SRA Submission Quick Start Guide

National Center for Biotechnology Information (NCBI)
National Library of Medicine
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The Sequence Read Archive (SRA) stores raw sequencing data from the next generation of sequencing platforms including Roche 454 GS System®, Illumina Genome Analyzer®, Life Technologies AB SOLiD System® , Helicos Biosciences Heliscope®, Complete Genomics®, and Pacific Biosciences SMRT®. This Guide is intended for new and low volume submitters to the SRA.

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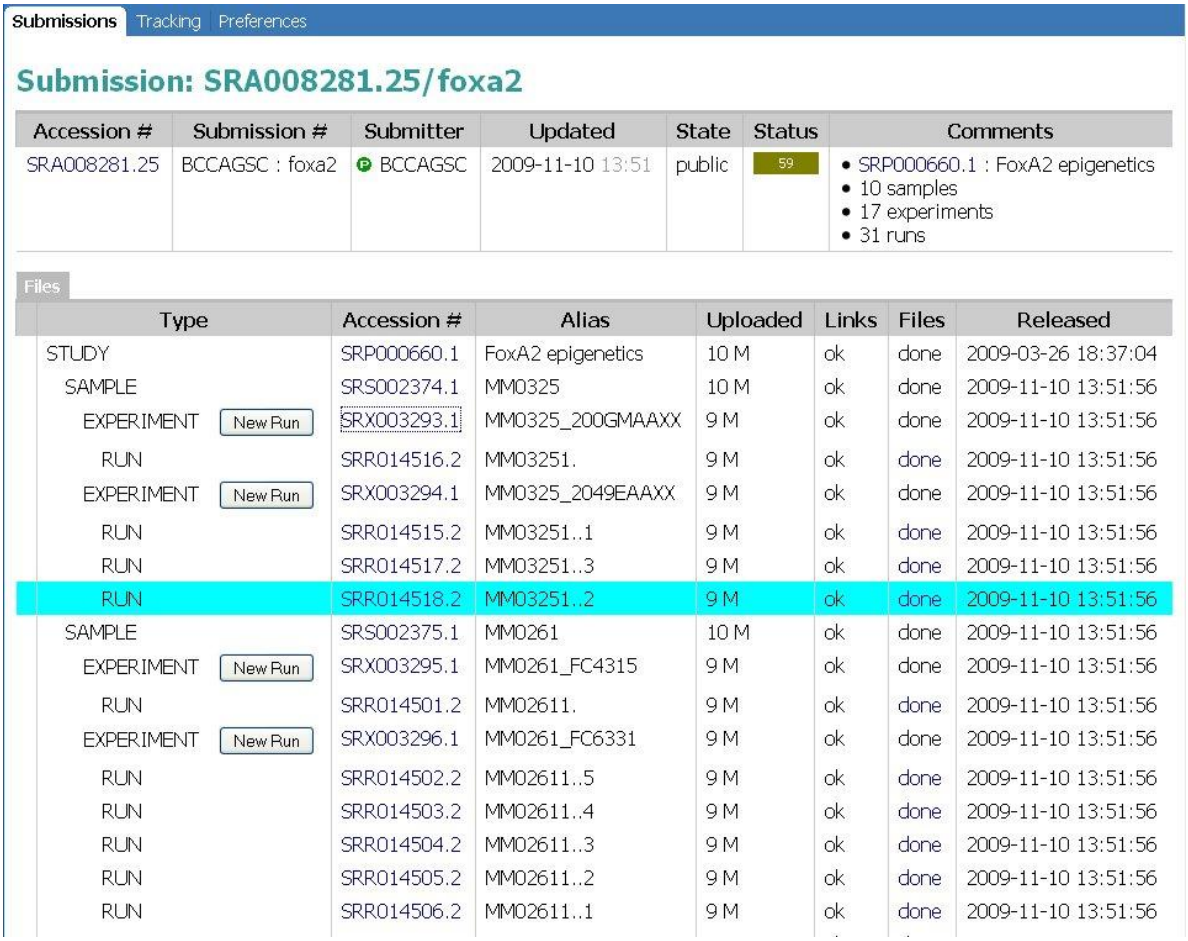

Submissions | Tracking | Preferences

Submission: SRA008281.25/foxa2

Accession #	Submission #	Submitter	Updated	State	Status	Comments
SRA008281.25	BCCAGSC : foxa2	BCCAGSC	2009-11-10 13:51	public	59	• SRP000660.1 : FoxA2 epigenetics • 10 samples • 17 experiments • 31 runs

Files

Type	Accession #	Alias	Uploaded	Links	Files	Released
STUDY	SRP000660.1	FoxA2 epigenetics	10 M	ok	done	2009-03-26 18:37:04
SAMPLE	SRS002374.1	MM0325	10 M	ok	done	2009-11-10 13:51:56
EXPERIMENT New Run	SRX003293.1	MM0325_200GMAAXX	9 M	ok	done	2009-11-10 13:51:56
RUN	SRR014516.2	MM03251.	9 M	ok	done	2009-11-10 13:51:56
EXPERIMENT New Run	SRX003294.1	MM0325_2049EAAXX	9 M	ok	done	2009-11-10 13:51:56
RUN	SRR014515.2	MM03251..1	9 M	ok	done	2009-11-10 13:51:56
RUN	SRR014517.2	MM03251..3	9 M	ok	done	2009-11-10 13:51:56
RUN	SRR014518.2	MM03251..2	9 M	ok	done	2009-11-10 13:51:56
SAMPLE	SRS002375.1	MM0261	10 M	ok	done	2009-11-10 13:51:56
EXPERIMENT New Run	SRX003295.1	MM0261_FC4315	9 M	ok	done	2009-11-10 13:51:56
RUN	SRR014501.2	MM02611.	9 M	ok	done	2009-11-10 13:51:56
EXPERIMENT New Run	SRX003296.1	MM0261_FC6331	9 M	ok	done	2009-11-10 13:51:56
RUN	SRR014502.2	MM02611..5	9 M	ok	done	2009-11-10 13:51:56
RUN	SRR014503.2	MM02611..4	9 M	ok	done	2009-11-10 13:51:56
RUN	SRR014504.2	MM02611..3	9 M	ok	done	2009-11-10 13:51:56
RUN	SRR014505.2	MM02611..2	9 M	ok	done	2009-11-10 13:51:56
RUN	SRR014506.2	MM02611..1	9 M	ok	done	2009-11-10 13:51:56

Figure 1 Example of a finished SRA Submission viewed from the Interactive Tool.

2 Login

From the SRA Homepage:

Click the ***Submit*** tab.
Then click ***NCBI PDA*** (If you do not have a PDA account already, one will need to be created.)

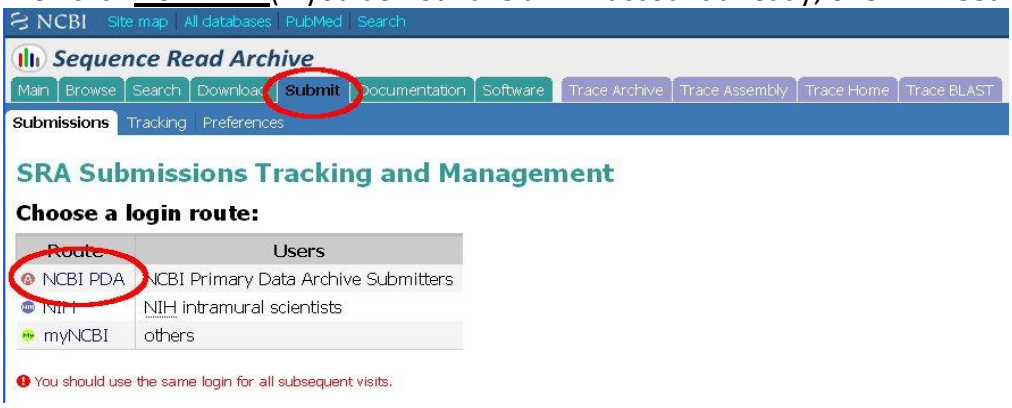

Figure 2 From the 'Submit' tab, click NCBI PDA to login for Submission.

3 Creating a New Submission

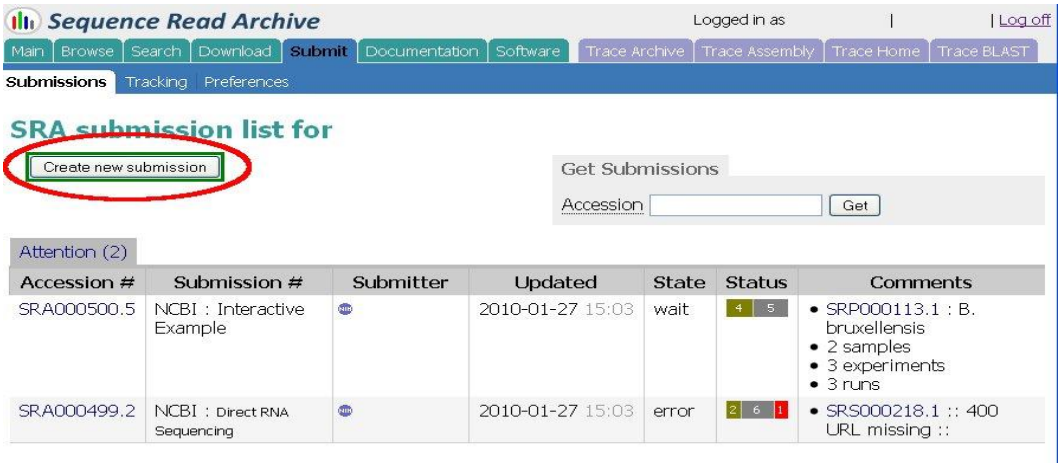

Figure 3 To start a Submission, click the 'Create new submission' button.

3.1 Submission Alias and Comment

Submission ID also known as **'Alias'** - will be used for tracking within the archive and for the submitter. This field should be something that makes sense to the submitter.
Example: *C. elegans resequencing project* (this field is NOT indexed in Entrez).

Submission Comment – area for submitter to enter a comment about the submission.
Example: *prepared with assistance by John Smith* (this field is NOT indexed in Entrez).

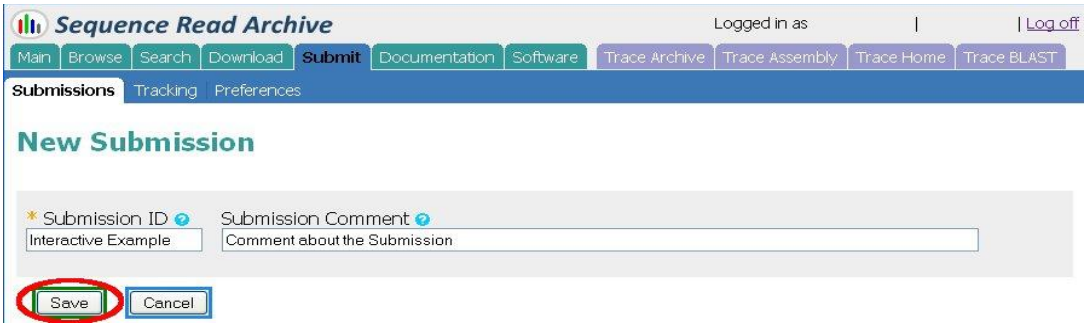

Figure 4 The Submission is not created until the 'Save' button is clicked.

4 Study

4.1 Creating a New Study

A Study identifies the sequencing study or project and may contain multiple experiments.
Study accessions are a good choice as the reference in a scientific journal article because the published Study provides a good landing page for users seeking to download data.

Figure 5 Create the Study by clicking the button for 'New Study'.

4.2 Describing a Study

Alias- Used as a reference for the submitter and archive. (NOT an indexed field)
Title- Publicly viewable title. A title from a journal article or other descriptive title should be used.
Study Type- Drop-down menu providing a selection of different categories for sequencing projects. Used as a method for users to find general types of studies. Pick the closest category and avoid 'other' if possible.
Abstract- Describes the goals, purpose, and scope of the study.
Description- Allows for more extensive and free-form description of the study.
Project Name- Name used by submitter for the project, if different from the Study Title.
Project ID- Genome Project ID. New Projects can be created here.
Links and Attributes- Used to add URLs, Entrez Links, or other Attributes in a key-value pair configuration. If linking to other databases, please use the correct database abbreviation.

- If the Study accompanies a journal article, enter the PubMed ID (pmid) as an 'entrez link' with "pubmed" as the 'DB' and the pmid as the 'ID'.

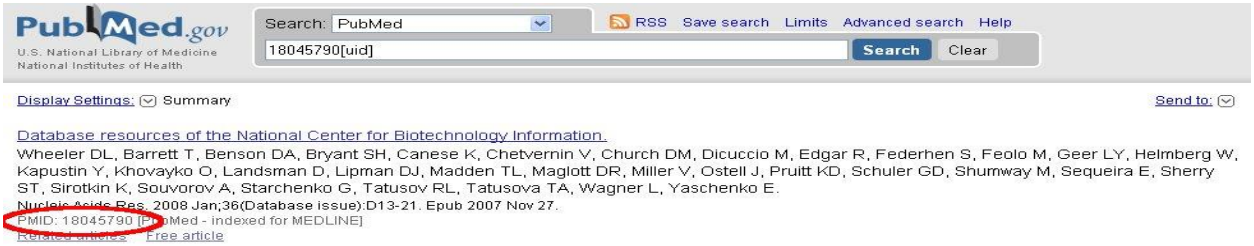

Figure 6 The PMID for an article is listed at the bottom of the article's PubMed Summary.

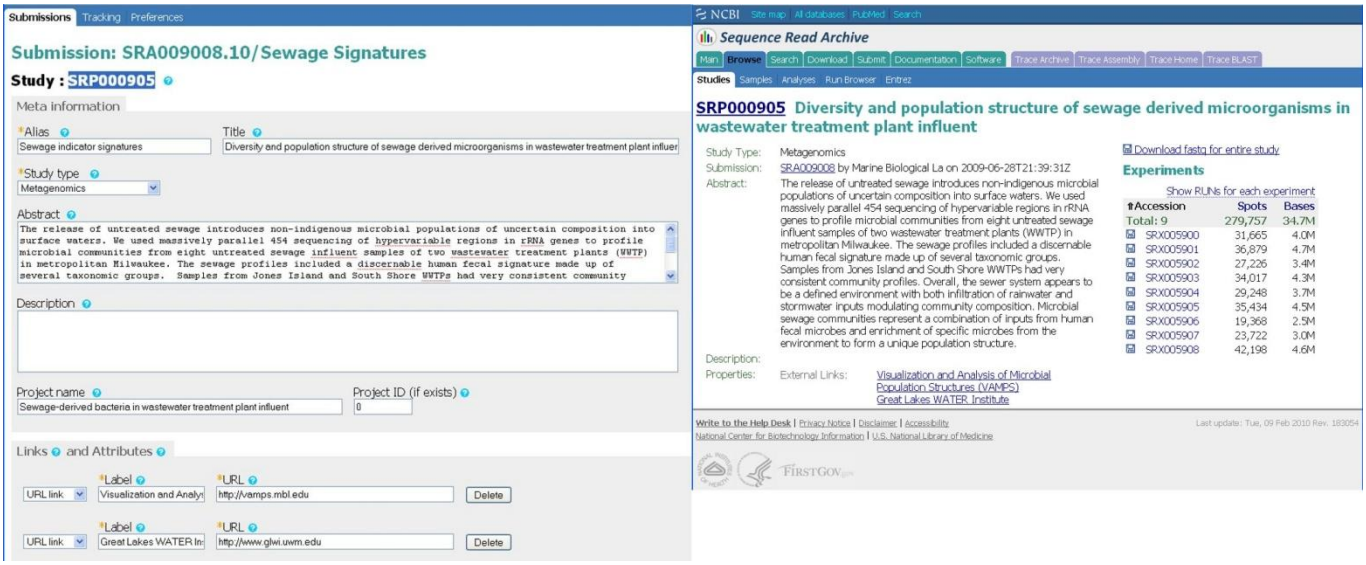

Figure 7 Example showing the SRA Interactive Tool (left) compared to the view of the same Study in Entrez (right).

Above Study in Entrez

5 Setting a Submission Release Date

A release date is required for all submissions. It is advisable to enter a release date before loading any data into a Submission. This will prevent accidental early release of data. Dates may be set for up to one year in the future in anticipation of a publication release date.

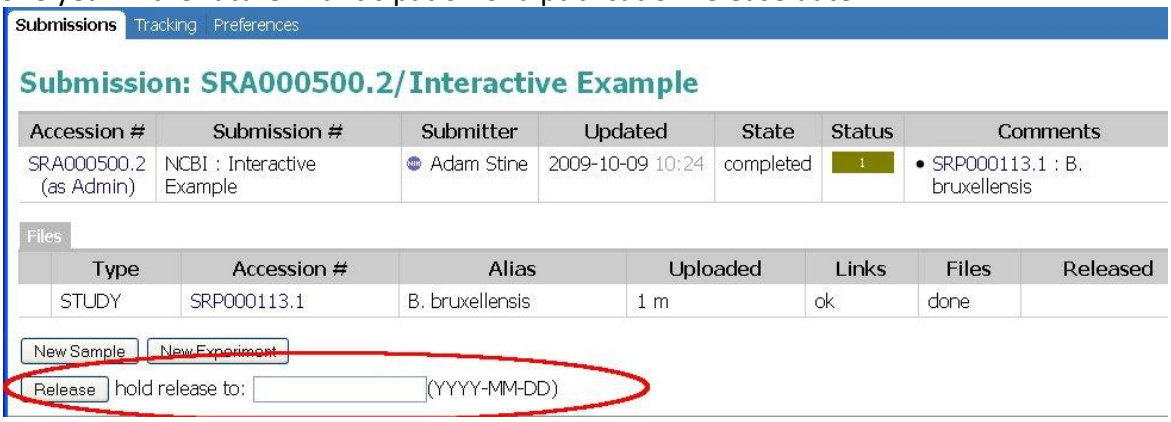

Figure 8 To save the date on which the submission is scheduled to be published/released to the public, enter a date in the box using a YYYY-MM-DD format, then click 'Release' The release date can be changed as long as the submission has not yet been made public

6 Status

Figure 9 The Status Bar

The status bar provides a visual representation of the current state of the submission and files in Tracking. **Done** (Dark Green) indicates the number of completed objects. **Wait** (Gray) further information or files uploads are needed. **Processing** (Light Blue- not shown) an object is currently being processed, if an object/file is processing for more than 48 hours, contact SRA. **Queue** (Dark Blue) the object will being processing when the pipeline is available. **Replaced** (Bright Green) an object/file was replaced by another. **Error** (Red) intervention is required, please contact SRA.

7 Sample

7.1 Creating Samples

Each unique sample used in a study needs to have its own sample object within the submission. The exception to that rule is when samples were intentionally pooled. A pooled sample is one sample but should explicitly describe as much as is known about what was in the pool. Please contact SRA for help with barcoded or indexed samples. A Study may contain multiple Samples.

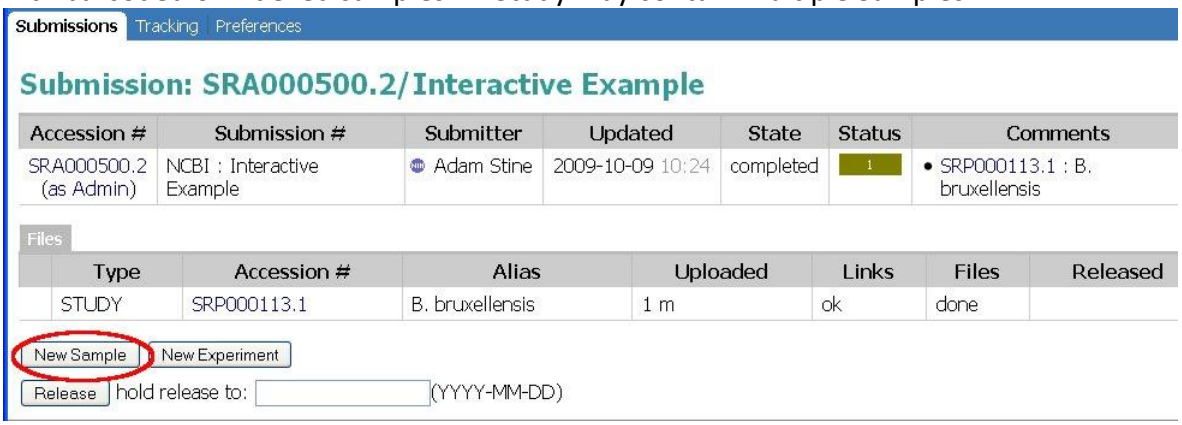

Figure 10 Click the 'New Sample' button to create a new Sample.

7.2 Describing a Sample

Alias- Used as a reference for the user and archive. (NOT an indexed field)

Title-Publicly viewable title. A formal title used to describe the Sample. If the submission goes along with a journal publication, the title should distinguish samples within the article.

Anonymized Name- Anonymous public name of the sample. For example, *HapMap human isolate NA12878*.

NCBI Taxon ID- ID number from the NCBI Taxonomy database. For samples that do not have an appropriate Taxonomy entry, the submitter will need to apply for a new or provisional Taxon ID. Email SRA for assistance to establish new or provisional Taxon IDs.

Description- Allows for more extensive and detailed description of the sample.

Links and Attributes- Used to add URLs, Entrez Links, or other Attributes in a key-value pair configuration. If linking to other databases, please use the correct database abbreviation.

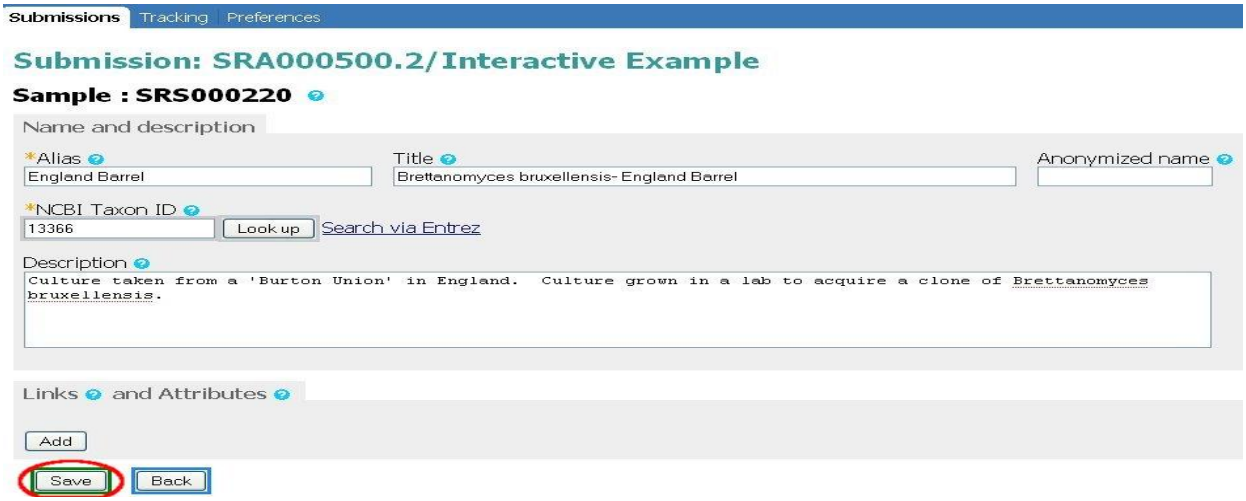

Figure 11 Samples should be fully described such that a user does not need to find an accompanying publication. The information is not stored until the 'Save' button is clicked. Saved samples can be updated as necessary.

8 Experiment

8.1 Creating Experiments

Experiment describes the library, platform selection, and processing parameters. Each change to the library or sequencer parameters requires the creation of a new experiment. A Sample can contain multiple experiments but each experiment contains only one library.

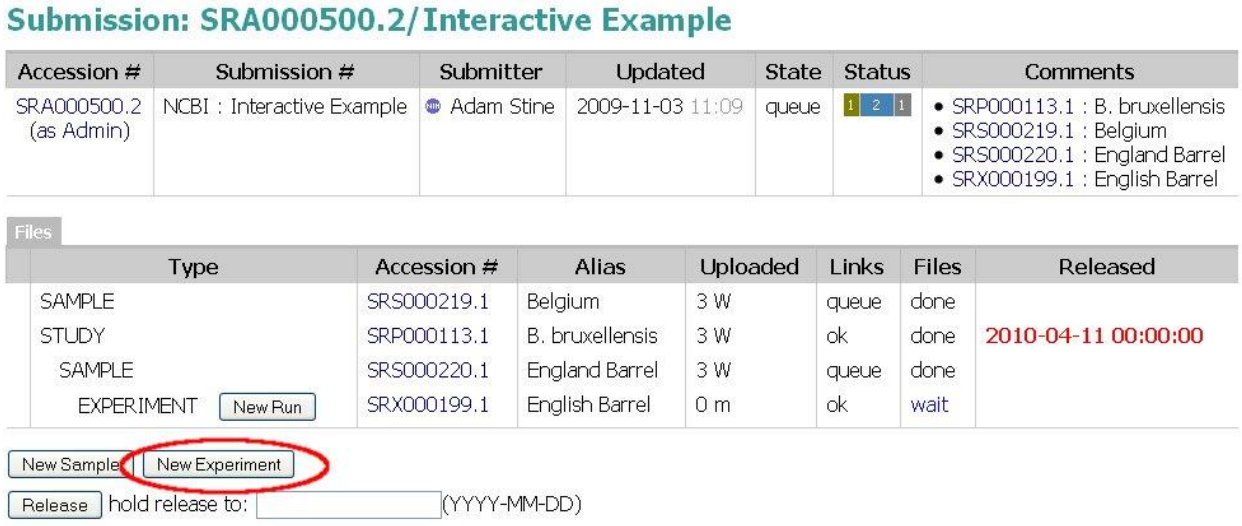

Figure 12 Click the 'New Experiment' button to begin creating an Experiment.

8.2 Describing an Experiment

- ***Meta Information***

Platform- This describes the sequencing platform used in the experiment.
Alias- Used as a reference for the user and archive. (NOT an indexed field)
Title- A publicly viewable and formal title used to describe the Experiment.
Study Accession– Links this Experiment to a previously created Study

Sample Accession- Links this Experiment to a previously created Sample
Design Description- Describes the setup and goals of this Experiment

- **Library**

Name- Name of the Library that was sequenced
Strategy- Sequencing strategy used in the experiment
Source- Type of genetic source material sequenced
Selection- Method of selection or enrichment used in the Experiment
Layout- Configuration of the read layout. Paired, Fragment, etc.
Nominal Size (paired)– Size of the insert for Paired reads. (Required)
Nominal Standard Deviation (paired)- Standard deviation of insert size (typically ~10% of Nominal Size)
Library Construction Protocol- An area to give a description on the library construction techniques and reagents used.(Required)

- **Processing**

This section varies with the sequencer selected. Please pay close attention to the answers provided in this section, as they may affect proper loading of data.

Links and Attributes- Used to add URLs, Entrez Links, or other Attributes in a key-value pair configuration. If linking to other databases, please use the correct database abbreviation.

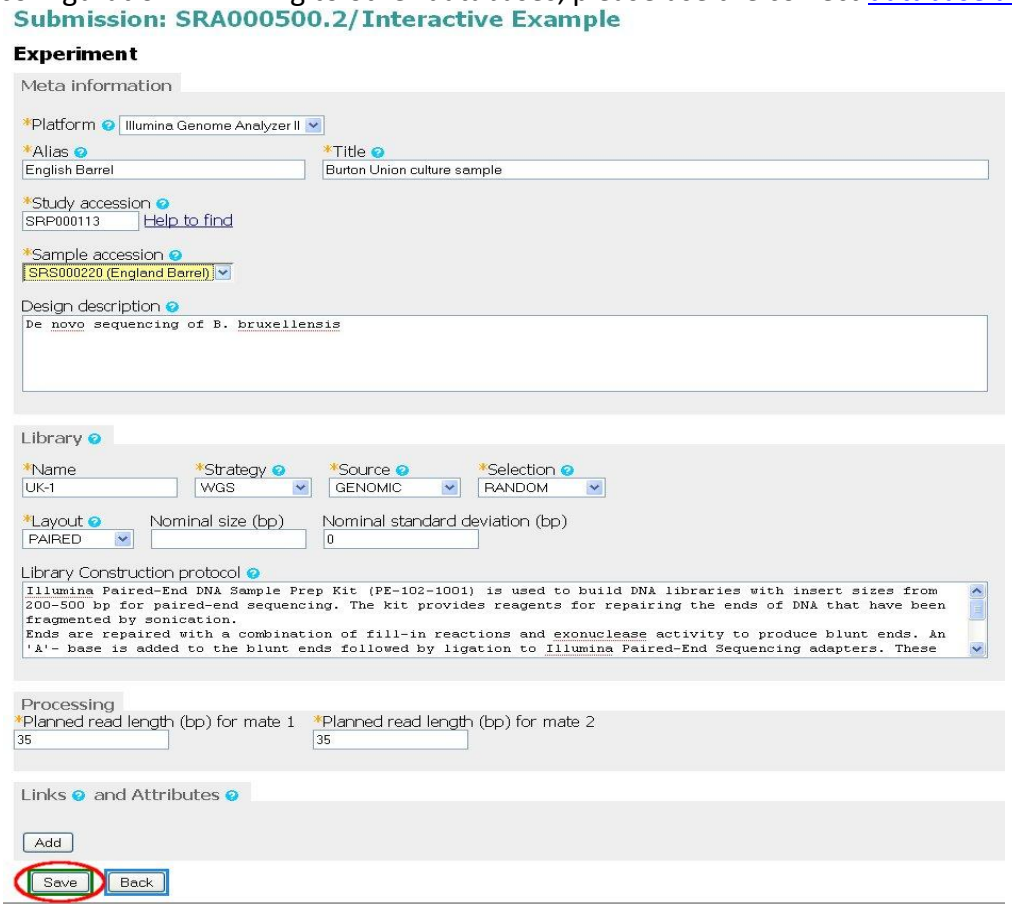

Figure 13 Click the 'Save' button to store the Experiment information. Saved Experiments can be updated as necessary.

9 Run

9.1 Creating Runs

Runs describe the files that belong to the previously created Experiments. Runs are divided by production run of the sequencer. Experiments may contain many Runs depending on how many sequencer runs were involved in data acquisition.

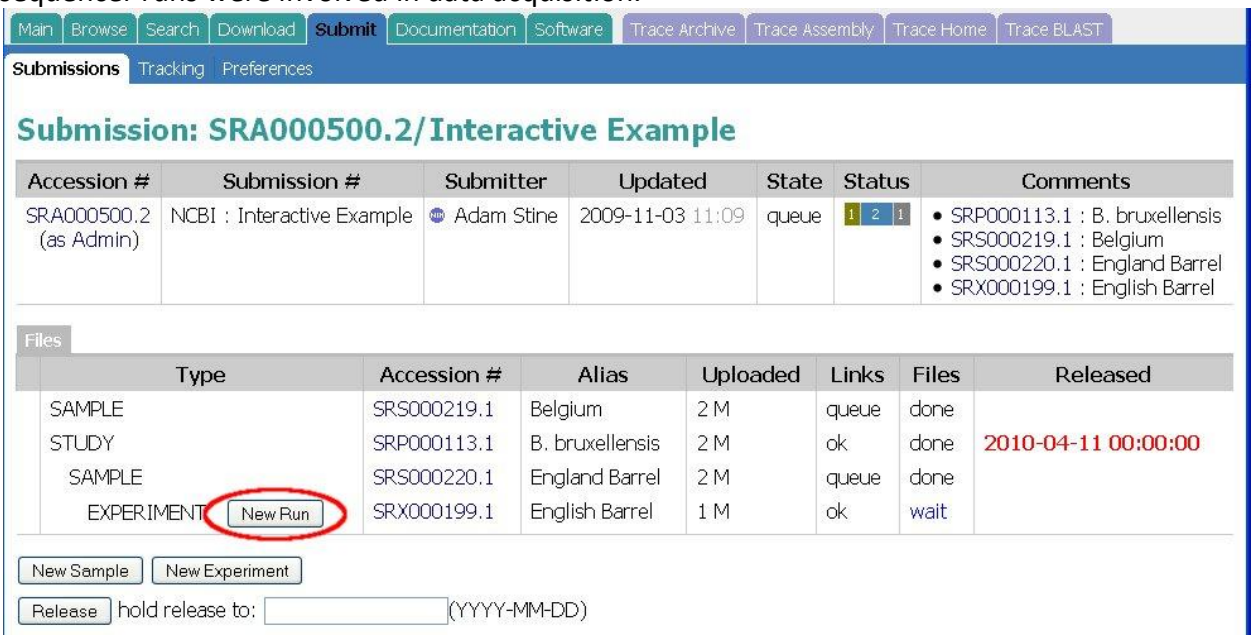

Figure 14 Click the 'New Run' button to the right of the Experiment for which a Run is needed. Each Experiment will have its own 'New Run' button.

9.2 Describing a Run

Alias- Used as a reference for the user and archive. (NOT an indexed field)

Run data file type- The storage format (srf, sff, fastq, etc) of the sequence data being submitted. More information about the file types currently accepted by the SRA can be found in the SRA Submission Guidelines.

File Name- Name of the file transferred to the SRA including any file extensions. Some data types require multiple files to be combined into a tar archive and some require single files.

MD5 checksum- A checksum or hash sum generated for the file listed in 'File Name' that is used to detect errors introduced through storage or transfer. SRA uses the file name and md5 checksum to track and link files to their proper Runs.

Unix- `md5sum <file>`

OS X- `md5 <file>`

Windows- Application required. Fsum Frontend and WinMD5Sum are two possible options.

Plate and Region- Only seen on certain file types like FASTQ. Because some file types have limited addressing information, these fields allow the user to provide the address information for the sequencing media used.

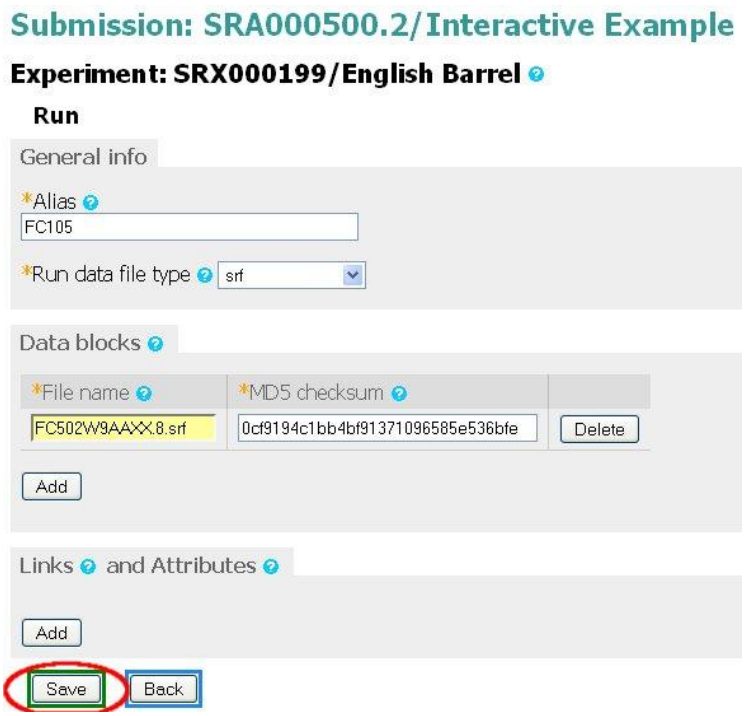

Figure 15 Click the 'Save' button to store the Run information. Runs can only be updated until data has been loaded for the Run. Once there is data in a Run, it will be locked from further updates. Contact SRA for changes to be made to locked Runs.

10 Data Transfer

After the metadata is entered, you may upload data to the SRA.

Upload via FTP:
ftp://sra:61c6lwoE6!@ftp-private.ncbi.nih.gov/
(Windows Explorer or an FTP client may be used)
FileZilla is one of many free FTP clients.

Or from unix/linux
Address: ftp-private.ncbi.nih.gov
Login: sra
Password: 61c6lwoE6! (contact SRA for the current password)
If everything is correct files will be linked and loaded automatically.
Additional information on data transfer methods is available in the SRA Submission Guidelines.

Please write to sra@ncbi.nlm.nih.gov for answers to submission questions.