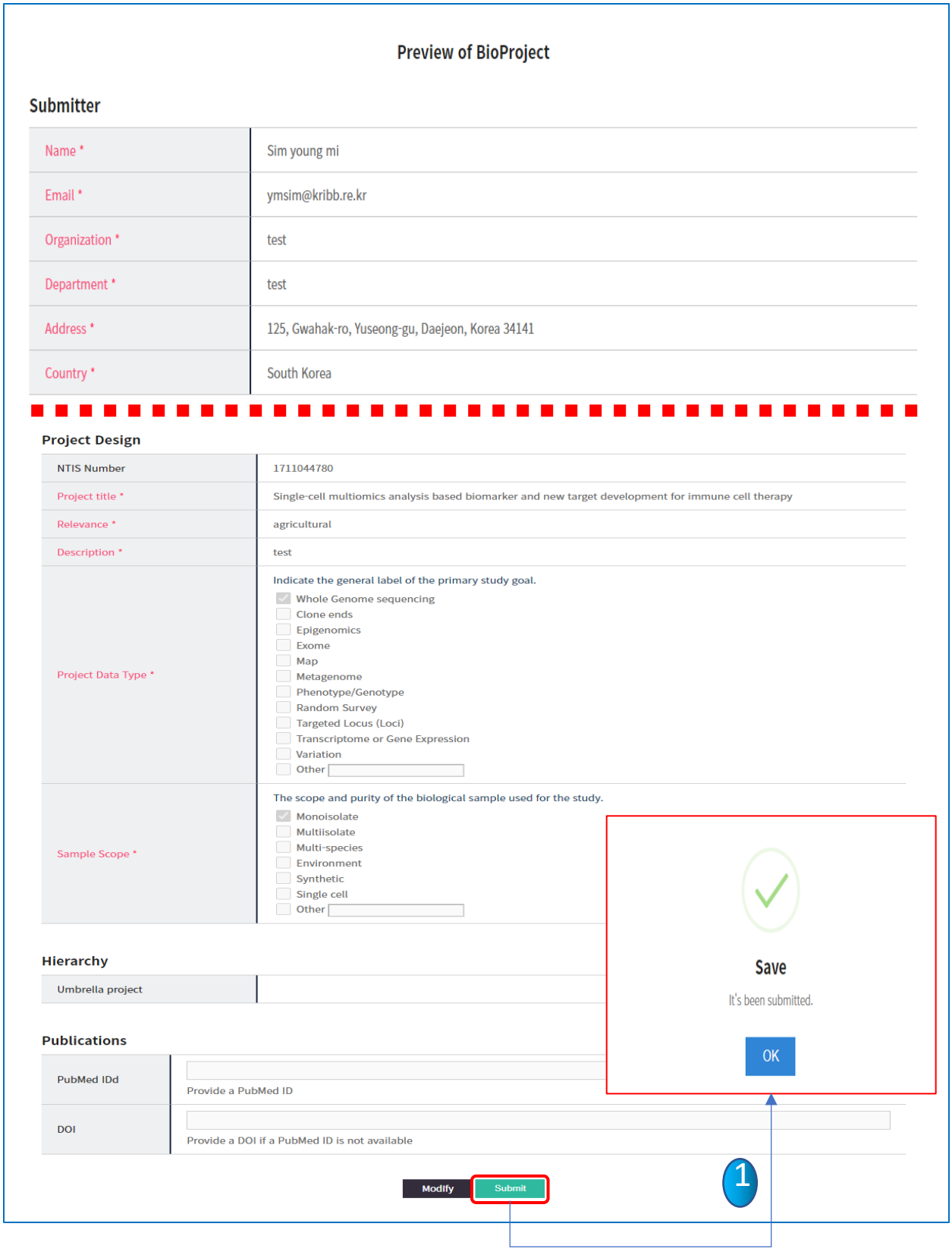
7. BioProject 제출

① 해당 항목을 모두 기입 후 [Save] 버튼을 선택

② 데이터가 저장되었다는 [알림] 팝업창 확인

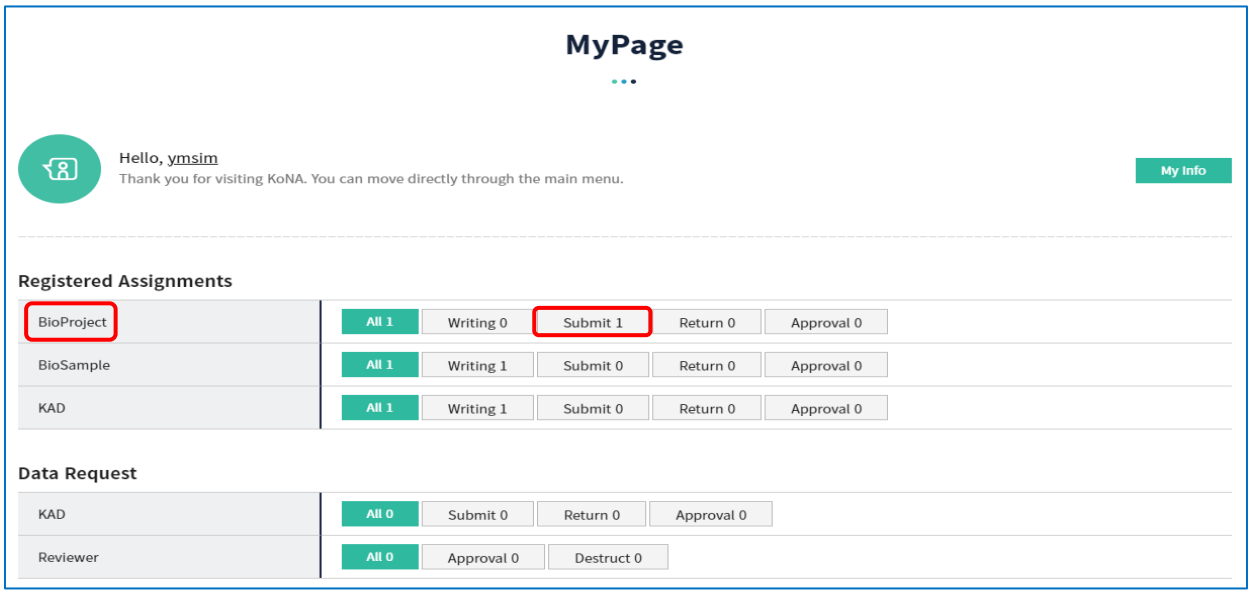


③ [Submit] 버튼을 클릭하여 BioProject 제출 완료



④ 제출된 BioProject는 MyPage에서 확인 가능

* BioProject의 승인 진행 사항을 확인 할 수 있음

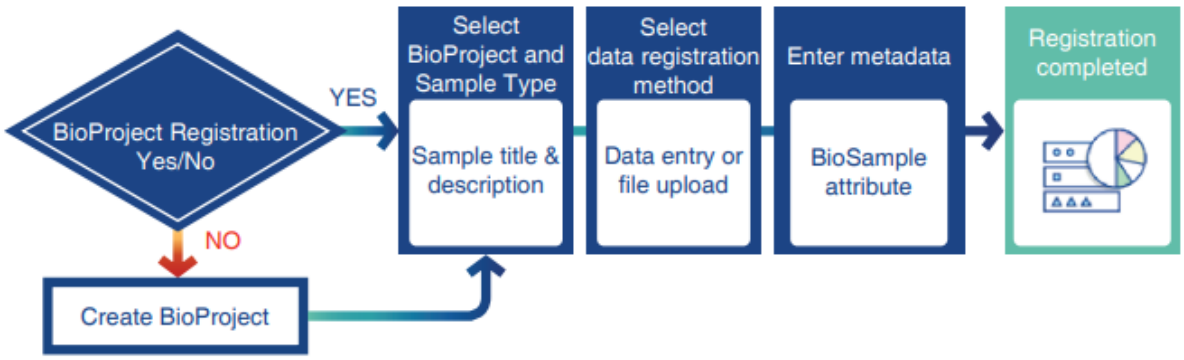


2-4. Submit sample information (BioSample)

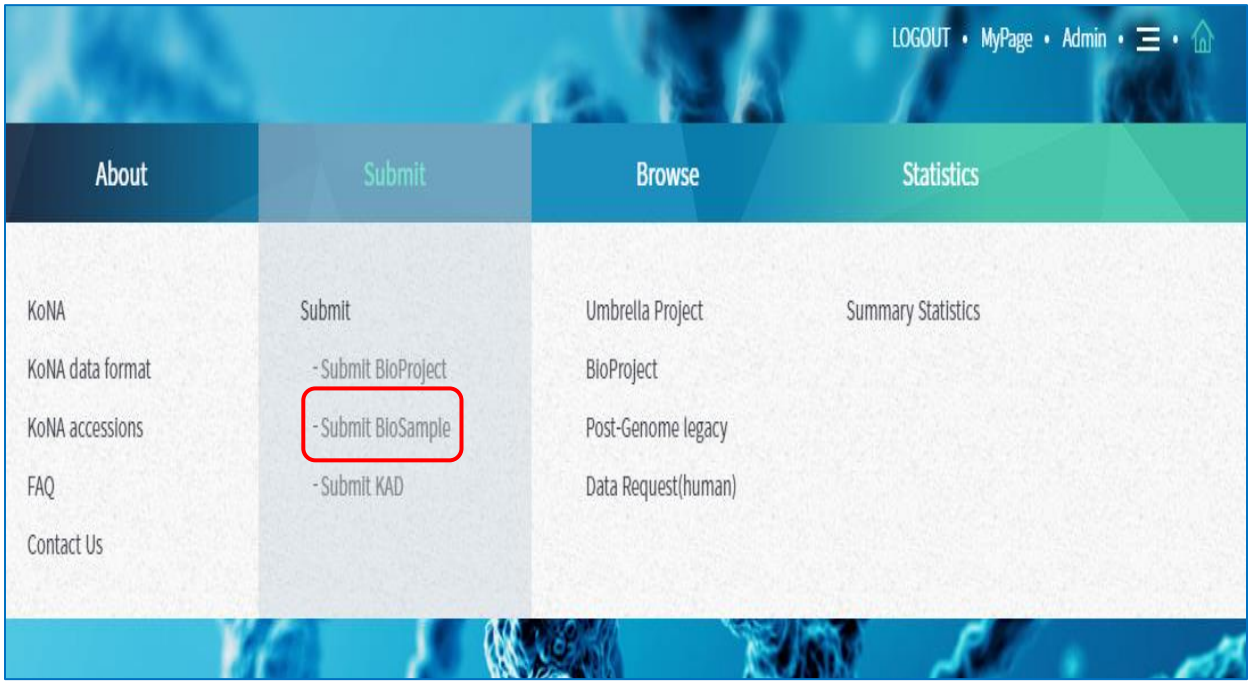
◎ 기본 샘플 정보 (BioSample)

생물 유래 샘플 대상으로 실험하여 얻은 실험 데이터를 등록하기 전에 필수 등록해야 하는 정보로서 그 샘플에 대한 개괄적인 정보를 등록하기 위해 사용, 샘플 (BioSample) 정보 작성 및 제출

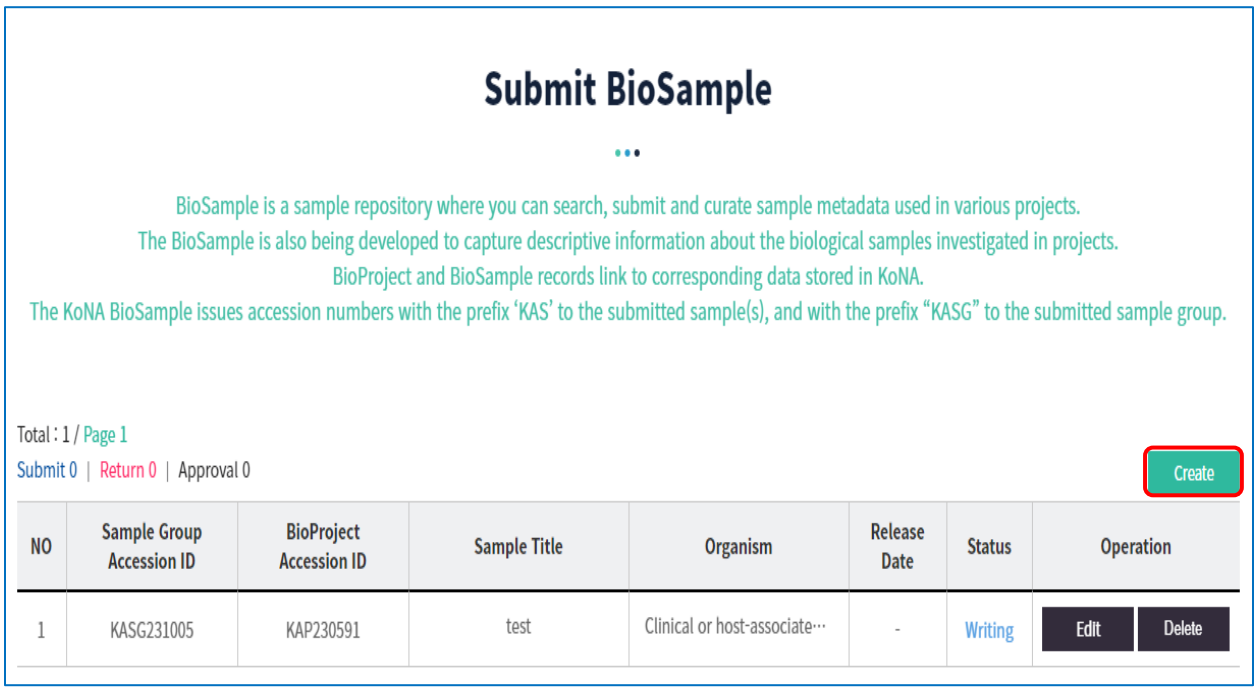
• BioSample 작성단계



1. 데이터 등록을 위하여 KoNA 메인페이지(https://www.kobic.re.kr/kona/) 상단 메뉴의 [Submit 》 Submit



2. Create 메뉴를 눌러 새로운 BioSample 페이지를 활성화 한다.



3. 프로젝트 및 샘플설명 작성

※ BioProject 제출을 선행하지 않은 경우, BioProject 등록 절차에 따라 작성 및 등록 진행

① BioProject 제출 후, [Search] 버튼을 클릭하고 창이 나오면 앞서 제출 또는 등록된 BioProject 중, 샘플 등록을 위한 BioProject 를 선택

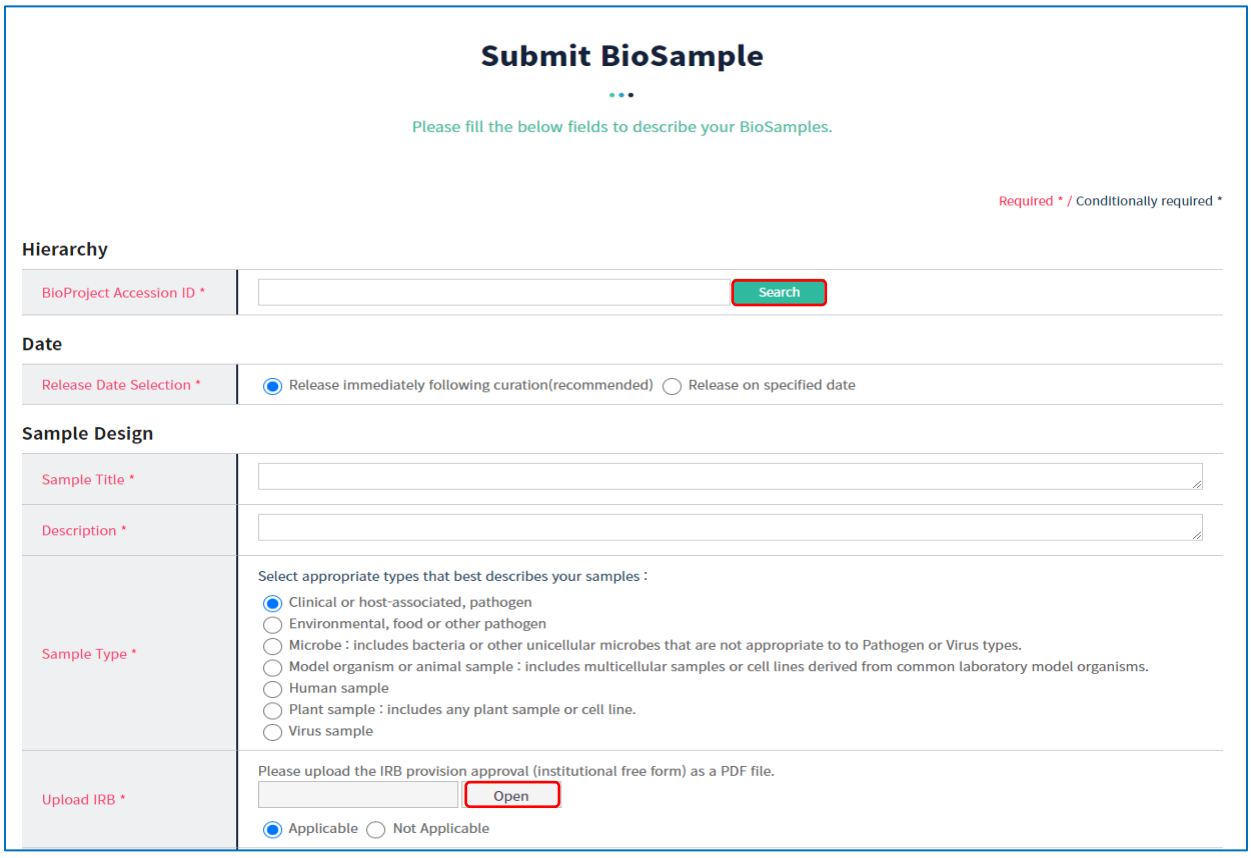
② 등록하고자 하는 샘플의 공개 날짜를 선택, 즉시 공개와 공개 일자 지정을 할 수 있음

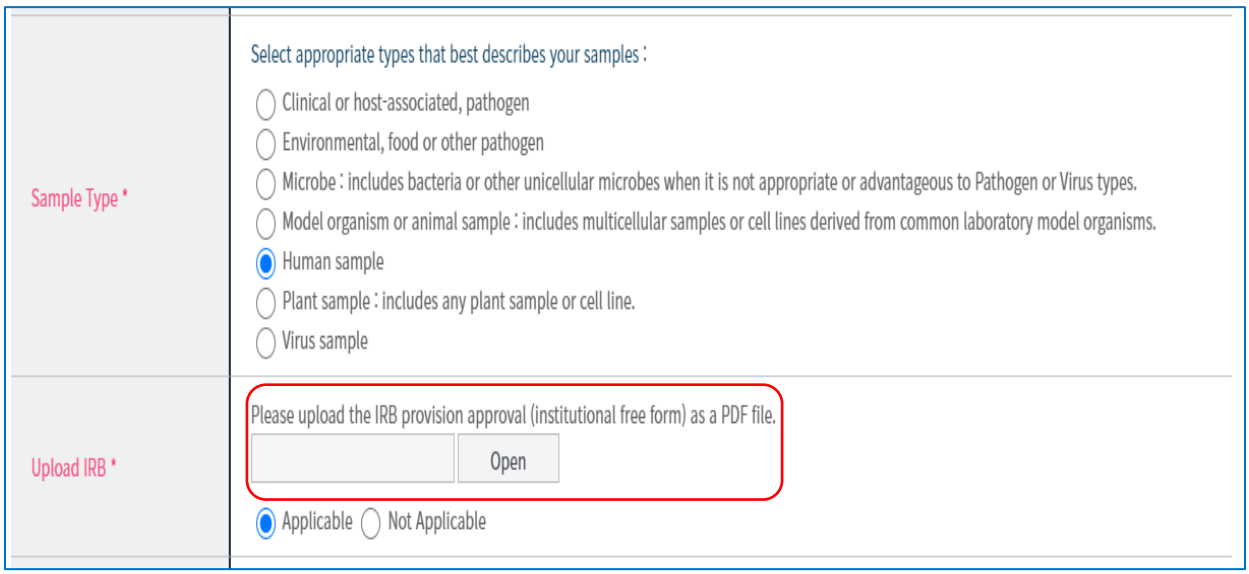
③ Sample Design에 Sample에 대한 Title과 설명을 작성

④ 등록하고자 하는 Sample typle을 선택

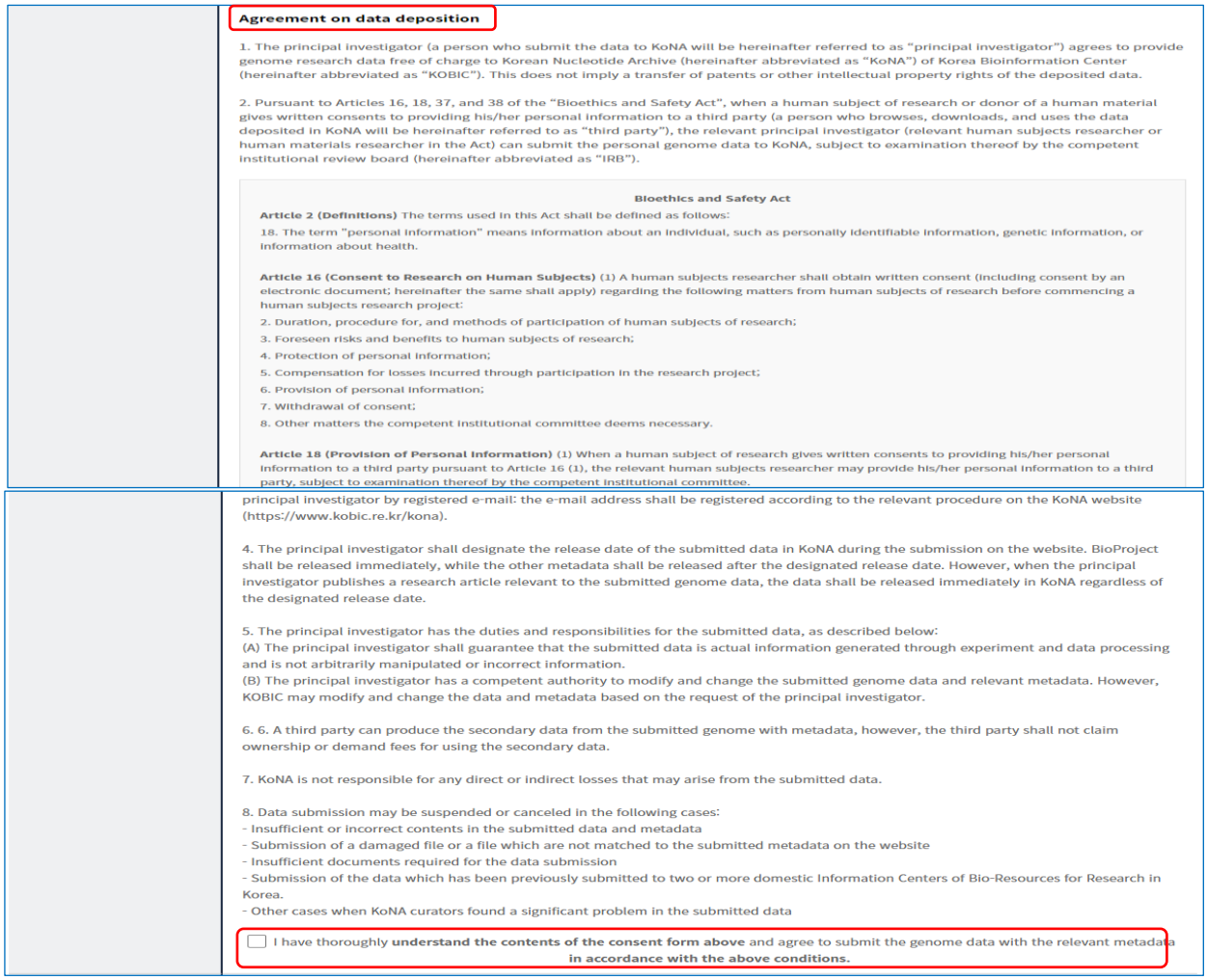
▶ Sample typle (Human Sample 일 경우 신청 한 IRB를 함께 등록 해야 함)

Type	Category
Sample type	Clinical or host-associated pathogen
	Environmental, food or other pathogen
	Microbe
	Model organism or animal sample
	Human sample
	Plant sample
	Virus sample





⑤ 샘플 등록에 대한 약관을 꼼꼼히 읽은 후 동의란에 체크



4. 데이터 등록방법

① Sample Data Input Type 의 [직접 입력] 또는 [파일 업로드] 선택

1) [직접 입력] 다음 단계인 메타데이터 입력 시 하단 Spread sheet 에 직접 입력하는 방식으로 처음 작성하는 경우나 데이터가 많지 않은 경우에 적합

2) [파일 업로드 방식] 다음 단계 메타데이터 입력 시 Spread sheet 파일 형태의 양식 파일을 다운로드하여 작성 후 업로드하는 방식으로 많은 데이터를 입력하는 경우에 적합

5. 메타데이터

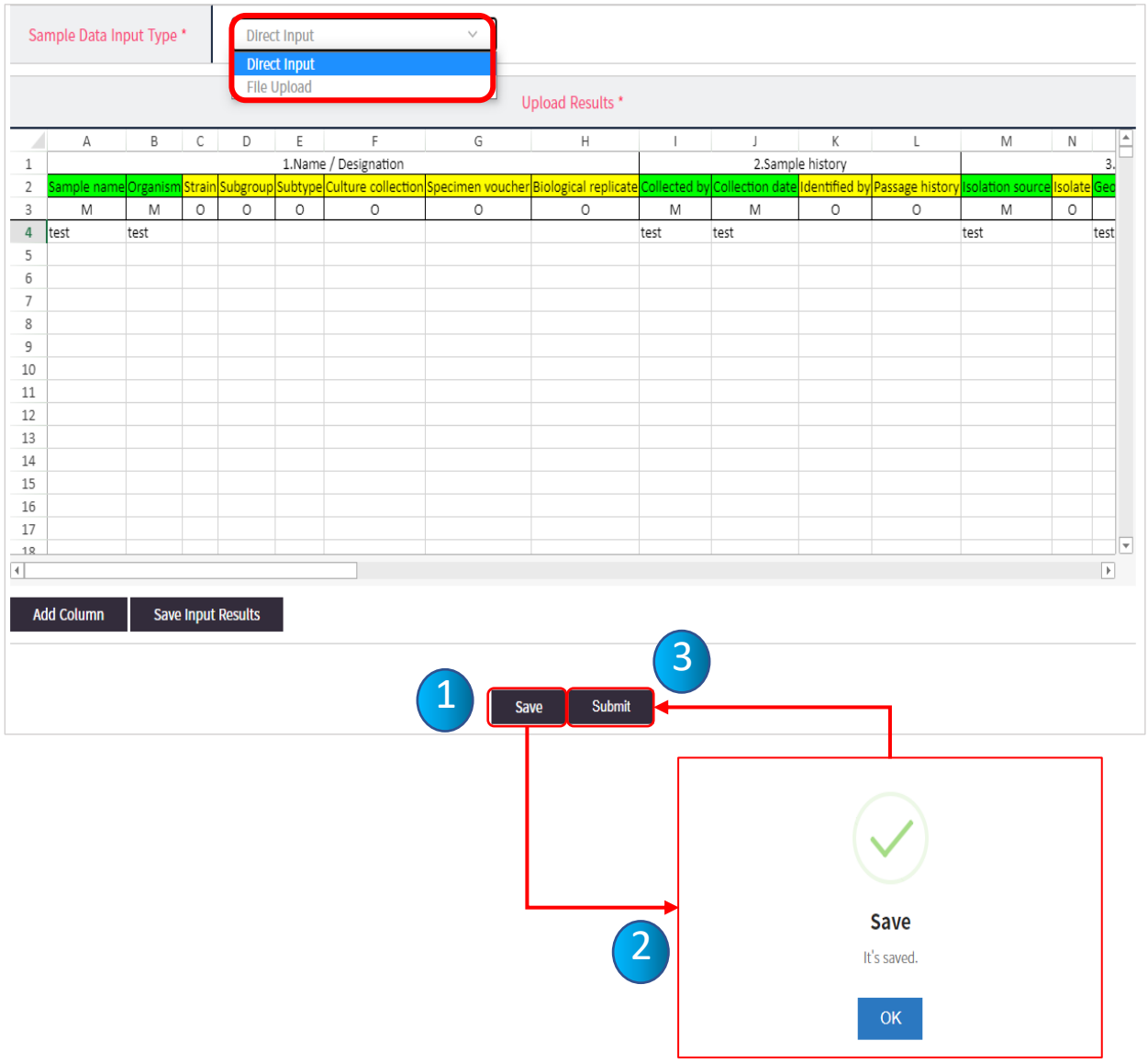
① 각 항목에 대한 설명과 예시에 따라 작성하고 *필수 항목은 반드시 작성

*M : 필수항목, O : 선택 항목

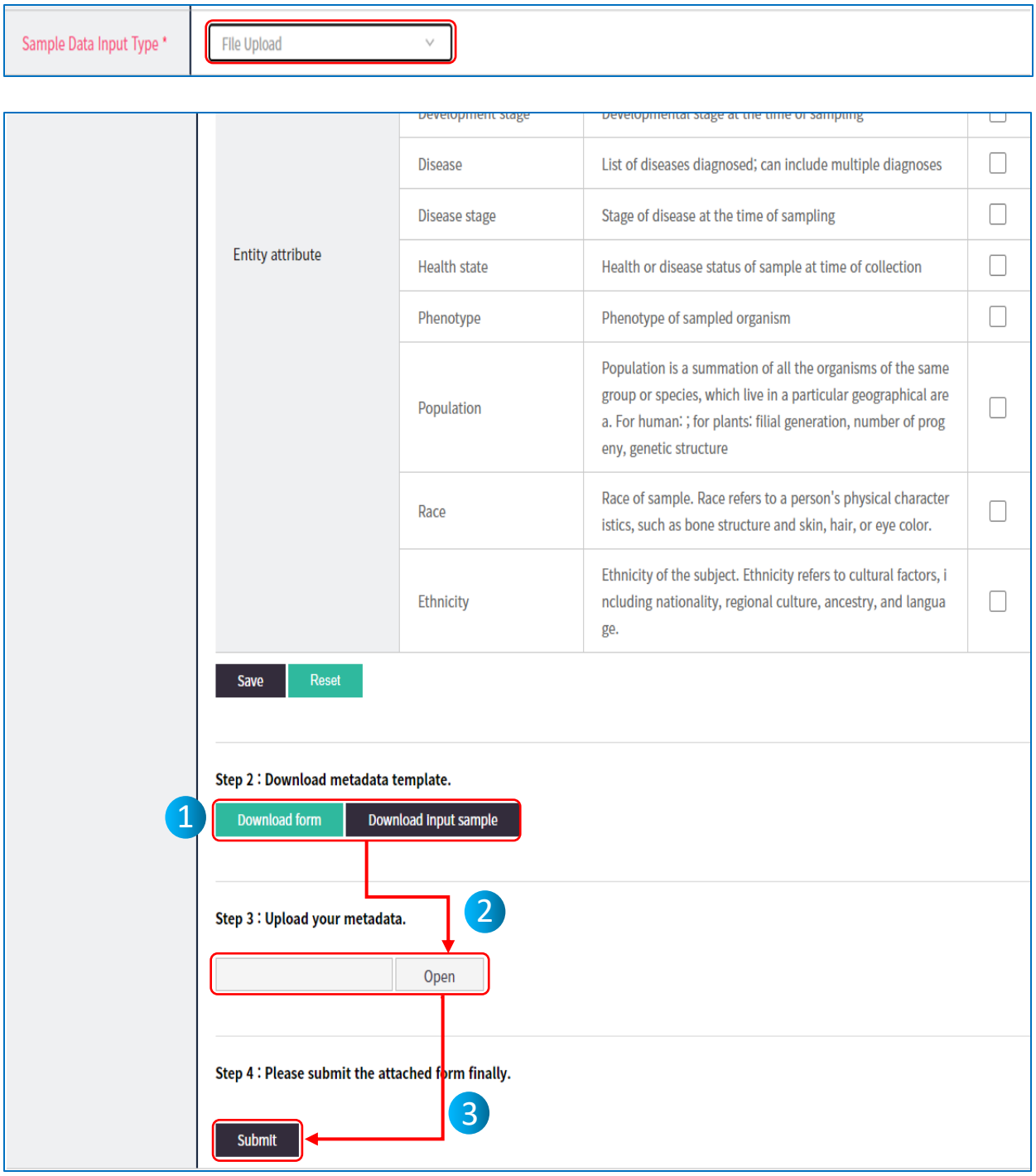
② [직접 입력]의 경우 하단 Spread sheet 에 작성해야 할 정보를 항목별로 확인 후, 빠짐없이 작성하고 아래의 [Save] 클릭하여 저장됨

③ 오른쪽의 [Submit] 버튼을 클릭하여 BioSample 제출 완료

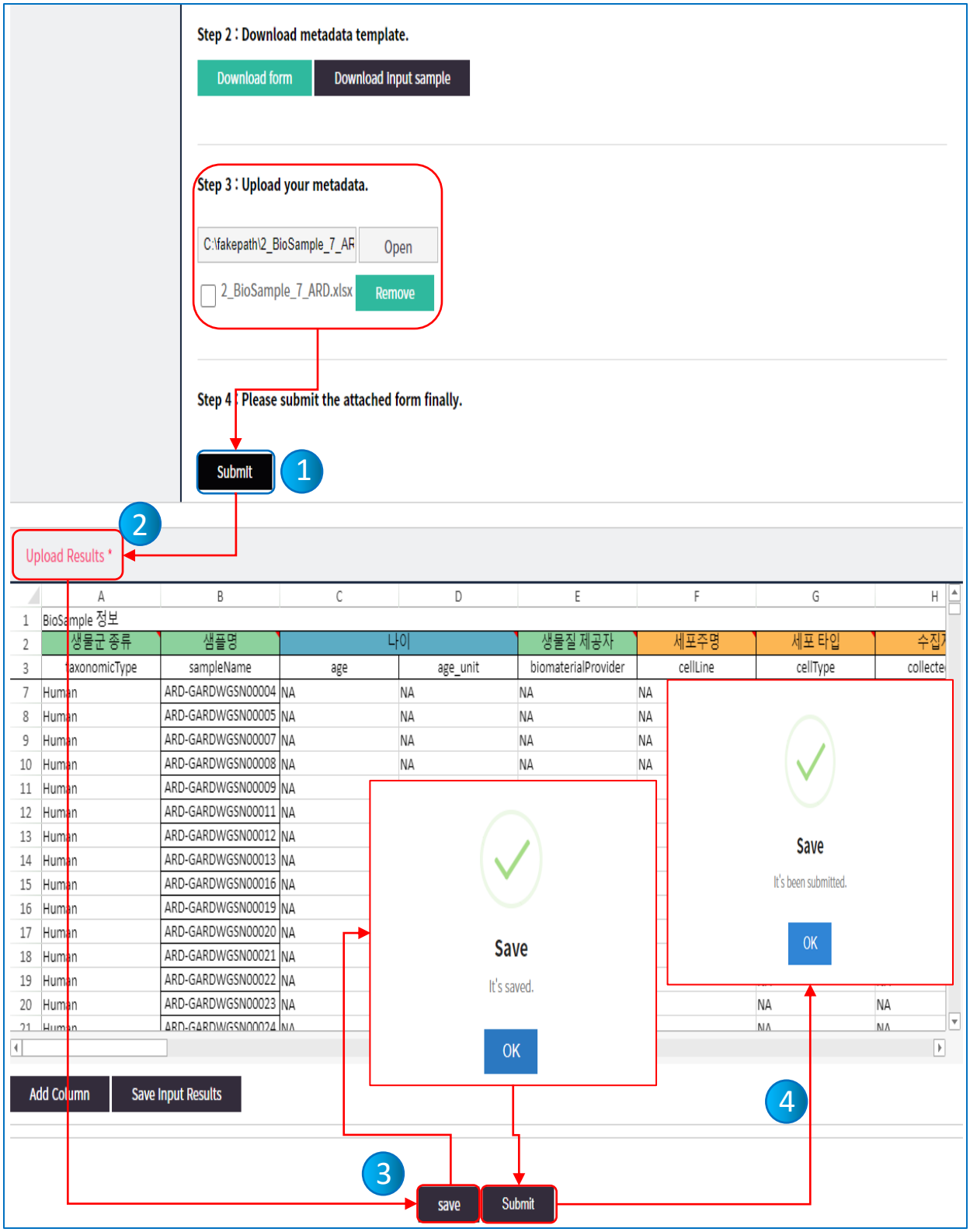
※ 제출을 진행하면 품질관리자 반려 전에는 수정 및 삭제가 불가능


Sample Data Input Type *
Direct Input
Direct Input
File Upload
Upload Results *
1.Name / Designation
2.Sample history
Sample name
Organism
Strain
Subgroup
Subtype
Culture collection
Specimen voucher
Biological replicate
Collected by
Collection date
Identified by
Passage history
Isolation source
Isolate
M
O
test
Add Column
Save Input Results
1
2
3
Save
Submit
Save
It's saved.
OK

④ [파일 업로드]의 경우 [Download form]을 클릭하여 양식을 다운받아 작성하고 [Open]을 클릭하여 작성한 양식을 업로드한 후 [Submit]을 클릭



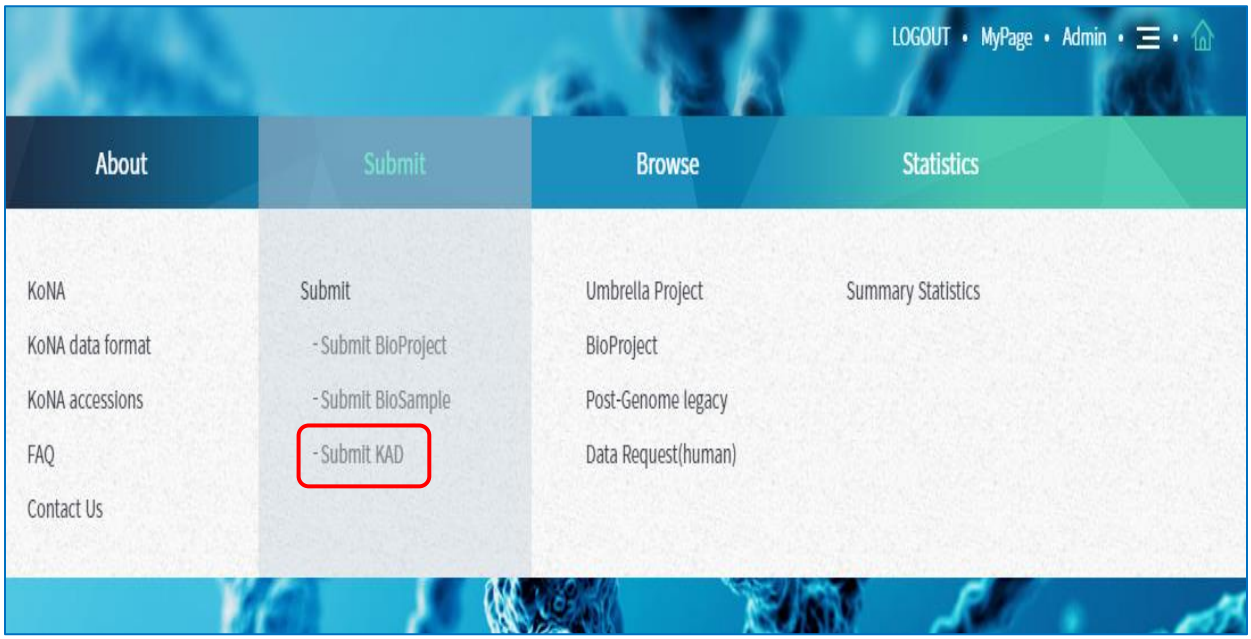
⑤ Submit 클릭 후 성공적으로 업로드가 되면, 하단 Spread sheet에 업로드한 파일의 정보가 입력됨. 내용 확인 후 Save 및 Submit를 클릭하여 BioSample 제출을 완료



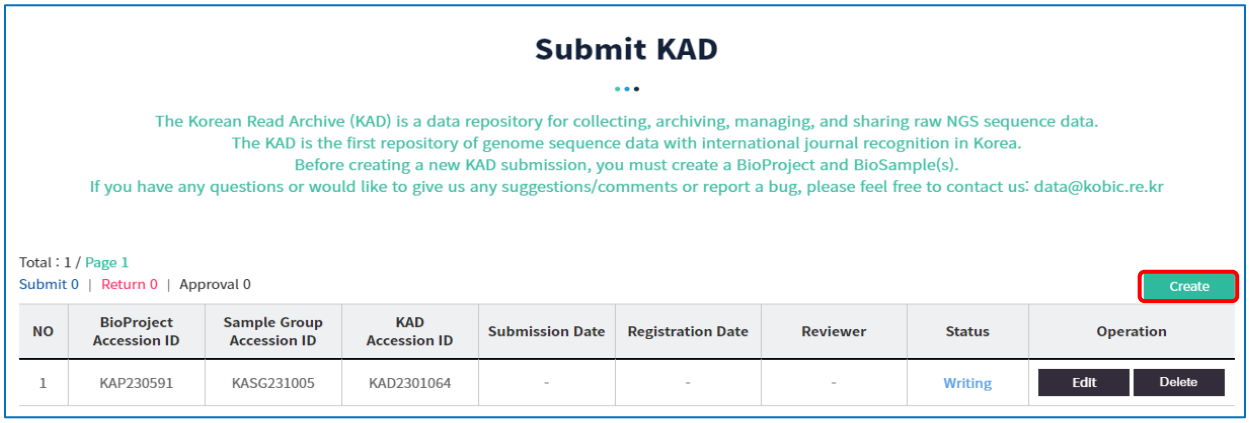
2-5. Submit NGS data (KRA)

◎ 실험 데이터 작성 및 등록

1. 데이터 등록을 위하여 KoNA 메인페이지(https://www.kobic.re.kr/kona/) 상단 메뉴의 [Submit 》 Submit KAD] 페이지로 이동



2. Create 메뉴를 눌러 새로운 KAD 페이지를 활성화 한다.



3. 실험 데이터 입력에 앞서 해당 BioProject와 BioSample 선택

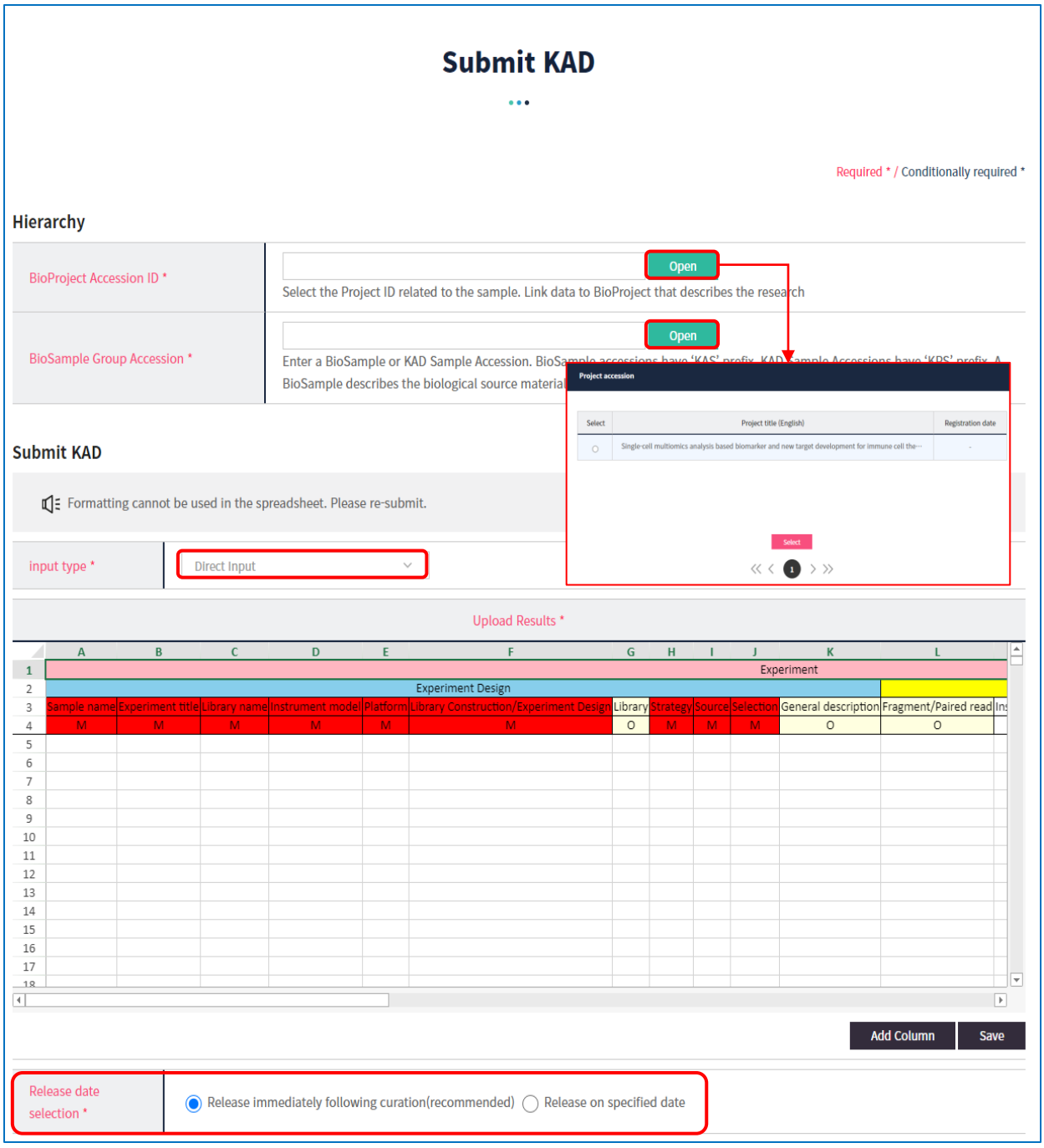
① [Open] 버튼을 클릭하고 창이 나오면 앞서 제출 또는 등록된 BioProject와 BioSample 선택

② 등록하고자 하는 실험 데이타의 공개 날짜를 선택, 즉시 공개와 공개 일자 지정을 할 수 있음

③ [데이터 등록방법]을 선택 [데이터 등록 방법]에는 다음과 아래와 같은 방법이 있음

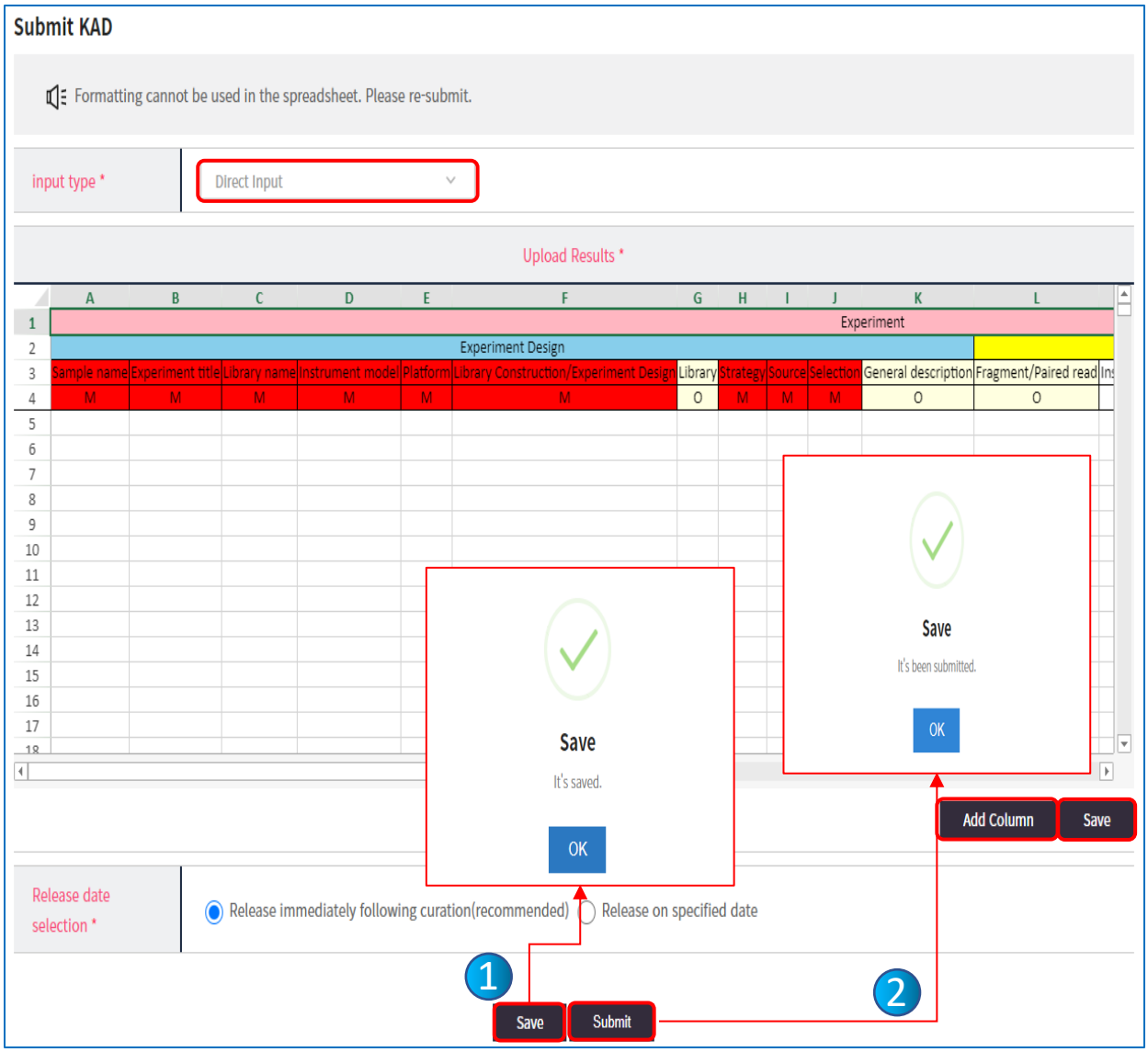
1) 직접 입력 : 실데이터 경로와 메타데이터를 웹 양식에 직접 입력하는 방식

2) 파일 업로드 : 여러 개의 실데이터경로와 메타데이터를 한 번에 파일로 업로드하는 방식



4. 메타데이터 작성 및 제출

1) 데이터 등록 방법에서 “직접 입력”을 선택한 경우



① 빅데이터 고속 전송 시스템(*GBox)를 통해 KoNA스토리지로 실데이터 파일을 업로드

* GBox 다운로드, 설치 및 데이터 업로드에 대한 상세한 설명은 Appendix의 ” GBox user guide ” 참고

② 메타데이터 작성 항목은 *필수항목과 선택항목으로 이루어져 있으며, 필수항목에 빠짐없이 실험 정보를 입력 후 저장하면 하단 Spread sheet 창에 적용

*M : 필수항목, O : 선택 항목

③ Gbox를 다운로드 받아 해당 폴더에 옮긴 실데이터의 경로를 하단 Spread sheet의 path 부분에 작성

④ Run 부분에 추가 되는 파일이 있을 경우, [Add Column]을 클릭하여 OTHER column 옆에 새로운 column이 생성 추가 파일을 입력 할 수 있음.

⑤ 스프레드시트 밑에 Save 버튼을 눌러 작성한 내용을 저장

⑥ 공개일자 지정 후 창 하단의 [Save]을 클릭하여 전체적인 내용을 저장 후 [Submit] 클릭하여 제출 완료

2)데이터 등록 방법에서 “파일 업로드”를 선택한 경우

Submit KAD

Input Type * : File Upload

Proceed with Sample typeUpload는 in thr following order.

Step 1 : Select data entry form.
- To enter data, check 'Enter or not'.
- If you have a field that you want to keep data private, please select 'Private status'.
- After selecting all, select 'Save'. If not saved, the selection information will not reflected.

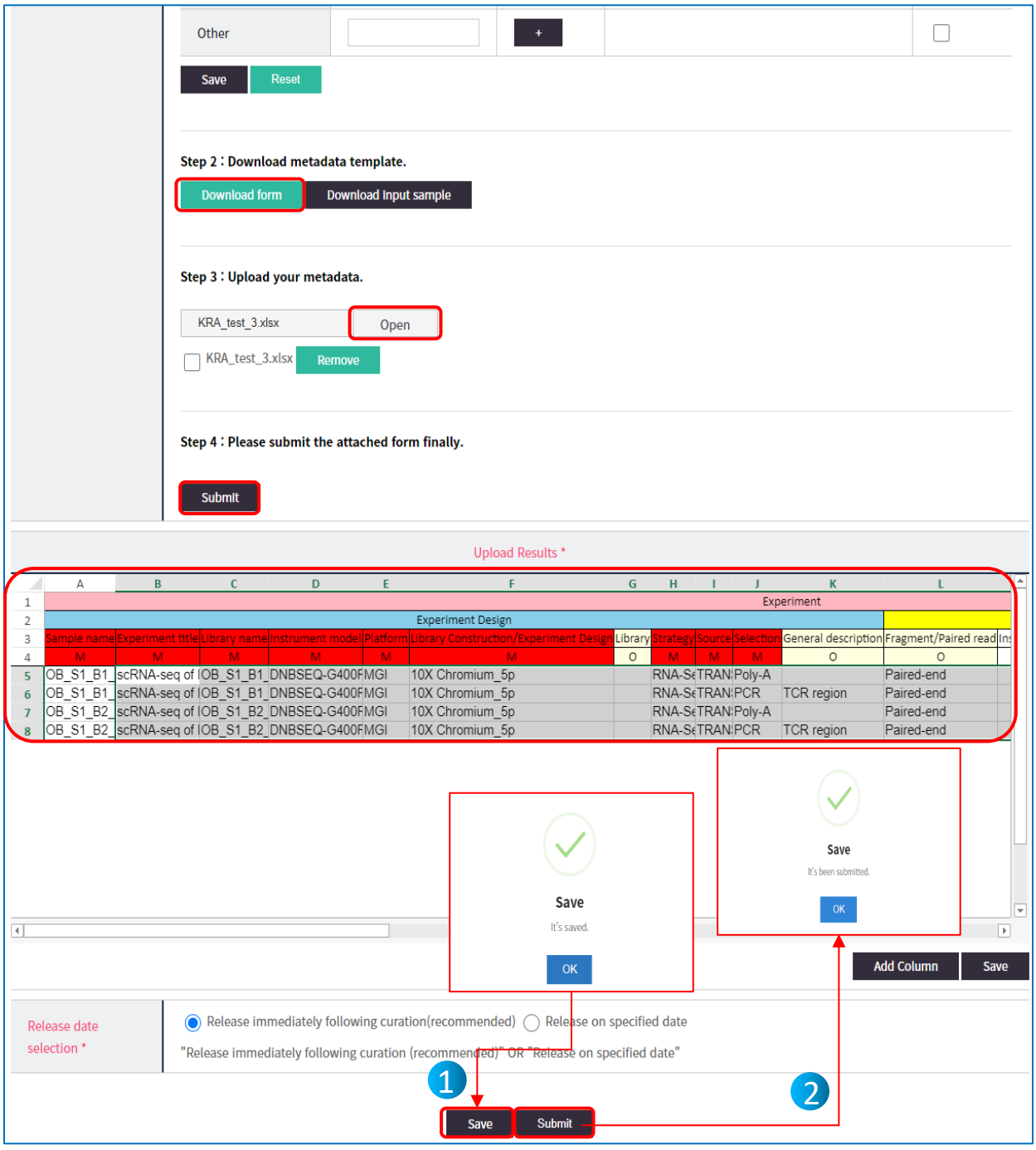
카테고리	필드	M/O	설명	입력여부
sample	Sample name	M	A name that you choose for the sample. It can have any format, but we suggest that you make it concise, unique and consistent within your lab, and as informative as possible. Every Sample Name from a single Submitter must be unique.	
Experiment Design	Experiment title (English)	M	"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)	M	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	M	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	M	Sequencing platform	
	Instrument model	M	Sequencing platform 중 Instrument model 부분	
	Library Construction/Experiment Design	M	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: - the protocols used to extract and prepare the material to be sequenced - the library construction protocol - name of the library preparation kit	

① 빅데이터 고속 전송 시스템(*GBox)를 통해 KoNA스토리지로 실데이터 파일을 업로드

* GBox 다운로드, 설치 및 데이터 업로드에 대한 상세한 설명은 Appendix의 " GBox user guide " 참고

② [파일 업로드]의 경우 [Download form]을 클릭하여 양식을 다운로드 받아 실험 정보를 작성하고 [Open]을 클릭하여 작성한 파일을 업로드한 후 [Submit]을 클릭

성공적으로 업로드가 되면, 하단 Spread sheet에 업로드한 파일의 정보가 입력됨.



③ 이때도 직접입력 방식과 마찬가지로 Gbox 폴더에 옮긴 실데이터의 경로를 다운받은 엑셀 파일의 path 부분에 작성

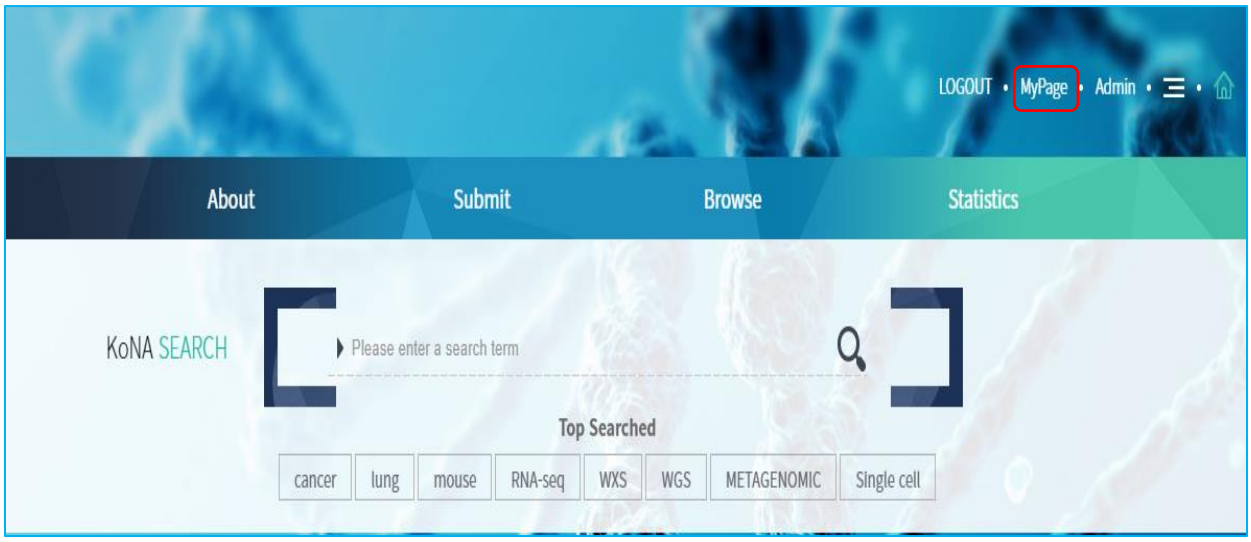
④ 제출된 실험 정보를 Spread sheet 창에서 다시 한번 검토하고 공개 일자 지정 후 창 하단의 [Save]을 클릭하여 전체적인 내용을 저장 후 [Submit] 클릭하여 제출 완료

2-6 Manage my submission (MyPage)

◎ 제출 이후 절차 안내

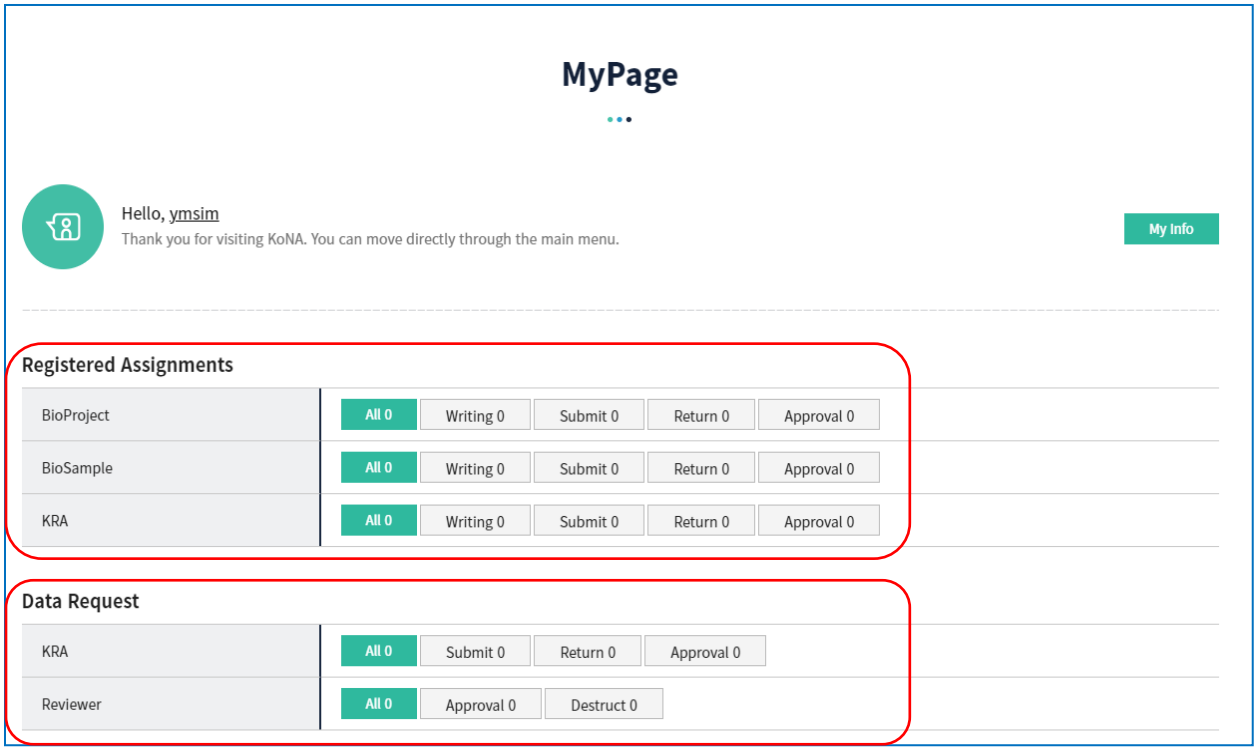
◎ 제출 후 검토 단계

▶ 제출 이후 진행 과정은 [MYPAGE]에서 확인 가능



▶ 검토 단계는 품질관리자가 제출된 데이터를 검수

▶ 검토 단계를 통과하면 '승인'되어 등록이 가능한 상태로 변경되고, 통과하지 못한 데이터에 대해서는 '반려' 처리가 되어 제출자가 수정하여 재제출 필요



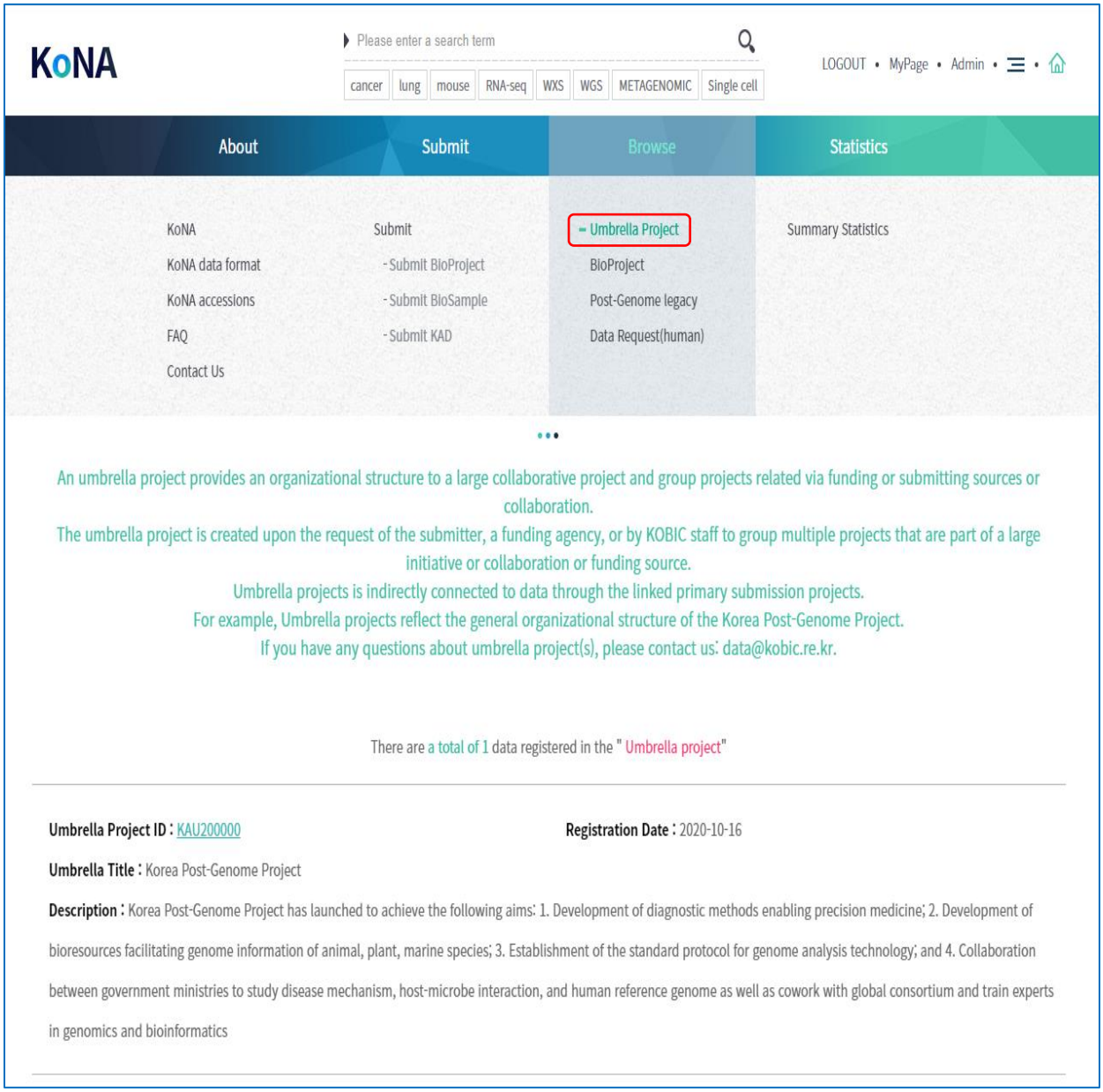
◎ 등록 이후

검토 이후 최종 등록이 완료되면, 등록번호가 부여되고, 입력한 공개 일자에 데이터는 공개됨

III DATA SEARCH AND DOWNLOAD

3-1. Search Umbrella BioProject

1. KoNA 메인페이지(https://www.kobic.re.kr/kona/) 상단 메뉴의 [Browse 》 Umbrella Project] 페이지로 이동, 등록된 Umbrella Project를 확인 할 수 있음

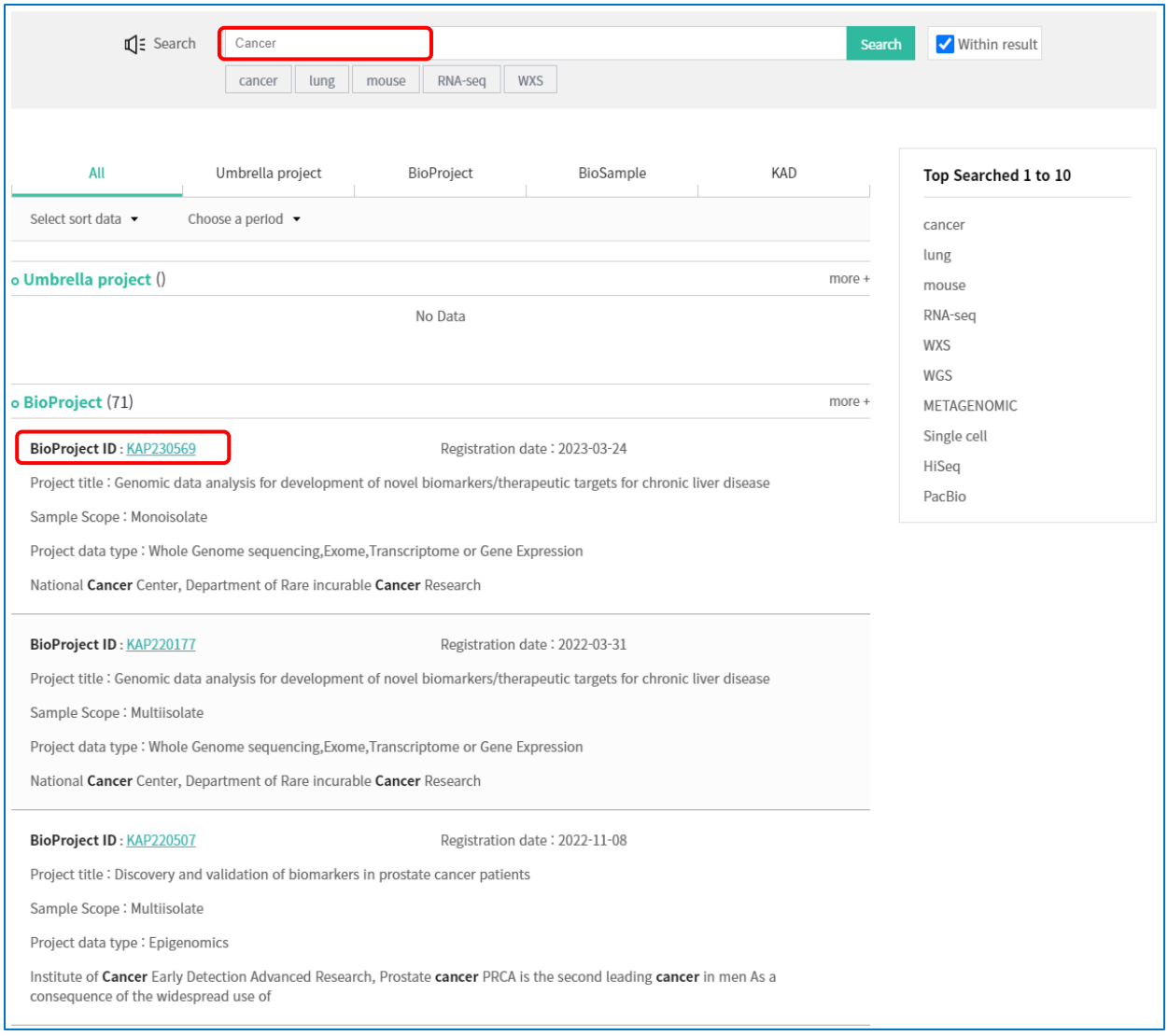


3-2. Search BioProject

◎ 메인페이지 통합 검색

1. 메인페이지의 검색 바에서 원하는 검색어(예: cancer)를 입력 후, 우측 아이콘을 클릭

2. 입력한 검색어에 대한 BioProject 와 BioSample Group, KAD 에서 원하는 데이터를 선택



BioSample Group (136)

more +

Sample Group accession ID : KASG210092 Registration date : 2021-09-08

Sample title : microRNA sequencing data generated from ovarian cancer stem cells and ovarian non-cancer stem cells

Sample type : Human sample

microRNA sequencing data generated from ovarian **cancer** stem cells and ovarian non-**cancer** stem cells, 난소암 **cancer** stem cells과 non-**cancer** stem cells에서 생산한 마이크로알엔에이 시퀀싱 데이터, To detect differentially expressed microRNAs between ovarian **cancer** stem cells and ovarian non-**cancer**, 마이크로알엔에이 시퀀싱 데이터 분석을 통하여 난소암 **cancer** stem cell과 non-**cancer** stem cell에서 차별발현되는 마이크로알엔에이를 발굴함

Sample Group accession ID : KASG220245 Registration date : 2022-04-12

Sample title : Whole genome sequencing of lung cancer

Sample type : Human sample

Whole genome sequencing of lung **cancer**, Whole genome sequence of **cancer** tissues and surrounding normal tissues of lung **cancer** patients

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Sample Group accession ID : KASG220268 Registration date : 2022-04-12

Sample title : Whole genome sequencing on lung cancer

Sample type : Human sample

Whole genome sequencing on lung **cancer**, Whole genome seq analysis of **cancer** tissues and surrounding normal tissues of lung **cancer** patients

---

KAD (95)

more +

KAD accession ID : KAD2000013 Registration date : 2020-12-16

Platform : BGISEQ Strategy : WGS Selection : other (not size selecti...

Extraction of ctDNA from blood samples of patients with triple negative breast **cancer** 2.

KAD accession ID : KAD2100122 Registration date : 2021-09-08

Platform : ILLUMINA Strategy : smRNA-Seq Selection : size fractionation

curcumin-untreated SK-OV-3 **cancer** stem cells_miRNA-Seq,curcumin-treated SK-OV-3 **cancer** stem cells_miRNA-Seq, curcumin을 처리하지 않은 SK-OV-3 **cancer** stem cell의 miRNA,curcumin을 처리한 SK-OV-3 **cancer** stem cell의 miRNA,curcumin을

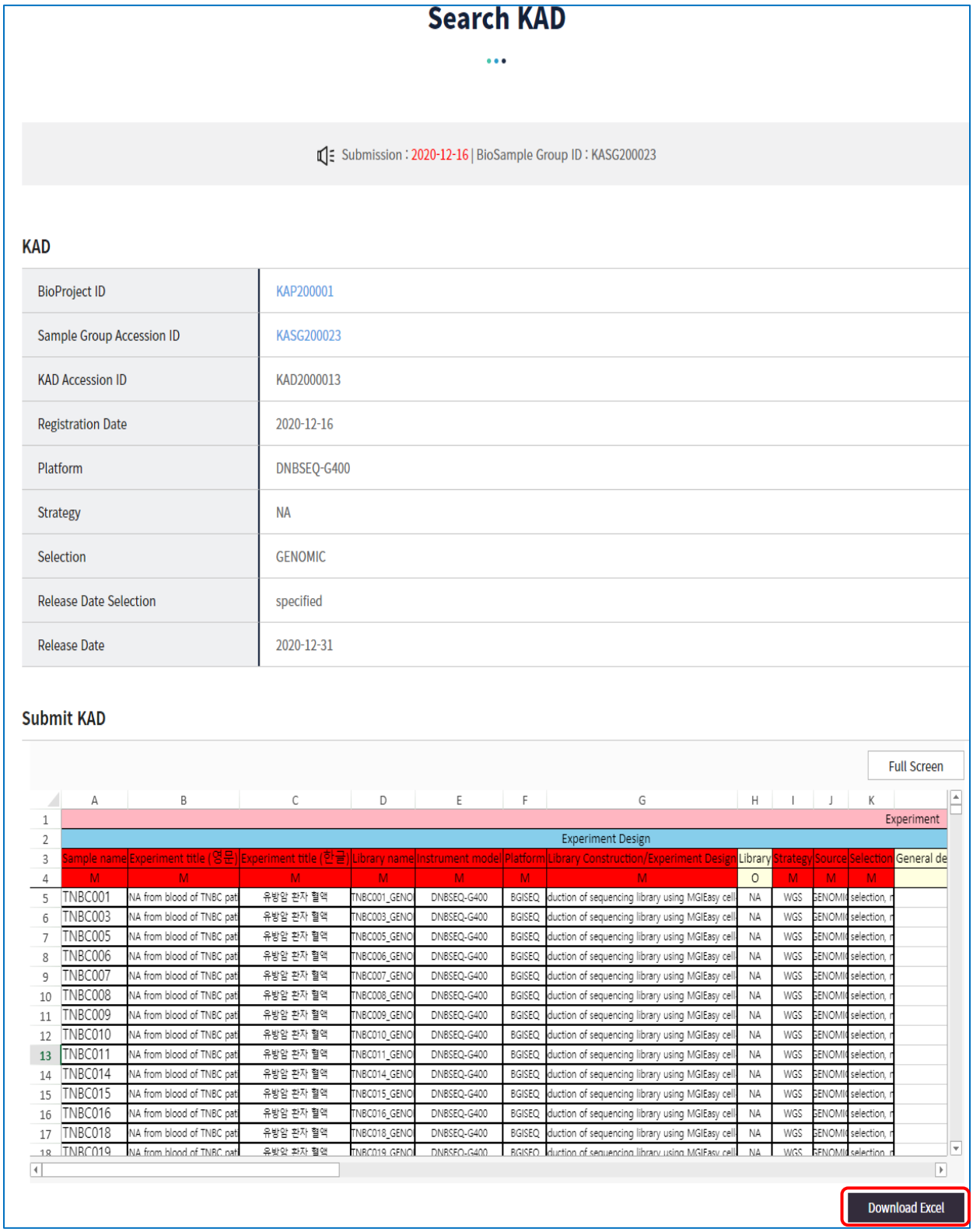
KAD accession ID : KAD2100074 Registration date : 2021-03-22

Platform : ION_TORRENT,Illumina Strategy : Targeted-Capture Selection : PCR,Hybrid Selection

The development of kit for screening of **cancer** related target genes with high sensitivity in the liquid, Lung **Cancer** Panel-Targeted Sequencing (LCPT-Seq), Lung **Cancer** Panel-Targeted Sequencing (LCPT-Seq)

---

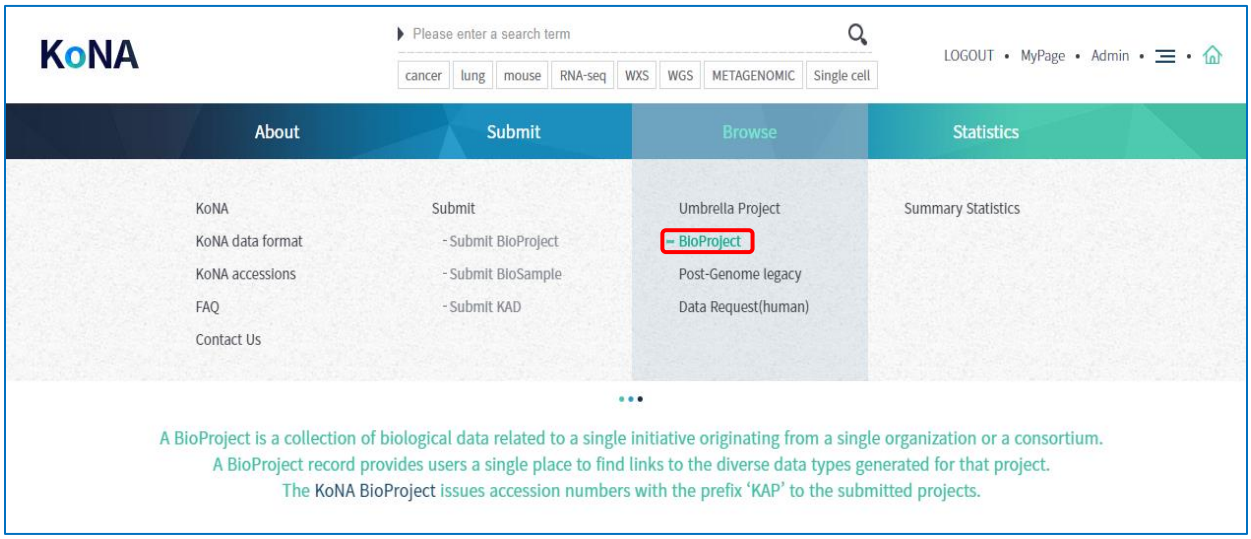
3. 선택한 데이터에 대한(공개일자가 지난데이터) 메타데이터(웹상 엑셀파일로 바로 다운로드) 및 실데이터의(Gbox 사용) 다운로드가 가능

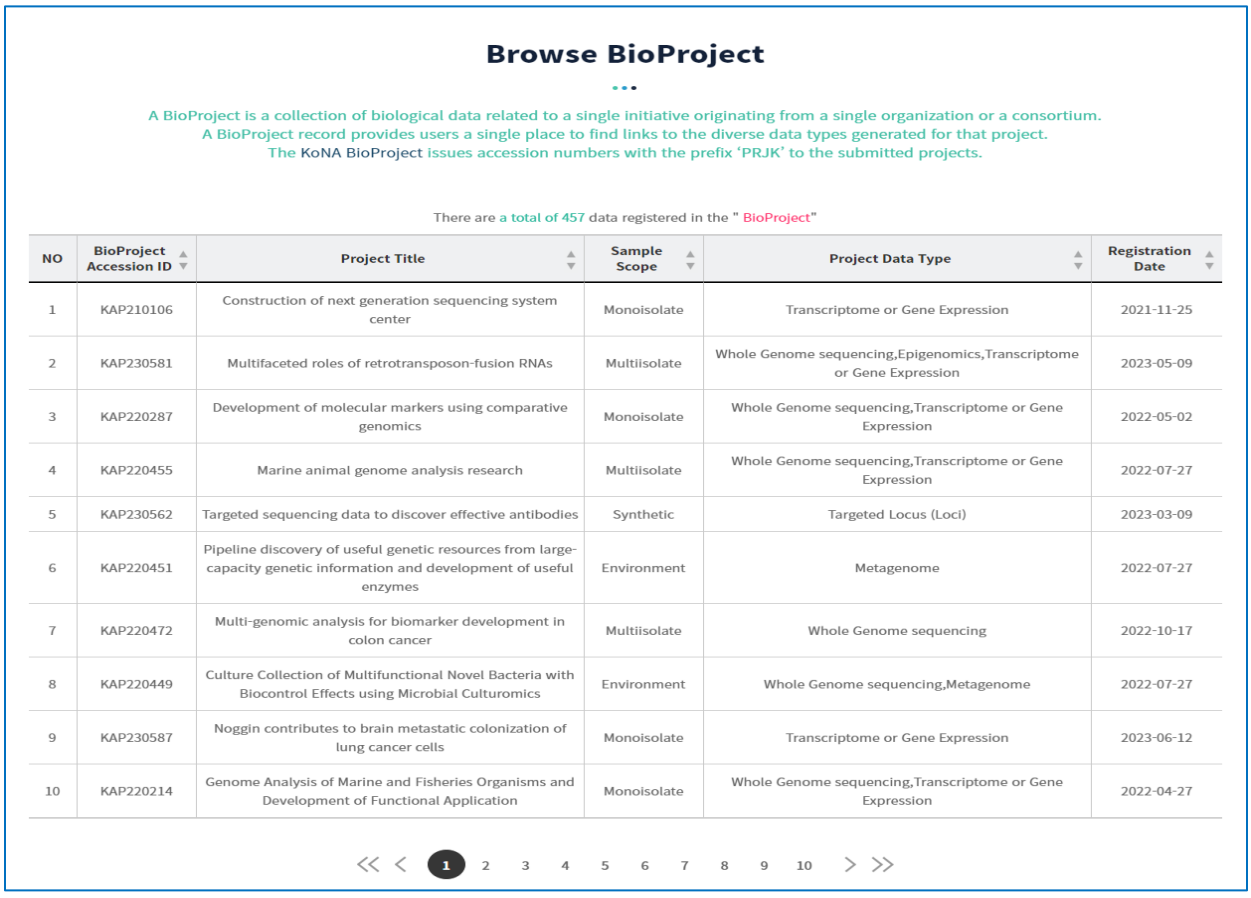


	A	B	C	D	E	F	G	H	I	J	K
1											Experiment
2							Experiment Design				
3	Sample name	Experiment title (영문)	Experiment title (한글)	Library name	Instrument model	Platform	Library Construction/Experiment Design	Library	Strategy	Source	Selection	General de
4	M	M	M	M	M	M	M	O	M	M	M	
5	TNBC001	NA from blood of TNBC pat	유방암 환자 혈액	TNBC001_GENO	DNBSEQ-G400	BGISEQ	duction of sequencing library using MGIEasy cell	NA	WGS	GENOMI	selection, r	
6	TNBC003	NA from blood of TNBC pat	유방암 환자 혈액	TNBC003_GENO	DNBSEQ-G400	BGISEQ	duction of sequencing library using MGIEasy cell	NA	WGS	GENOMI	selection, r	
7	TNBC005	NA from blood of TNBC pat	유방암 환자 혈액	TNBC005_GENO	DNBSEQ-G400	BGISEQ	duction of sequencing library using MGIEasy cell	NA	WGS	GENOMI	selection, r	
8	TNBC006	NA from blood of TNBC pat	유방암 환자 혈액	TNBC006_GENO	DNBSEQ-G400	BGISEQ	duction of sequencing library using MGIEasy cell	NA	WGS	GENOMI	selection, r	
9	TNBC007	NA from blood of TNBC pat	유방암 환자 혈액	TNBC007_GENO	DNBSEQ-G400	BGISEQ	duction of sequencing library using MGIEasy cell	NA	WGS	GENOMI	selection, r	
10	TNBC008	NA from blood of TNBC pat	유방암 환자 혈액	TNBC008_GENO	DNBSEQ-G400	BGISEQ	duction of sequencing library using MGIEasy cell	NA	WGS	GENOMI	selection, r	
11	TNBC009	NA from blood of TNBC pat	유방암 환자 혈액	TNBC009_GENO	DNBSEQ-G400	BGISEQ	duction of sequencing library using MGIEasy cell	NA	WGS	GENOMI	selection, r	
12	TNBC010	NA from blood of TNBC pat	유방암 환자 혈액	TNBC010_GENO	DNBSEQ-G400	BGISEQ	duction of sequencing library using MGIEasy cell	NA	WGS	GENOMI	selection, r	
13	TNBC011	NA from blood of TNBC pat	유방암 환자 혈액	TNBC011_GENO	DNBSEQ-G400	BGISEQ	duction of sequencing library using MGIEasy cell	NA	WGS	GENOMI	selection, r	
14	TNBC014	NA from blood of TNBC pat	유방암 환자 혈액	TNBC014_GENO	DNBSEQ-G400	BGISEQ	duction of sequencing library using MGIEasy cell	NA	WGS	GENOMI	selection, r	
15	TNBC015	NA from blood of TNBC pat	유방암 환자 혈액	TNBC015_GENO	DNBSEQ-G400	BGISEQ	duction of sequencing library using MGIEasy cell	NA	WGS	GENOMI	selection, r	
16	TNBC016	NA from blood of TNBC pat	유방암 환자 혈액	TNBC016_GENO	DNBSEQ-G400	BGISEQ	duction of sequencing library using MGIEasy cell	NA	WGS	GENOMI	selection, r	
17	TNBC018	NA from blood of TNBC pat	유방암 환자 혈액	TNBC018_GENO	DNBSEQ-G400	BGISEQ	duction of sequencing library using MGIEasy cell	NA	WGS	GENOMI	selection, r	
18	TNBC019	NA from blood of TNBC pat	유방암 환자 혈액	TNBC019_GENO	DNBSEQ-G400	BGISEQ	duction of sequencing library using MGIEasy cell	NA	WGS	GENOMI	selection, r	

◎ BioProject 데이터 활용 검색

1. [메인페이지 》Browse》BioProject] 페이지로 이동
2. 주요 과제 중 관심 BioProject 클릭하여 이동
3. 해당 BioProject 의 데이터에 대한(공개일자가 지난데이터) 메타데이터(웹상 엑셀 파일로 바로 다운로드) 및 실데이터의(Gbox 사용) 다운로드가 가능





3-3. Search BioSample

◎ BioSample 데이터 활용 검색

1. [메인페이지 》Browse》BioProject] 페이지로 이동
2. 선택한 BioPreoject 내 사용하고자 하는 Sample 데이터를 클릭하여 이동
3. 해당 Sample Group ID 의 데이터에 대한(공개일자가 지난데이터) 메타데이터(웹상 엑셀파일로 바로 다운로드) 및 실데이터의(Gbox 사용) 다운로드 가능

Sample Group

BioSample Accession ID	Project Title	Sample Type	Registration Date
KASG230995	Cancer cell line	Human sample	2023-05-24
KASG230983	ONT whole genome sequencing for colorectal cancer patients	Human sample	2023-05-09

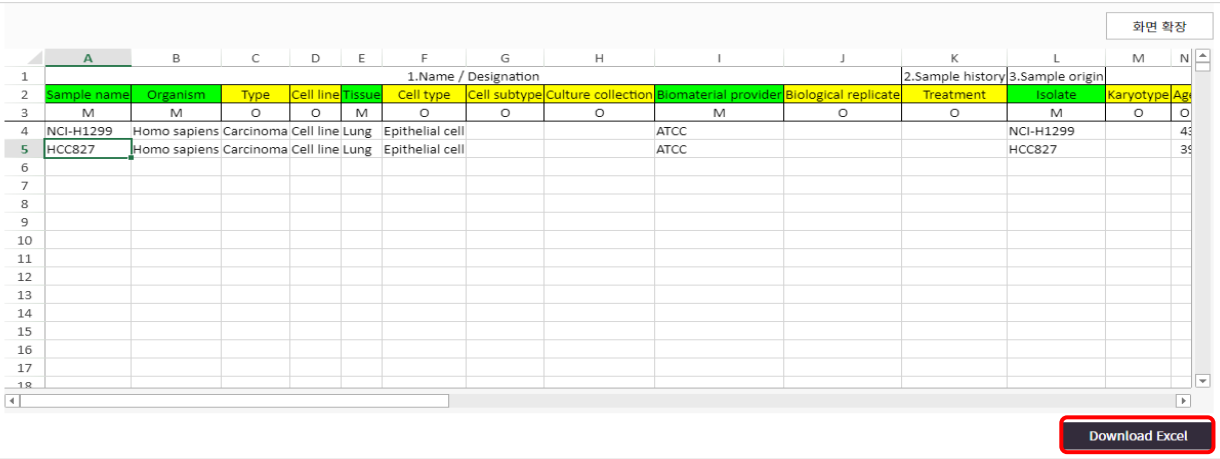
Submitters's Submissions

BioProject Accession ID	Project Title	Sample Scope	Project Data Type	Registration Date
KAP220480	Single cell transcriptome based biomarker development in colorectal cancer	Multiisolate	Whole Genome sequencing,Transcriptome or Gene Expression	2022-10-17
KAP220465	Single-cell multiomics analysis based biomarker and new target development for immune cell therapy	Single cell	Transcriptome or Gene Expression	2022-09-14
KAP220466	Development of prognosis-treatment prediction biomarkers based on single-cell transcripts for colorectal cancer	Single cell	Transcriptome or Gene Expression	2022-09-14
KAP220477	Single cell transcriptome based biomarker development in colorectal cancer	Multiisolate	Whole Genome sequencing	2022-10-17
KAP220479	Single cell transcriptome based biomarker development in colorectal cancer	Multiisolate	Whole Genome sequencing,Transcriptome or Gene Expression	2022-10-17
KAP220355	Single-cell multiomics analysis based biomarker and new target development for immune cell therapy	Single cell	Transcriptome or Gene Expression	2022-07-05
KAP230581	Multifaceted roles of retrotransposon-fusion RNAs	Multiisolate	Whole Genome sequencing,Epigenomics,Transcriptome or Gene Expression	2023-05-09

Sample Group

BioProject ID	KAP230581
Sample Group Accession ID	KASG230995
Sample Title	Cancer cell line
Description	Lung cancer cell line samples (H1299, HCC827)
Sample Type	Human sample
Registration Date	2023-05-24
Number of BioSamples	2
Number of Experiments	2

Sample Group Information



KRA

BioProject ID	Sample Group Accession ID	KRA Accession ID	Registration Date	Platform	Strategy	Selection
KAP230581	KASG230995	KAD02301058	2023-05-24	ILLUMINA	RNA-Seq	PolyA

3-4. Search KAD and download raw data

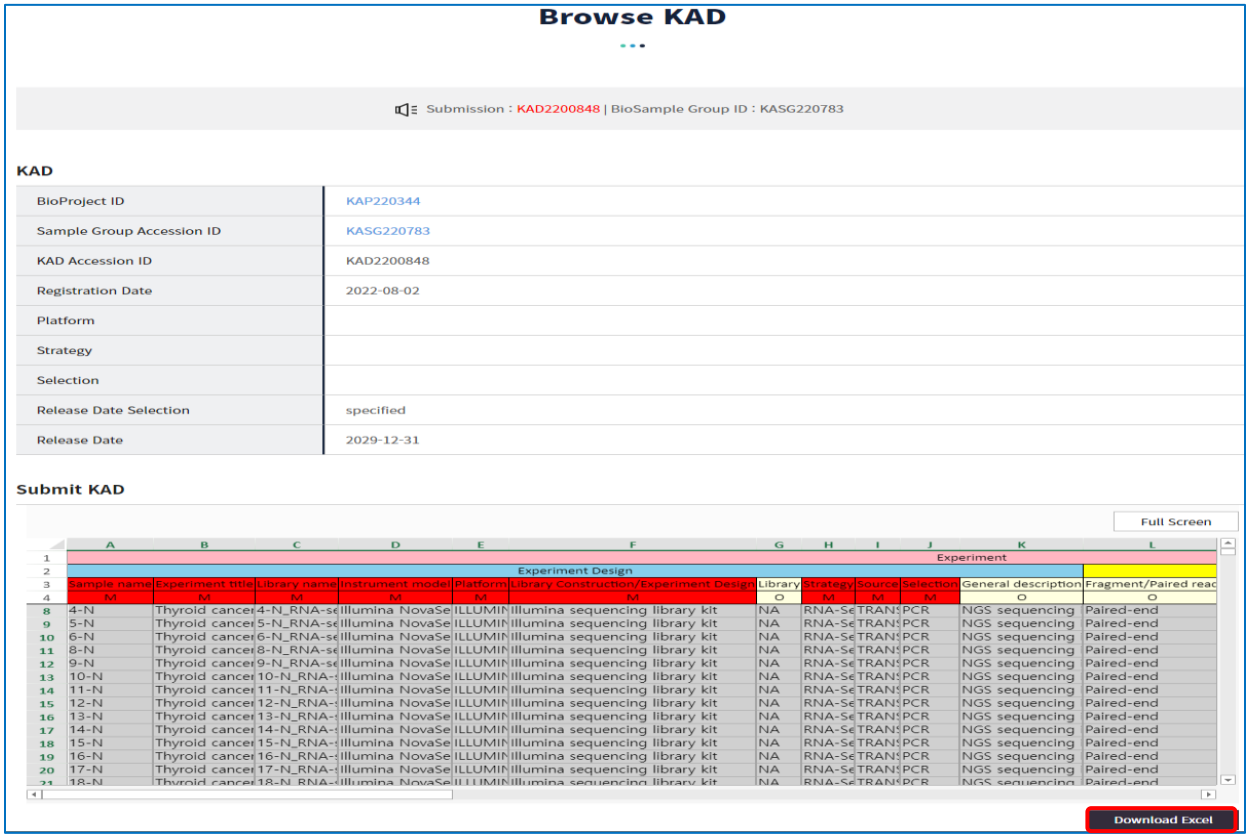
◎ KAD 데이터 활용 검색

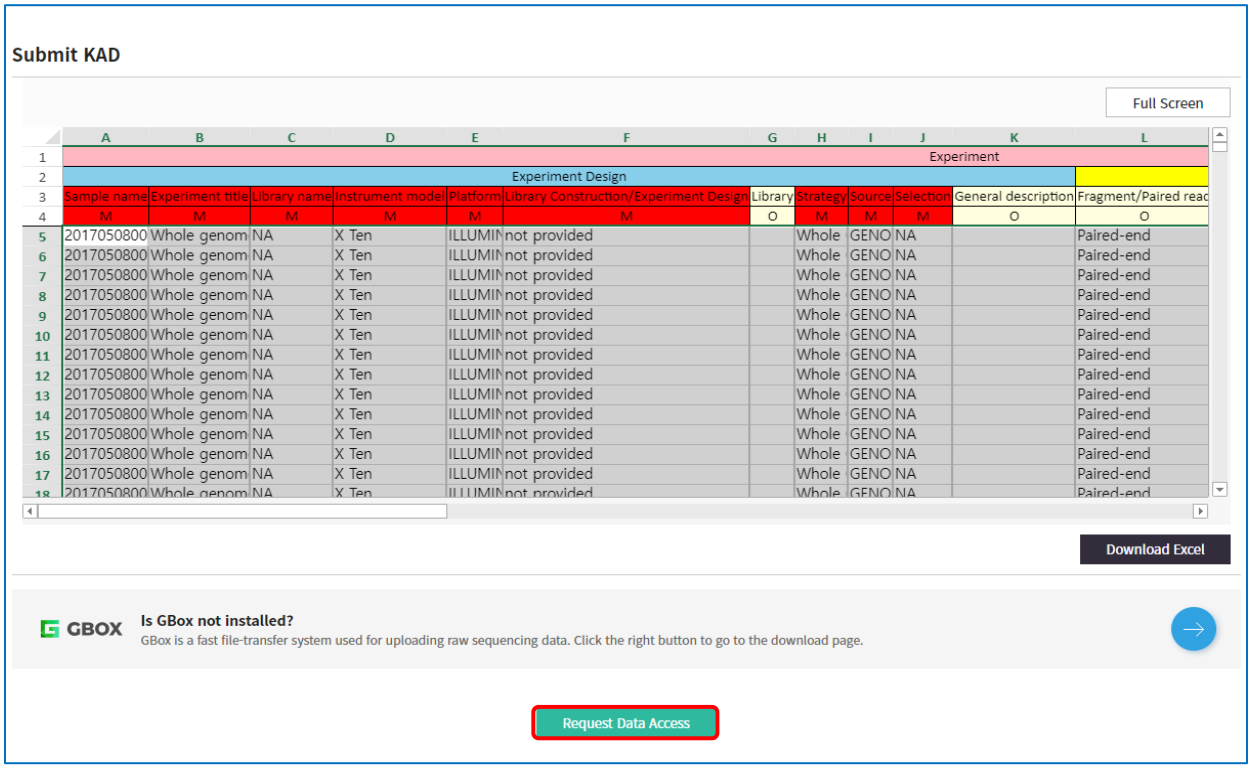
1. [메인페이지 》 Browse》 BioProject] 페이지로 이동
2. 선택한 BioPreoject 내 사용하고자 하는 Sample 데이터를 클릭하여 이동
3. 해당 Sample Group ID 에 링크된 KAD 데이터에 대한(공개일자가 지난데이터) 메타데이터(웹상 엑셀 파일로 바로 다운로드) 및 실데이터의(Gbox 사용) 다운로드 가능

① 본 사용자 가이드 통하여 원하는 데이터를 검색 및 선택하여 페이지로 이동

② [Download Excel] 버튼을 클릭하여 데이터 다운로드 ※ 공개 전 데이터는 다운로드 가능

③ 실데이터는 하단의 [Request Data Access]를 클릭하여 요청 한 뒤 본인 계정의 Gbox 로 들어가면 요청된 실데이터 다운로드가 가능



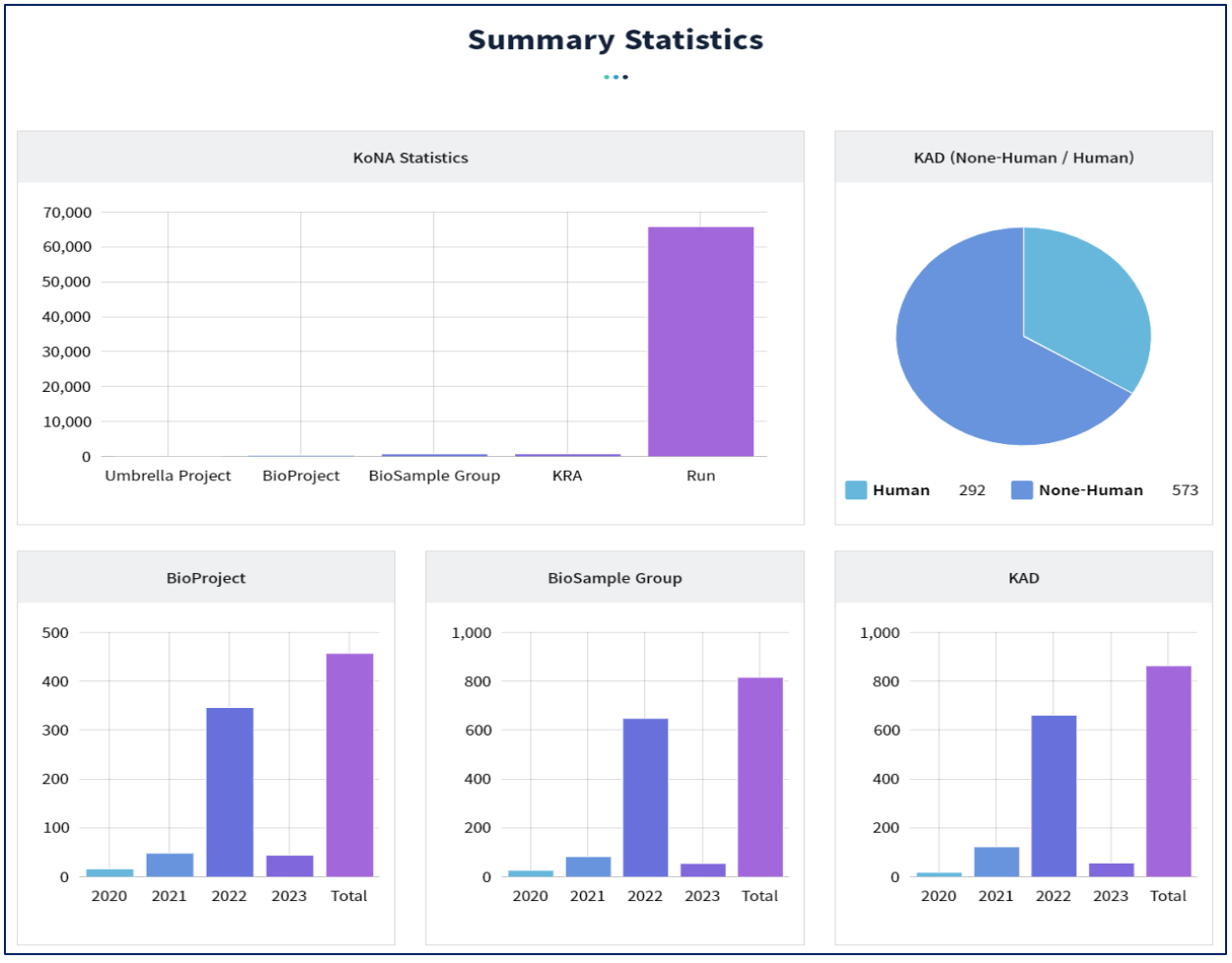


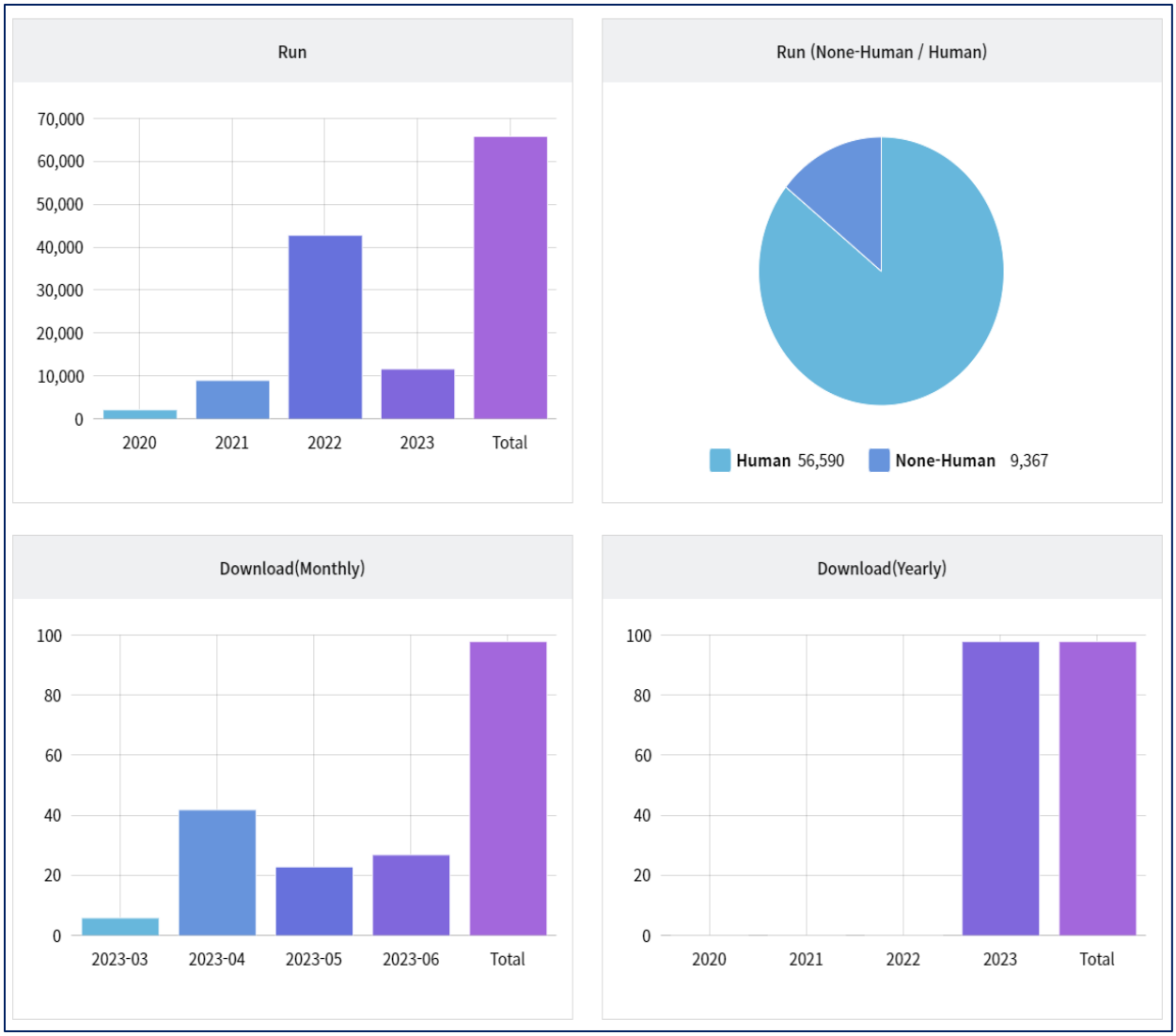
3-4. Statistics

◎ 데이터 타입별 통계

1. [메인페이지 》 Statistics 》 Summary Statistics] 페이지로 이동

2. "데이터 통계" 페이지에서 데이터별 등록 현황, 등록 추이 및 년도별 등록 현황 확인




Run
70,000
60,000
50,000
40,000
30,000
20,000
10,000
0
2020
2021
2022
2023
Total
Run (None-Human / Human)
Human 56,590
None-Human 9,367
Download(Monthly)
100
80
60
40
20
0
2023-03
2023-04
2023-05
2023-06
Total
Download(Yearly)
100
80
60
40
20
0
2020
2021
2022
2023
Total

IV FAQ

F : How many samples and experiments do I need?

A : A1. You may have more than one experiment per samples.
SAMPLE is a record of biological isolate with unique physical properties.
Please refer to the KoNA Guide for detailed descriptions and guideline.
EXPERIMENT is a unique sequencing result for a specific sample.
A2. In the KoNA Metatdata template, EXPERIMENT is represented by a combination of library + strategy + layout + instrument model and corresponds to one row in the table.
Please refer to the KoNA Metadata Overview for better understanding of KoNA data organization.

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

A : A1. We recommend using the BioProject accession (KAP#) in publications.
A BioProject is an umbrella for all data submitted to the NCBI for a given study.
Each BioProject can be associated with more than one submission in KoNA. After you have
successfully completed your submission, the KoNA will send an email notification with the BioProject accession.

F : My manuscript reviewer is requesting a link to my submission, how do I get one?

A : Log into the KoNA's MyPage Interface
Find BioProject of interest by browsing, searching, or filtering all your data
Press the button "Reviewer link"

F : Why doesn't my GBox upload work?

A : For troubleshooting GBox service please refer to Bio-Express Support

F : How do I create more than one EXPERIMENT (library/replicate) per SAMPLE for the KAD submission in Bio-Sub menu?

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.

F : How do I create more than one RUN per EXPERIMENT in Bio-Sub menu?

A : Only one RUN per EXPERIMENT is allowed for KRA submission in the Bio-Sub Portal. When libraries are indeed identical (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.

F : How do I delete my submission (SUB#: e.g., BIOPROJECT#, BIOSAMPLE GROUP#, and KAD#) in Bio-Sub menu?

A : To delete KoNA submissions please contact KoNA staff for assistance at data@kobic.kr. Provide SUB# and reason.

F : How do I add more samples to my KAD submission in Bio-Sub menu?

A : KAD Submission is a descrete 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 umbrella for all data submitted to the NCBI 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. This will ensure that all pertinent data are linked to the same accession in Entrez and become searchable across databases.

F : My manuscript has been published. How do I update my KoNA submission with the publication?

A : Please refer to the How to cite in KoNA

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

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

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

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

F : How do I withdraw my KoNA BIOPRJECT, BIOSAMPLE GROUP, KAD in KoNA (KAP#/KASG#/KAD#)?

A : Contact the KoNA staff for assistance at data@kobic.kr. Provide KAP#, KASG#, KAD#, etc.

F : How do I re-name my EXPERIMENT/RUN?

A : Aliases of EXPERIMENTs and RUNs cannot be changed.

F : How do I change the PLATFORM in my EXPERIMENTs?

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

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

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

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

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

F : Contact KoNA

A : If you were unable to resolve your problem after reading this F&Q, contact KoNA staff at data@kobic.kr..

VI APPENDIX

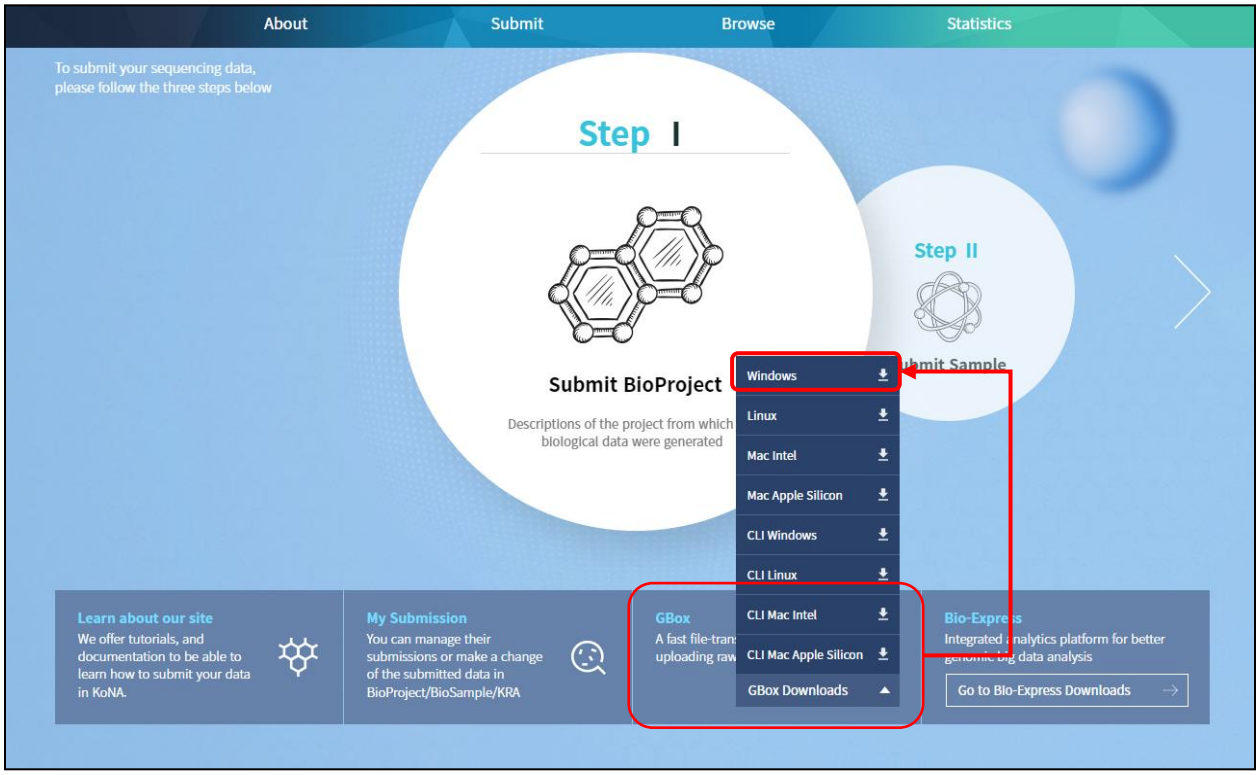
4-1. 빅데이터 고속 전송 시스템 (GBox)

◎ 빅데이터 고속 전송 시스템 소개

GBox 고속 전송 시스템은 가속기 등의 추가적인 하드웨어 구축이나 ActiveX와 같은 별도의 플러그인 설치 없이 소프트웨어 기술만으로 사용자의 대용량 데이터를 고속으로 전송할 수 있는 시스템

• 프로그램 다운로드 및 설치

[메인페이지 ⇨ 하단 G-Box] 클릭, 본인의 컴퓨터 환경에 맞는 것을 선택하여 다운로드



※ **KRA upload raw data**

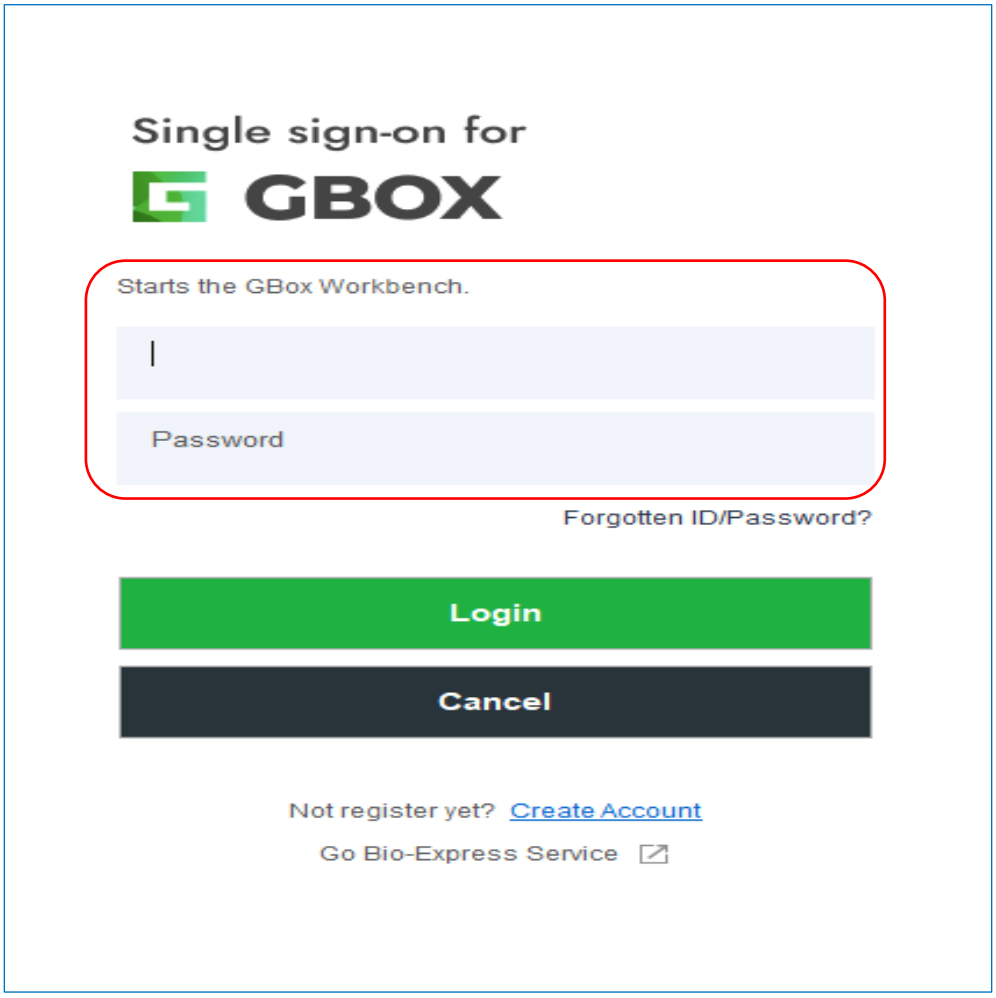
▶ 홈페이지상의 Gbox를 각 연구자의 컴퓨터 환경 설정에 맞게 다운로드 하여 설치

▶ 설치된 Gbox를 실행 후 로그인 하여 업로드 하고자 하는 raw data를 이동 복사

▶ 데이터가 이동된 디렉토리의 path를 메타데이터 작성시 Run column에 입력

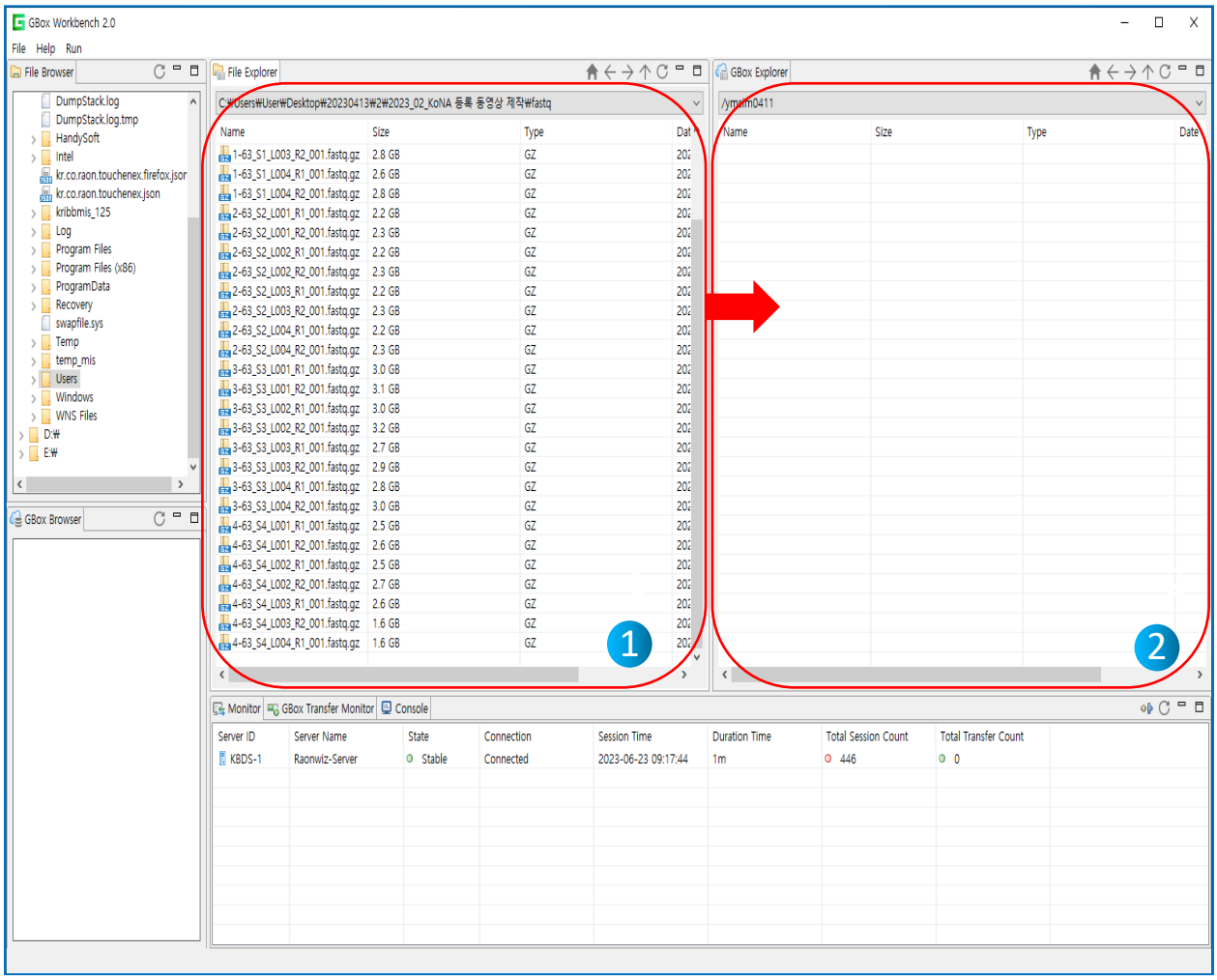
• 데이터 업로드 및 다운로드

1. 아래 그림의 GBox 프로그램을 통해 사용자는 KoNA 스토리지에 데이터를 업로드하거나 사용자의 PC 로 다운로드할 수 있음



① **[File Browser]**나 **[File Explorer]**를 통해 사용자 PC의 업로드 할 데이터가 있는 폴더로 이동

② 업로드 할 폴더 또는 파일을 선택한 후 **[GBox Explorer]**로 드래그하거나 **[마우스 우클릭]** 후 팝업되는 메뉴 창에서 Upload 하면 **[KoNA스토리지]** 경로로 선택한 폴더 및 파일이 업로드됨



③ **[File Explorer]** 창에서 **[마우스 우클릭]**을 통해 데이터 업로드, 폴더 및 파일 생성, rename, 복사/붙여넣기, 삭제, refresh 기능을 지원

④ KoNA 스토리지 내 사용자의 경로는 **"/[사용자아이디]"로 시작. 업로드한 폴더 및 파일의 경로는 /[사용자아이디/업로드한 폴더/업로드한 파일"**로 사용

예1) 사용자 아이디 : test, 업로드한 폴더 : RNA_seq, 해당폴더 내 파일명 : sample.fq.gz

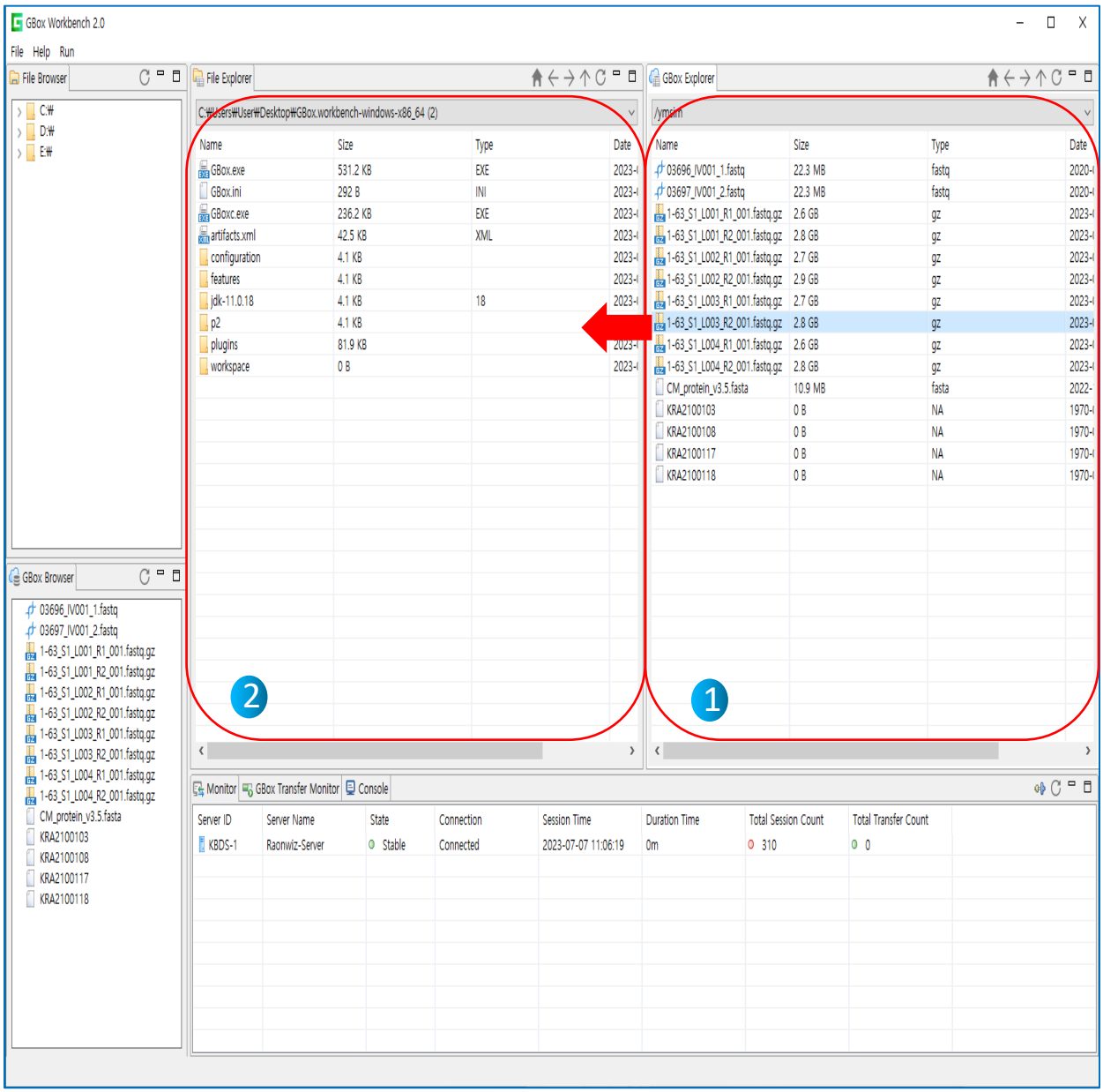
⇒ 업로드한 폴더 및 파일의 경로 : /test/RNA_seq/sample.fq.gz

예2) 사용자 아이디 : test, 업로드한 파일명 : sample.fq.gz

⇒ 업로드한 폴더 및 파일의 경로 : /test/sample.fq.gz

⑤ **[현재 KoNA 스토리지]** 서버와 연결 상태를 확인 가능. Connection 창의 상태가 "Connected"가 일 때만 데이터 업로드/다운로드가 가능

⑥데이터를 사용자 PC로 다운로드할 때는 **[GBox Explorer]**창의 폴더 또는 파일을 **[File Explorer]**로 드래그하거나 GBox Explorer의 파일 및 폴더를 우클릭해 다운로드



• 업로드한 데이터 경로 확인

① **[데이터 업로드]**가 시작되면 하단의 progress 창에서 업로드 현황 확인이 가능. 폴더

를 업로드하는 경우 폴더 내의 모든 파일에 대한 파일 크기 측정이 완료된 후 업로드가 시작되며 파일 개수에 따라 측정 시간이 추가로 소요

② **[업로드]**가 완료되면 GBox Explorer창에 업로드된 파일 또는 폴더가 나타남

③ **[이 파일 및 폴더의 위치]**는 표시된 [현재 KoNA스토리지 내 경로] 하위에 파일명 및 폴더명으로 저장

④ 업로드한 파일 및 폴더의 경로를 확인하는 다른 방법은 GBox Explorer 창에서 파일 또는 폴더를 선택하고 **[마우스 우클릭]**을 하여 팝업되는 메뉴에서 Path Copy를 선택하면 해당 파일 또는 폴더의 전체 경로가 복사

⑤ 이후 KoNA 웹 페이지에서 직접 입력 등록 또는 파일 업로드 등록 시 입력할 파일명은 파일명이 아닌 위의 방식으로 파악한 파일의 "**전체 경로명(절대경로)"**을 기입

4-2. 상세 설명 가이드

1. Sample Design - Sample Type

1.1 Clinical or host-associated pathogen
Description : Clinical or host-associated pathogen

Mandatory Attributes

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) (e.g. "Candida metapsilosis"; "Hepacivirus C"; "Homo sapiens"; "metagenome")
Collected by	Name(s) of person(s) or institute who collected the sample (e.g. "Korea Research Institute of Bioscience & Biotechnology(KRIBB)"; "Dan Janzen")
Collection date	Date of sampling (YYYY-MM-DD) (e.g. "1989-09-20")
Isolation source	Describes the physical, environmental and/or local geographical source of the biological sample from which the sample was derived (e.g. "rumen isolates from standard Pelleted ration-fed steer #67"; "permanent Antarctic sea ice"; "denitrifying activated sludge from carbon_limited continuous reactor")

Geographic location	Geographical origin of the sample; Use a colon to separate the country or ocean from more detailed information about the location (e.g "Korea: Seoul"; "Korea")
Latitude and longitude	The geographical coordinates of the location where the sample was collected. Specify as degrees latitude and longitude in format "d[d.dddd] N|S d[dd.dddd] W|E", e.g., 38.98 N 77.11 W (e.g. "47.9412 N 28.1201 E")
Host	Name of the natural (as opposed to laboratory) host species to the organism from which the sample was obtained (e.g. "Homo sapiens"; "Gallus gallus domesticus")
Host disease	Name of relevant disease, e.g. Salmonella gastroenteritis (e.g. "Salmonella gastroenteritis"; "Hepatitis C")

Optional Attributes

Strain	microbial or eukaryotic strain name, number or designation (e.g. "MG1234"; "K12"; "BALB/c")
Subgroup	Taxonomy below subspecies; sometimes used in viruses to denote subgroups taken from a single isolate (e.g. "Clostridium botulinum Group I")
Subtype	Used as classifier in viruses (e.g. HIV type 1, Group M, Subtype A) (e.g. HIV type 1, Group M, Subtype A)
Culture collection	* Name of source institute and unique culture identifier. * Provide the following information only if the sequenced sample you are submitting was retrieved directly from the indicated culture collection, or the sequenced sample was deposited in the indicated culture collection. * This should be provided using the following format 'institution-code:(optional collection-code):culture-id'. culture-id and institution-code are mandatory. See the list of allowed institutes (ftp://ftp.ncbi.nlm.nih.gov/pub/taxonomy/coll_dump.txt) (e.g. "ATCC:26370")
Specimen voucher	* Identifier for the physical specimen that remains after the sample has been obtained. * Provide the following information only if the sequenced sample you are submitting was retrieved directly from the indicated museum/collection, or the sequenced sample was deposited in the indicated museum/collection. * This should be provided using the following format 'institution-code:(optional collection-code):specimen-id'. specimen-id is mandatory, collection-code is optional; institution-code is mandatory when collection code is provided. (e.g. "UAM:Mamm:52179"; "AMCC:101706"; "USNM:field series 8798"; "personal:Dan Janzen:99-SRNP-2003"; "99-SRNP-2003")
Biological replicate	Please clarify BioSamples in a same group (e.g. same species, type of cells, genotype or treatment condition) by using Biological replicate identifier. (e.g. "Sample name_1")
Identified by	The name of the taxonomist who identified the specimen. This field reports the name(s) of the specific person(s) who identified the TAXONOMY of the sample. This does not mean the person(s) in the laboratory who identified the submitted sample. (e.g. "Dan Janzen")

Passage history	Number of passages and passage method (e.g. "13"; "Gentle cell dissociation reagent (STEMCELL Technologies, 07174) was used to passage cPP cells as aggregates which were then seeded at a 1:6 split ratio.")
Isolate	Identification or description of the specific individual from which this sample was obtained (e.g. "Patient #152"; "DGGE band PSBAC-13"; "MattSeq37C_S93")
Genotype	observed genotype (e.g. "SB0140"; "Wild Type")
Host subject id	a unique identifier by which each subject can be referred to, de-identified, e.g. #131 (e.g. "#131")
Host tissue sampled	Type of tissue the initial sample was taken from (e.g. "leaves"; "liver")
Host age	Age of host at the time of sampling (e.g. "12 years old"; "2.5 month")
Host sex	Gender or physical sex of the host (e.g. "male"; "female"; "mixed"; "hermaphrodite"; "not determined"; "missing"; "not applicable"; "not collected")
Host disease stage	Stage of disease at the time of sampling (e.g. "Stage 2"; "IIIa"; "de novo AML")
Host health state	Information regarding health state of the individual sampled at the time of sampling (e.g. "death"; "chronic disease"; "recovery")
Host disease outcome	Final outcome of disease, e.g., death, chronic disease, recovery (e.g. "death"; "chronic disease"; "recovery")
Host description	Additional information not included in other defined vocabulary fields (e.g. "Patient received prior antiviral therapy but did not achieve sustained virological response.")
Pathotype	Some bacterial specific pathotypes (e.g. "Escherichia coli -STEC, UPEC"; "Extended-spectrum beta-lactamase (ESBL)")
Serotype	Taxonomy below subspecies; a variety (in bacteria, fungi or virus) usually based on its antigenic properties. e.g. serotype="H1N1" in Influenza A virus CY098518 (e.g. "H1N1"; "B1")
Serovar	Taxonomy below subspecies; a variety (in bacteria, fungi or virus) usually based on its antigenic properties. Same as serovar and serotype. Sometimes used as species identifier in bacteria with shaky taxonomy (e.g. "Leptospira, serovar saopaolo S76607 (65357 in Entrez)"; "Salmonella enterica subsp. enterica serovar Braenderup"; "O157

1.2 Environmental, food or other pathogen

Description : Environmental, food or other pathogen

Mandatory Attributes

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) (e.g. "Candida metapsilosis"; "Hepacivirus C"; "Homo sapiens"; "metagenome")
Collected by	Name(s) of person(s) or institute who collected the sample (e.g. "Korea Research Institute of Bioscience & Biotechnology(KRIBB)"; "Dan Janzen")

Collection date	Date of sampling (YYYY-MM-DD) (e.g. "1989-09-20")
Isolation source	Describes the physical, environmental and/or local geographical source of the biological sample from which the sample was derived (e.g. "rumen isolates from standard Pelleted ration-fed steer #67"; "permanent Antarctic sea ice"; "denitrifying activated sludge from carbon_limited continuous reactor")
Geographic location	Geographical origin of the sample; Use a colon to separate the country or ocean from more detailed information about the location (e.g "Korea: Seoul"; "Korea")
Latitude and longitude	The geographical coordinates of the location where the sample was collected. Specify as degrees latitude and longitude in format "d[d.dddd] N|S d[dd.dddd] W|E", e.g., 38.98 N 77.11 W (e.g. "47.9412 N 28.1201 E")

Optional Attributes

Strain	microbial or eukaryotic strain name, number or designation (e.g. "MG1234"; "K12"; "BALB/c")
Subgroup	Taxonomy below subspecies; sometimes used in viruses to denote subgroups taken from a single isolate (e.g. "Clostridium botulinum Group I")
Subtype	Used as classifier in viruses (e.g. HIV type 1, Group M, Subtype A) (e.g. HIV type 1, Group M, Subtype A)
Culture collection	* Name of source institute and unique culture identifier. * Provide the following information only if the sequenced sample you are submitting was retrieved directly from the indicated culture collection, or the sequenced sample was deposited in the indicated culture collection. * This should be provided using the following format 'institution-code:(optional collection-code):culture-id'. culture-id and institution-code are mandatory. See the list of allowed institutes (ftp://ftp.ncbi.nlm.nih.gov/pub/taxonomy/coll_dump.txt) (e.g. "ATCC:26370")
Specimen voucher	* Identifier for the physical specimen that remains after the sample has been obtained. * Provide the following information only if the sequenced sample you are submitting was retrieved directly from the indicated museum/collection, or the sequenced sample was deposited in the indicated museum/collection. * This should be provided using the following format 'institution-code:(optional collection-code):specimen-id'. specimen-id is mandatory, collection-code is optional; institution-code is mandatory when collection code is provided. (e.g. "UAM:Mamm:52179"; "AMCC:101706"; "USNM:field series 8798"; "personal:Dan Janzen:99-SRNP-2003"; "99-SRNP-2003")
Biological replicate	Please clarify BioSamples in a same group (e.g. same species, type of cells, genotype or treatment condition) by using Biological replicate identifier (e.g. "Sample name_1")
Identified by	The name of the taxonomist who identified the specimen. This field reports the name(s) of the specific person(s) who identified the TAXONOMY of the

	sample. This does not mean the person(s) in the laboratory who identified the submitted sample (e.g. "Dan Janzen").
Passage history	Number of passages and passage method (e.g. "13"; "Gentle cell dissociation reagent (STEMCELL Technologies, 07174) was used to passage cPP cells as aggregates which were then seeded at a 1:6 split ratio.")
Isolate	Identification or description of the specific individual from which this sample was obtained (e.g. "Patient #152"; "DGGE band PSBAC-13"; "MattSeq37C_S93")
Temperature	temperature of the sample at time of sampling (e.g. "27 ℃")
Genotype	observed genotype (e.g. "SB0140"; "Wild Type")
Pathotype	Some bacterial specific pathotypes (example Escherichia coli -STEC, UPEC) (e.g."Escherichia coli -STEC, UPEC"; "Extended-spectrum beta-lactamase (ESBL)")
Serotype	Taxonomy below subspecies; a variety (in bacteria, fungi or virus) usually based on its antigenic properties. e.g. serotype="H1N1" in Influenza A virus CY098518 (e.g. "H1N1"; "B1")
Serovar	Taxonomy below subspecies; a variety (in bacteria, fungi or virus) usually based on its antigenic properties. Same as serovar and serotype. Sometimes used as species identifier in bacteria with shaky taxonomy (e.g. "Leptospira, serovar saopaolo S76607 (65357 in Entrez)"; "Salmonella enterica subsp. enterica serovar Braenderup"; "O157

1.3 Microbe

Description : Use for bacteria or other unicellular microbes when it is not appropriate or advantageous to use MIxS, Pathogen or Virus packages.

Mandatory Attributes

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) (e.g. "Candida metapsilosis"; "Hepacivirus C"; "Homo sapiens"; "metagenome")
Strain	microbial or eukaryotic strain name, number or designation (e.g. "MG1234"; "K12"; "BALB/c")
Collection date	Date of sampling (YYYY-MM-DD) (e.g "1989-09-20")
Isolation source	Describes the physical, environmental and/or local geographical source of the biological sample from which the sample was derived (e.g. "rumen isolates from standard Pelleted ration-fed steer #67"; "permanent Antarctic sea ice"; "denitrifying activated sludge from carbon_limited continuous reactor")
Geographic location	Geographical origin of the sample; Use a colon to separate the country or ocean from more detailed information about the location (e.g "Korea: Seoul"; "Korea")

Optional Attributes

Culture collection	* Name of source institute and unique culture identifier. * Provide the following information only if the sequenced sample you are submitting was retrieved directly from the indicated culture collection, or the sequenced sample was deposited in the indicated culture collection. * This should be provided using the following format 'institution-code:(optional collection-code):culture-id'. culture-id and institution-code are mandatory. See the list of allowed institutes (ftp://ftp.ncbi.nlm.nih.gov/pub/taxonomy/coll_dump.txt) (e.g. "ATCC:26370")
Specimen voucher	* Identifier for the physical specimen that remains after the sample has been obtained. * Provide the following information only if the sequenced sample you are submitting was retrieved directly from the indicated museum/collection, or the sequenced sample was deposited in the indicated museum/collection. * This should be provided using the following format 'institution-code:(optional collection-code):specimen-id'. specimen-id is mandatory, collection-code is optional; institution-code is mandatory when collection code is provided. (e.g. "UAM:Mamm:52179"; "AMCC:101706"; "USNM:field series 8798"; "personal:Dan Janzen:99-SRNP-2003"; "99-SRNP-2003")
Biomaterial provider	* The name and address of the lab or PI, or a culture collection identifier who provided the sample to the submitter. * This field is used to annotate source material in biological collections that do not fit into either the 'Culture collection' or the 'Specimen voucher' field categories: * Physical specimens from zoos, aquaria, stock centers, seed banks, germplasm repositories, or DNA banks. * Provide the following information only if the sequenced sample was retrieved directly from the indicated collection, or the sequenced sample was deposited in the indicated collection. * If the value of the field modifier is the name and address of the lab or PI, "Biomaterial provider" and "Collected by" fields can have the same value. * If the value of the field modifier is a culture collection, the identifier should be provided using the following format 'institution-code:(optional collection-code):specimen-id'. specimen-id is mandatory, collection-code is optional; institution-code is mandatory when collection code is provided. (e.g. "Korea Research Institute of Bioscience & Biotechnology(KRIBB)"; "Dan Janzen"; "CGC:CB3912")
Biological replicate	Please clarify BioSamples in a same group (e.g. same species, type of cells, genotype or treatment condition) by using Biological replicate identifier. (e.g. "Sample name _1")
Collected by	Name(s) of person(s) or institute who collected the sample (e.g. "Korea Research Institute of Bioscience & Biotechnology(KRIBB)"; "Dan Janzen")
Identified by	The name of the taxonomist who identified the specimen. This field reports the name(s) of the specific person(s) who identified the TAXONOMY of the

	sample. This does not mean the person(s) in the laboratory who identified the submitted sample. (e.g. "Dan Janzen")
Passage history	Number of passages and passage method (e.g. "13"; "Gentle cell dissociation reagent (STEMCELL Technologies, 07174) was used to passage cPP cells as aggregates which were then seeded at a 1:6 split ratio.")
Sample size	Amount or size of sample (volume, mass or area) that was collected (e.g. "1 L"; "0.3 kg"; "0.1 m2")
Environment biome	descriptor of the broad ecological context of a sample. Examples include: desert, taiga, deciduous woodland, or coral reef. EnvO terms can be found via the link (https://www.ebi.ac.uk/ols/ontologies/envo) (e.g. "desert"; "taiga"; "deciduous woodland"; "coral reef")
Latitude and longitude	The geographical coordinates of the location where the sample was collected. Specify as degrees latitude and longitude in format "d[d.dddd] N|S d[dd.dddd] W|E", e.g., 38.98 N 77.11 W (e.g. "47.9412 N 28.1201 E")
Altitude	The altitude of the sample is the vertical distance between Earth's surface above Sea Level and the sampled position in the air (e.g. "-256 m"; "330.12 m")
Depth	Depth is defined as the vertical distance below surface, e.g. for sediment or soil samples depth is measured from sediment or soil surface, respectively. Depth can be reported as an interval for subsurface samples (e.g. "15m depth")
Temperature	temperature of the sample at time of sampling (e.g. "27 ℃")
Genotype	observed genotype (e.g. "SB0140"; "Wild Type")
Host	Name of the natural (as opposed to laboratory) host species to the organism from which the sample was obtained (e.g. "Homo sapiens"; "Gallus gallus domesticus")
Host tissue sampled	Type of tissue the initial sample was taken from (e.g. "leaves"; "liver")
Lab host	Scientific name and description of the laboratory host used to propagate the source organism or material from which the sample was obtained, e.g., Escherichia coli DH5a, or Homo sapiens HeLa cells (e.g. "Escherichia coli DH5a"; "Homo sapiens HeLa cell")
Serotype	Taxonomy below subspecies; a variety (in bacteria, fungi or virus) usually based on its antigenic properties. e.g. serotype="H1N1" in Influenza A virus CY098518 (e.g. "H1N1"; "B1")
Serovar	Taxonomy below subspecies; a variety (in bacteria, fungi or virus) usually based on its antigenic properties. Same as serovar and serotype. Sometimes used as species identifier in bacteria with shaky taxonomy (e.g. "Leptospira, serovar saopaolo S76607 (65357 in Entrez)"; "Salmonella enterica subsp. enterica serovar Braenderup"; "O157

1.4 Model organism or animal sample

Description : Use for multicellular samples or cell lines derived from common laboratory model organisms, e.g., mouse, rat, Drosophila, worm, fish, frog, or large mammals including zoo and farm animals.

Mandatory Attributes

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) (e.g. "Candida metapsilosis"; "Hepacivirus C"; "Homo sapiens"; "metagenome")
Tissue	Type of tissue the sample was taken from (e.g "leaves"; "liver")
Biomaterial provider	* The name and address of the lab or PI, or a culture collection identifier who provided the sample to the submitter. * This field is used to annotate source material in biological collections that do not fit into either the 'Culture collection' or the 'Specimen voucher' field categories: * Physical specimens from zoos, aquaria, stock centers, seed banks, germplasm repositories, or DNA banks. * Provide the following information only if the sequenced sample was retrieved directly from the indicated collection, or the sequenced sample was deposited in the indicated collection. * If the value of the field modifier is the name and address of the lab or PI, "Biomaterial provider" and "Collected by" fields can have the same value. * If the value of the field modifier is a culture collection, the identifier should be provided using the following format 'institution-code:(optional collection-code):specimen-id'. specimen-id is mandatory, collection-code is optional; institution-code is mandatory when collection code is provided. (e.g. "Korea Research Institute of Bioscience & Biotechnology(KRIBB)"; "Dan Janzen"; "CGC:CB3912")
Sex	physical sex of sampled organism (e.g. "male"; "female"; "mixed"; "hermaphrodite"; "not determined"; "missing"; "not applicable"; "not collected")

Optional Attributes

Strain	microbial or eukaryotic strain name, number or designation (e.g. "MG1234"; "K12"; "BALB/c")
Breed	breed name -chiefly used in domesticated animals or plants (e.g "mixed"; "Beagle")
Cell line	Name of the cell line (e.g "HepG2 cell")
Cell type	Type of cell of the sample or from which the sample was obtained (e.g "T cell")
Cell subtype	The subtype of cell (e.g "CD4+ T cell")
Culture collection	* Name of source institute and unique culture identifier. * Provide the following information only if the sequenced sample you are submitting was retrieved directly from the indicated culture collection, or the sequenced sample was deposited in the indicated culture collection. * This should be provided using the following format 'institution-code:(optional collection-code):culture-id'. culture-id and institution-code are mandatory. See the list of allowed institutes

	(ftp://ftp.ncbi.nlm.nih.gov/pub/taxonomy/coll_dump.txt) (e.g. "ATCC:26370")
Specimen voucher	* Identifier for the physical specimen that remains after the sample has been obtained. * Provide the following information only if the sequence you are submitting was obtained from a sample you retrieved directly from the indicated museum/collection, or the sequence was obtained from a sample that you deposited in the indicated museum/collection. * This should be provided using the following format 'institution-code:(optional collection-code):specimen-id'. specimen-id is mandatory, collection-code is optional; institution-code is mandatory when collection code is provided. (e.g. "UAM:Mamm:52179"; "AMCC:101706"; "USNM:field series 8798"; "personal:Dan Janzen:99-SRNP-2003"; "99-SRNP-2003")
Study book number	Study book number of sample
Biological replicate	Please clarify BioSamples in a same group (e.g. same species, type of cells, genotype or treatment condition) by using Biological replicate identifier. (e.g. "Sample name _1")
Collected by	Name(s) of person(s) or institute who collected the sample (e.g. "Korea Research Institute of Bioscience & Biotechnology(KRIBB)"; "Dan Janzen")
Growth protocol	The protocol of growth (e.g. "ES cell–derived NS cells were routinely generated by re-plating d 7 adherent neural differentiation cultures (typically 2–3 × 106 cells into a T75 flask) on uncoated plastic in NS-A medium (Euroclone, Milan, Italy) supplemented with modified N2 and 10 ng/ml of both EGF and FGF-2 (NS expansion medium).")
Storage conditions	Explain how and for how long the sample was stored before DNA extraction
Treatment	Treatment of sample (e.g. "Adalimumab treatment")
Isolation source	Describes the physical, environmental and/or local geographical source of the biological sample from which the sample was derived (e.g. "rumen isolates from standard Pelleted ration-fed steer #67"; "permanent Antarctic sea ice"; "denitrifying activated sludge from carbon_limited continuous reactor")
Geographic location	Geographical origin of the sample; Use a colon to separate the country or ocean from more detailed information about the location (e.g "Korea: Seoul"; "Korea")
Latitude and longitude	The geographical coordinates of the location where the sample was collected. Specify as degrees latitude and longitude in format "d[d.dddd] N|S d[dd.dddd] W|E", e.g., 38.98 N 77.11 W (e.g. "47.9412 N 28.1201 E")
Genotype	observed genotype (e.g. "SB0140"; "Wild Type")
Age	age at the time of sampling; relevant scale depends on species and study (e.g. "12 years old"; "2.5 month")
Birth date	The date of birth (e.g. "1989-09-20")
Birth location	The location of birth (e.g. "Seoul, Korea")
Breeding history	The history of breeding

Breeding method	The method of breeding (e.g. "Clinical veterinary/Client-owned dog")
Death date	The date of death (e.g. "1989-09-20")
Development stage	Developmental stage at the time of sampling (e.g. "adult"; "Dairy cows second seasonal lactation")
Disease	List of diseases diagnosed; can include multiple diagnoses (e.g. "Rheumatoid arthritis"; "Lung cancer")
Disease stage	Stage of disease at the time of sampling (e.g. "Stage 2"; "IIIa"; "de novo AML")
Health state	Health or disease status of sample at time of collection (e.g. "death"; "chronic disease"; "recovery")
Phenotype	Phenotype of sampled organism (e.g. "Leaf senescence"; "decreased tolerance to Al stress")

1.5 Human sample

Description : WARNING: Only use for human samples or cell lines that have no privacy concerns. For all studies involving human subjects, it is the submitter's responsibility to ensure that the information supplied protects participant privacy in accordance with all applicable laws, regulations and institutional policies. Make sure to remove any direct personal identifiers from your submission. If there are patient privacy concerns regarding making data fully public, please submit samples and data to NCBI's dbGaP database. dbGaP has controlled access mechanisms and is an appropriate resource for hosting sensitive patient data. For samples isolated from humans use the Pathogen, Microbe or appropriate MIxS package.

Mandatory Attributes

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) (e.g. "Candida metapsilosis"; "Hepacivirus C"; "Homo sapiens"; "metagenome")
Tissue	Type of tissue the sample was taken from (e.g "leaves"; "liver")
Biomaterial provider	* The name and address of the lab or PI, or a culture collection identifier who provided the sample to the submitter. * This field is used to annotate source material in biological collections that do not fit into either the 'Culture collection' or the 'Specimen voucher' field categories: * Physical specimens from zoos, aquaria, stock centers, seed banks, germplasm repositories, or DNA banks. * Provide the following information only if the sequenced sample was retrieved directly from the indicated collection, or the sequenced sample was deposited in the indicated collection. * If the value of the field modifier is the name and address of the lab or PI, "Biomaterial provider" and "Collected by" fields can have the same value. * If the value of the field modifier is a culture collection, the identifier should be provided using the following format 'institution-code:(optional

	collection-code):specimen-id'. specimen-id is mandatory, collection-code is optional; institution-code is mandatory when collection code is provided. (e.g. "Korea Research Institute of Bioscience & Biotechnology(KRIBB)"; "Dan Janzen"; "CGC:CB3912")
Isolate	Identification or description of the specific individual from which this sample was obtained (e.g. "Patient #152"; "DGGE band PSBAC-13"; "MattSeq37C_S93")
Sex	physical sex of sampled organism (e.g. "male"; "female"; "mixed"; "hermaphrodite"; "not determined"; "missing"; "not applicable"; "not collected")

Optional Attributes

Type	Sample type, such as cell culture, mixed culture, tissue sample, whole organism, single cell, and metagenomics assembly
Cell line	Name of the cell line (e.g "HepG2 cell")
Cell type	Type of cell of the sample or from which the sample was obtained (e.g "T cell")
Cell subtype	The subtype of cell (e.g "CD4+ T cell")
Culture collection	* Name of source institute and unique culture identifier. * Provide the following information only if the sequenced sample you are submitting was retrieved directly from the indicated culture collection, or the sequenced sample was deposited in the indicated culture collection. * This should be provided using the following format 'institution-code:(optional collection-code):culture-id'. culture-id and institution-code are mandatory. See the list of allowed institutes (ftp://ftp.ncbi.nlm.nih.gov/pub/taxonomy/coll_dump.txt) (e.g. "ATCC:26370")
Biological replicate	Please clarify BioSamples in a same group (e.g. same species, type of cells, genotype or treatment condition) by using Biological replicate identifier. (e.g. "Sample name_1")
Treatment	Treatment of sample (e.g. "Adalimumab treatment")
Karyotype	Karyotype of sampled organism. karyotype is the number and appearance of chromosomes in the nucleus of a eukaryotic cell. (e.g. "copy neutral loss of heterozygosity"; "47XY+21_1"; "haploid")
Age	age at the time of sampling; relevant scale depends on species and study (e.g. "12 years old"; "2.5 month")
Development stage	Developmental stage at the time of sampling (e.g. "adult"; "Dairy cows second seasonal lactation")
Disease	List of diseases diagnosed; can include multiple diagnoses (e.g. "Rheumatoid arthritis"; "Lung cancer")
Disease stage	Stage of disease at the time of sampling (e.g. "Stage 2"; "IIIa"; "de novo AML")
Health state	Health or disease status of sample at time of collection (e.g. "death"; "chronic disease"; "recovery")
Phenotype	Phenotype of sampled organism (e.g. "Leaf senescence"; "decreased tolerance to Al stress")

Population	Population is a summation of all the organisms of the same group or species, which live in a particular geographical area. For human: ; for plants: filial generation, number of progeny, genetic structure (e.g. "F2 population")
Race	Race of sample. Race refers to a person's physical characteristics, such as bone structure and skin, hair, or eye color. (e.g. "Hair color: black"; "Eye color: black")
Ethnicity	Ethnicity of the subject. Ethnicity refers to cultural factors, including nationality, regional culture, ancestry, and language. (e.g. "Korean"; "Chinese Han"; "Asian"; "Caucasian")

1.6 Plant sample

Description : Use for any plant sample or cell line.

Mandatory Attributes

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	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. (e.g. "Candida metapsilosis"; "Hepacivirus C"; "Homo sapiens"; "metagenome")
Cultivar	Cultivar name: cultivated variety of plant from which the sample was obtained
Tissue	Type of tissue the sample was taken from (e.g "leaves"; "liver")
Biomaterial provider	* The name and address of the lab or PI, or a culture collection identifier who provided the sample to the submitter. * This field is used to annotate source material in biological collections that do not fit into either the 'Culture collection' or the 'Specimen voucher' field categories: * Physical specimens from zoos, aquaria, stock centers, seed banks, germplasm repositories, or DNA banks. * Provide the following information only if the sequenced sample was retrieved directly from the indicated collection, or the sequenced sample was deposited in the indicated collection. * If the value of the field modifier is the name and address of the lab or PI, "Biomaterial provider" and "Collected by" fields can have the same value. * If the value of the field modifier is a culture collection, the identifier should be provided using the following format 'institution-code:(optional collection-code):specimen-id'. specimen-id is mandatory, collection-code is optional; institution-code is mandatory when collection code is provided. (e.g. "Korea Research Institute of Bioscience & Biotechnology(KRIBB)"; "Dan Janzen"; "CGC:CB3912")

Sex	physical sex of sampled organism (e.g. "male"; "female"; "mixed"; "hermaphrodite"; "not determined"; "missing"; "not applicable"; "not collected")

Optional Attributes

Type	Sample type, such as cell culture, mixed culture, tissue sample, whole organism, single cell, and metagenomics assembly
Cell line	Name of the cell line (e.g "HepG2 cell")
Cell type	Type of cell of the sample or from which the sample was obtained (e.g "T cell")
Culture collection	* Name of source institute and unique culture identifier. * Provide the following information only if the sequenced sample you are submitting was retrieved directly from the indicated culture collection, or the sequenced sample was deposited in the indicated culture collection. * This should be provided using the following format 'institution-code:(optional collection-code):culture-id'. culture-id and institution-code are mandatory. See the list of allowed institutes (ftp://ftp.ncbi.nlm.nih.gov/pub/taxonomy/coll_dump.txt) (e.g. "ATCC:26370")
Specimen voucher	* Identifier for the physical specimen that remains after the sample has been obtained. * Provide the following information only if the sequence you are submitting was obtained from a sample you retrieved directly from the indicated museum/collection, or the sequence was obtained from a sample that you deposited in the indicated museum/collection. * This should be provided using the following format 'institution-code:(optional collection-code):specimen-id'. specimen-id is mandatory, collection-code is optional; institution-code is mandatory when collection code is provided. (e.g. "UAM:Mamm:52179"; "AMCC:101706"; "USNM:field series 8798"; "personal:Dan Janzen:99-SRNP-2003"; "99-SRNP-2003")
Biological replicate	Please clarify BioSamples in a same group (e.g. same species, type of cells, genotype or treatment condition) by using Biological replicate identifier. (e.g. "Sample name_1")
Collected by	Name(s) of person(s) or institute who collected the sample ("Korea Research Institute of Bioscience & Biotechnology(KRIBB)"; "Dan Janzen")
Collection date	Date of sampling (YYYY-MM-DD) (e.g "1989-09-20")
Growth protocol	The protocol of growth (e.g. "ES cell–derived NS cells were routinely generated by re-plating d 7 adherent neural differentiation cultures (typically 2–3 × 106 cells into a T75 flask) on uncoated plastic in NS-A medium (Euroclone, Milan, Italy) supplemented with modified N2 and 10 ng/ml of both EGF and FGF-2 (NS expansion medium).")
Treatment	Treatment of sample (e.g. "Adalimumab treatment")
Isolation source	Describes the physical, environmental and/or local geographical source of the biological sample from which the sample was derived (e.g. "rumen isolates from standard Pelleted ration-fed steer #67"; "permanent

	Antarctic sea ice"; "denitrifying activated sludge from carbon_limited continuous reactor")
Latitude and longitude	The geographical coordinates of the location where the sample was collected. Specify as degrees latitude and longitude in format "d[d.dddd] N|S d[dd.dddd] W|E", e.g., 38.98 N 77.11 W (e.g. "47.9412 N 28.1201 E")
Temperature	temperature of the sample at time of sampling (e.g. "27 ℃")
Genotype	observed genotype (e.g. "SB0140"; "Wild Type")
Age	age at the time of sampling; relevant scale depends on species and study (e.g. "12 years old"; "2.5 month")
Development stage	Developmental stage at the time of sampling (e.g. "adult"; "Dairy cows second seasonal lactation")
Disease	List of diseases diagnosed; can include multiple diagnoses (e.g. "Rheumatoid arthritis"; "Lung cancer")
Disease stage	Stage of disease at the time of sampling (e.g. "Stage 2"; "IIIa"; "de novo AML")
Phenotype	Phenotype of sampled organism (e.g. "Leaf senescence"; "decreased tolerance to Al stress")
Height or length	Measurement of height or length (e.g. "Height: 135 cm")
Population	Population is a summation of all the organisms of the same group or species, which live in a particular geographical area. For human: ; for plants: filial generation, number of progeny, genetic structure (e.g. "F2 population")

1.7 Virus sample

Description : Use for all virus samples not directly associated with disease. Viral pathogens should be submitted using the Pathogen: Clinical or host-associated pathogen package.

Mandatory Attributes

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) (e.g. "Candida metapsilosis"; "Hepacivirus C"; "Homo sapiens"; "metagenome")
Collection date	Date of sampling (YYYY-MM-DD) (e.g. "1989-09-20")
Isolation source	Describes the physical, environmental and/or local geographical source of the biological sample from which the sample was derived (e.g. "rumen isolates from standard Pelleted ration-fed steer #67"; "permanent Antarctic sea ice"; "denitrifying activated sludge from carbon_limited continuous reactor")
Isolate	Identification or description of the specific individual from which this sample was obtained (e.g. "Patient #152"; "DGGE band PSBAC-13"; "MattSeq37C_S93")

Geographic location	Geographical origin of the sample; Use a colon to separate the country or ocean from more detailed information about the location (e.g "Korea: Seoul"; "Korea")
Host	Name of the natural (as opposed to laboratory) host species to the organism from which the sample was obtained (e.g. "Homo sapiens"; "Gallus gallus domesticus")

Optional Attributes

Strain	microbial or eukaryotic strain name, number or designation 칭(e.g. "MG1234"; "K12"; "BALB/c")
Subgroup	Taxonomy below subspecies; sometimes used in viruses to denote subgroups taken from a single isolate (e.g. "Clostridium botulinum Group I")
Subtype	Used as classifier in viruses (e.g. HIV type 1, Group M, Subtype A)
Culture collection	* Name of source institute and unique culture identifier. * Provide the following information only if the sequenced sample you are submitting was retrieved directly from the indicated culture collection, or the sequenced sample was deposited in the indicated culture collection. * This should be provided using the following format 'institution-code:(optional collection-code):culture-id'. culture-id and institution-code are mandatory. See the list of allowed institutes (ftp://ftp.ncbi.nlm.nih.gov/pub/taxonomy/coll_dump.txt) (e.g. "ATCC:26370")
Specimen voucher	* Identifier for the physical specimen that remains after the sample has been obtained. * Provide the following information only if the sequence you are submitting was obtained from a sample you retrieved directly from the indicated museum/collection, or the sequence was obtained from a sample that you deposited in the indicated museum/collection. * This should be provided using the following format 'institution-code:(optional collection-code):specimen-id'. specimen-id is mandatory, collection-code is optional; institution-code is mandatory when collection code is provided. (e.g. "UAM:Mamm:52179"; "AMCC:101706"; "USNM:field series 8798"; "personal:Dan Janzen:99-SRNP-2003"; "99-SRNP-2003")
Biomaterial provider	* The name and address of the lab or PI, or a culture collection identifier who provided the sample to the submitter. * This field is used to annotate source material in biological collections that do not fit into either the 'Culture collection' or the 'Specimen voucher' field categories: * Physical specimens from zoos, aquaria, stock centers, seed banks, germplasm repositories, or DNA banks. * Provide the following information only if the sequenced sample was retrieved directly from the indicated collection, or the sequenced sample was deposited in the indicated collection. * If the value of the field modifier is the name and address of the lab or PI, "Biomaterial provider" and "Collected by" fields can have the same value.

	* If the value of the field modifier is a culture collection, the identifier should be provided using the following format 'institution-code:(optional collection-code):specimen-id'. specimen-id is mandatory, collection-code is optional; institution-code is mandatory when collection code is provided. (e.g. "Korea Research Institute of Bioscience & Biotechnology(KRIBB)"; "Dan Janzen"; "CGC:CB3912")
Biological replicate	Please clarify BioSamples in a same group (e.g. same species, type of cells, genotype or treatment condition) by using Biological replicate identifier. (e.g. "Sample name_1")
Collected by	Name(s) of person(s) or institute who collected the sample ("Korea Research Institute of Bioscience & Biotechnology(KRIBB)"; "Dan Janzen")
Identified by	The name of the taxonomist who identified the specimen. This field reports the name(s) of the specific person(s) who identified the TAXONOMY of the sample. This does not mean the person(s) in the laboratory who identified the submitted sample. (e.g. "Dan Janzen")
Passage history	Number of passages and passage method (e.g. "13"; "Gentle cell dissociation reagent (STEMCELL Technologies, 07174) was used to passage cPP cells as aggregates which were then seeded at a 1:6 split ratio.")
Sample size	Amount or size of sample (volume, mass or area) that was collected 기(e.g. "1 L"; "0.3 kg"; "0.1 m2")
Environment biome	descriptor of the broad ecological context of a sample. Examples include: desert, taiga, deciduous woodland, or coral reef. EnvO terms can be found via the link (https://www.ebi.ac.uk/ols/ontologies/envo) (e.g. "desert"; "taiga"; "deciduous woodland"; "coral reef")
Latitude and longitude	The geographical coordinates of the location where the sample was collected. Specify as degrees latitude and longitude in format "d[d.dddd] N|S d[dd.dddd] W|E", e.g., 38.98 N 77.11 W (e.g. "47.9412 N 28.1201 E")
Altitude	The altitude of the sample is the vertical distance between Earth's surface above Sea Level and the sampled position in the air (e.g. "-256 m"; "330.12 m")
Depth	Depth is defined as the vertical distance below surface, e.g. for sediment or soil samples depth is measured from sediment or soil surface, respectively. Depth can be reported as an interval for subsurface samples (e.g. "15m depth")
Temperature	temperature of the sample at time of sampling (e.g. "27 ℃")
Genotype	observed genotype (e.g. "SB0140"; "Wild Type")
Host tissue sampled	Type of tissue the initial sample was taken from ("leaves"; "liver")
Disease	List of diseases diagnosed; can include multiple diagnoses (e.g. "Rheumatoid arthritis"; "Lung cancer")
Lab host	Scientific name and description of the laboratory host used to propagate the source organism or material from which the sample was obtained, e.g., Escherichia coli DH5a, or Homo sapiens HeLa cells (e.g. "Escherichia coli DH5a"; "Homo sapiens HeLa cell")
Serotype	Taxonomy below subspecies; a variety (in bacteria, fungi or virus) usually based on its antigenic properties. e.g. serotype="H1N1" in Influenza A virus CY098518 (e.g. "H1N1"; "B1")

2. Submit KAD (Experiment)

Description : Write experiment data related to BioSample according to the format below.

Mandatory Attributes

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"")
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) (e.g "Library2_AHX1609"; "sample name_Strategy" or "sample name_Source")
Platform	part of Instrument model of Sequencing Platform *table(1)
Instrument model	Sequencing platform -> Instrument model select *table(1)
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: - the protocols used to extract and prepare the material to be sequenced - the library construction protocol - name of the library preparation kit
Strategy	Sequencing technique intended for this library. *table(2)
Source	The library source specifies the type of source material that is being sequenced. *table (3)
Selection	Whether any method was used to select and/or enrich the material being sequenced. *table (4)
Release date selection	Select “Release immediately following curation (recommended)”or “Release on specified date”
Release date	If you select “Release date selection”in “Release on specified date”, must enter a public date. (form: YYYY-MM-DD, ex, 2018-12-22)
Read 1	File name
Read 2	File name

Optional Attributes

General description (영문)	Free-form description of the methods, including a brief ‘Materials and Methods’ section, that sere not described in the other fields.
Library	The library descriptor specifies the origin of the material being sequenced and any treatments that the material might have

	undergone that affect the sequencing result. This specification is needed even if the platform does not require a library construction step per se. This field may include: - adapter sequence(s) that can be contained in the sequencing results - RNA integrity number (RIN) of the sample, if the source of the sample is transcription product
Fragment/Paired read	Library Layout specifies whether to expect Single, Paired-end, or Other configuration of reads. In the case of paired reads, information about the relative distance and orientation is specified. (e.g “Single-end”; “Paired-end”; “Other configuration of reads")
Nominal standard deviation	Standard deviation of insert size (typically ~10% of Nominal Size)(0nly Paired read) (e.g "25")
Technical replicate	When libraries are indeed identical (same combination of library + strategy + layout + instrument model), please clarify each library (Run) by using technical replicate identifier. (e.g., "technical_rep_2")
Insert size	[For paired-end (Paired read 만 해당)] Average fragment size for Paired reads. Insert size can be a distance between a pair of adapters and estimated by using bioinformatics tools such as SAMtools after read alignment. You need to fill in either ‘Insert size’ or ‘Nominal size’ identifier. (e.g "250")
Nominal size	[For paired-end (Paired read 만 해당)] Size of the insert for Paired reads. The nominal size is the expected size of the insert. The insert being the fragment sequenced, as chosen from size fractionation (e.g., cutting out a band from an agarose gel). If nominal length is 500bp, put down "500" as the value. No decimals or ranges (e.g., 100-200) allowed, and it cannot be zero. This information guides sequence aligner algorithms to place the two mates of a pair of reads on the genome sequences separated by a reasonable distance. Therefore, the nominal length value does not need to be absolutely precise, but also should not be an order of magnitude off. You need to fill in either ‘Insert size’ or ‘Nominal size’ identifier. (e.g "250")

3. table 1

• Table 1 : Sequencing platform & Instrument model

Platforms	***Instrument model for each Platform***									
_LS454	**_LS454**	**ILLUMINA**	**HELICOS**	**ABI_SOLID**	**COMPLETE_GENOMICS**	**PACBIO_SMRT**	**ION_TORRENT**	**CAPILLARY**	**OXFORD_NANOPORE**	**BGISEQ**
ABI_SOLID	454 GS	HiSeq X Five	Helicos HeliScope	AB 5500 Geneti	Complete	PacBio RS	Ion Torre	AB 310 Genet	GridION	BGISEQ-500

			c Analyzer	Genomics		nt PGM	ic Analyzer	
BGISEQ	454 GS 20	HiSeq X Ten	AB 5500xl Genetic Analyzer		PacBio RS II	Ion Torrent Proton	AB 3130 Genetic Analyzer	MinION
CAPILLARY	454 GS FLX	Illumina Genome Analyzer	AB 5500x-Wl Genetic Analyzer		PacBio Sequel	Ion Torrent S5 XL	AB 3130xL Genetic Analyzer	PromethION
COMPLETE_GENOMICS	454 GS FLX+	Illumina Genome Analyzer II	AB SOLiD 3 Plus System		PacBio Sequel II	Ion Torrent S5	AB 3500 Genetic Analyzer	
HELICOS	454 GS FLX Titanium	Illumina Genome Analyzer IIx	AB SOLiD 4 System				AB 3500xL Genetic Analyzer	
ILLUMINA	454 GS Junior	Illumina HiScan SQ	AB SOLiD 4hq System				AB 3730 Genetic Analyzer	
ION_TORRENT		Illumina HiSeq 1000	AB SOLiD PI System				AB 3730xL Genetic Analyzer	
OXFORD_NANOPORE		Illumina HiSeq 1500	AB SOLiD System					

PACBIO_SMRT	Illumina HiSeq 2000	AB SOLiD System 2.0
	Illumina HiSeq 2500	AB SOLiD System 3.0
	Illumina HiSeq 3000	
	Illumina HiSeq 4000	
	Illumina iSeq 100	
	Illumina NovaSeq 6000	
	Illumina MiniSeq	
	Illumina MiSeq	
	NextSeq 500	
	NextSeq 550	

4. table 2

• Table 2 : Strategy

type	*Description*
WGA	Whole genome amplification. Random sequencing of the whole genome following non-PCR amplification
WGS	Whole genome sequencing. Random sequencing of the whole genome
WXS	Whole exome sequencing. Random sequencing of exonic regions selected from the genome
RNA-Seq	Random sequencing of whole transcriptome

smRNA-Seq	MicroRNA and other small non-coding RNA sequencing
WCS	Random sequencing of a whole chromosome or other replicon isolated from a genome
CLONE	Genomic clone based (hierarchical) sequencing
POOLCLONE	Shotgun of pooled clones (usually BACs and Fosmids)
AMPLICON	Sequencing of overlapping or distinct PCR or RT-PCR products
CLONEEND	Clone end (5', 3', or both) sequencing
FINISHING	Sequencing intended to finish (close) gaps in existing coverage
ChIP-Seq	Direct sequencing of chromatin immunoprecipitates
MNase-Seq	Direct sequencing following MNase digestion
DNase-Hypersensitivity	Sequencing of hypersensitive sites, or segments of open chromatin that are more readily cleaved by DNaseI
Bisulfite-Seq	Sequencing following treatment of DNA with bisulfite to convert cytosine residues to uracil depending on methylation status
Tn-Seq	Gene fitness determination through transposon seeding. Sequencing from transposon insertion sites
EST	Single pass sequencing of cDNA templates
FL-cDNA	Full-length sequencing of cDNA templates
CTS	Concatenated Tag Sequencing
MRE-Seq	Methylation-Sensitive Restriction Enzyme Sequencing strategy
MeDIP-Seq	Methylated DNA Immunoprecipitation Sequencing strategy
MBD-Seq	Direct sequencing of methylated fractions sequencing strategy
Synthetic-Long-Read	Binning and barcoding of large DNA fragments to facilitate assembly of the fragment
ATAC-Seq	Assay for Transposase-Accessible Chromatin (ATAC) strategy is used to study genome-wide chromatin accessibility. Alternative method to DNase-Seq that uses an engineered Tn5 transposase to cleave DNA and to integrate primer DNA sequences into the cleaved genomic DNA
ChIA-PET	Direct sequencing of proximity-ligated chromatin immune-precipitates
FAIRE-Seq	Formaldehyde Assisted Isolation of Regulatory Elements
Hi-C	Chromosome Conformation Capture technique where a biotin-labeled nucleotide is incorporated at the ligation junction, enabling selective purification of chimeric DNA ligation junctions followed by deep sequencing
ncRNA-Seq	Capture of other non-coding RNA types, including post-translation modification types such as snRNA (small nuclear RNA) or snoRNA (small nucleolar RNA), or expression regulation types such as siRNA (small interfering RNA) or piRNA/piwiRNA (piwi-interacting RNA).
RAD-Seq	Restriction Site Associated DNA Sequence

RIP-Seq	Direct sequencing of RNA immunoprecipitates (includes CLIP-Seq, HITS-CLIP and PAR-CLIP)
SELEX	Systematic Evolution of Ligands by EXponential enrichment
ssRNA-Seq	strand-specific RNA sequencing
Targeted-Capture	Targeted-Capture sequencing
Tethered Chromatin Conformation Capture	Tethered Chromatin Conformation Capture sequencing
OTHER	Library strategy not listed (please include additional info in the "Description" field of Experiment section)

5. table 3

• Table 3 : Source

type	*Description*
GENOMIC	Genomic DNA (includes PCR products from genomic DNA)
EPIGENOMIC	Genomic DNA used for studying epigenetic changes in a cell that affect gene expression without altering the DNA sequence
TRANSCRIPTOMIC	Transcription products or non-genomic DNA (EST, cDNA, RT-PCR, screened libraries)
METATRANSCRIPTOMIC	Transcription products from community targets
METAGENOMIC	Mixed material from metagenome
SYNTHETIC	Synthetic DNA
VIRAL RNA	Viral RNA
OTHER	Other, unspecified, or unknown library source material (please include additional info in the "Description" of Experiment design)

6. table 4

• Table 4 : Selection

type	*Description*
unspecified	Library enrichment, screening, or selection is not specified (please include additional info in the "Description" of Experiment design)
RANDOM	Random selection by shearing or other method
PCR	Source material was selected by designed primers
RANDOM PCR	Source material was selected by randomly generated primers
RT-PCR	Source material was selected by reverse transcription PCR
HMPR	Hypo-methylated partial restriction digest
MF	Methyl Filtrated
CF-S	Cot-filtered single/low-copy genomic DNA
CF-M	Cot-filtered moderately repetitive genomic DNA

CF-H	Cot-filtered highly repetitive genomic DNA
CF-T	Cot-filtered theoretical single-copy genomic DNA
MDA	Multiple displacement amplification
MSLL	Methylation Spanning Linking Library
cDNA	complementary DNA
ChIP	Chromatin immunoprecipitation
MNase	Micrococcal Nuclease (MNase) digestion
DNAse	Deoxyribonuclease (DNase) digestion
Hybrid Selection	Selection by hybridization in array or solution
Reduced Representation	Reproducible genomic subsets, often generated by restriction fragment size selection, containing a manageable number of loci to facilitate re-sampling
Restriction Digest	DNA fractionation using restriction enzymes
5-methylcytidine antibody	Selection of methylated DNA fragments using an antibody raised against 5-methylcytosine or 5-methylcytidine (m5C)
MBD2 protein methyl-CpG binding domain	Enrichment by methyl-CpG binding domain
CAGE	Cap-analysis gene expression
RACE	Rapid Amplification of cDNA Ends
size fractionation	Physical selection of size appropriate targets
Padlock probes capture method	Circularized oligonucleotide probes
Poly-A	polyA enriched RNA-Seq
other	Other library enrichment, screening, or selection process (please include additional info in the "Description" of Experiment design)