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## Recommended browsers

- Google Chrome (version49+)
- Firefox (version45+)
- Microsoft Edge (version25+)
- Internet Explorer (version11+)
- Safari (version9+)\*

The latest version is recommended for every browser.

\*Safari may have a problem when trying to upload more than 1000 files at a time.

This service requires cookies and JavaScript. Be sure to allow them in your browser settings.

## How to cite jPOST Repository

jPOSTrepo: an international standard data repository for proteomes

Shujiro Okuda; Yu Watanabe; Yuki Moriya; Shin Kawano; Tadashi Yamamoto; Masaki Matsumoto; Tomoyo Takami; Daiki Kobayashi; Norie Araki; Akiyasu C. Yoshizawa; Tsuyoshi Tabata; Naoyuki Sugiyama; Susumu Goto; Yasushi Ishihama

Nucleic Acids Research 45 (D1): D1107-D1111 (2017).

doi: 10.1093/nar/gkw1080

[Copy citation text](#)

## Before submission

At first, read carefully [the ProteomeXchange \(PX\) guideline](#).

If you deposit the data on human proteome project (HPP), we recommend that you follow [the HPP guidelines](#) published by [Deutsch, E. et al. J. Proteome Res. 2016](#).

## Preparing for submission

You have to sign in with a verified e-mail address to submit data. The server will send you an e-mail containing a specific token (URL). By visiting the URL, you can verify your e-mail address. If you have lost that e-mail, you can resend it from [My page](#).

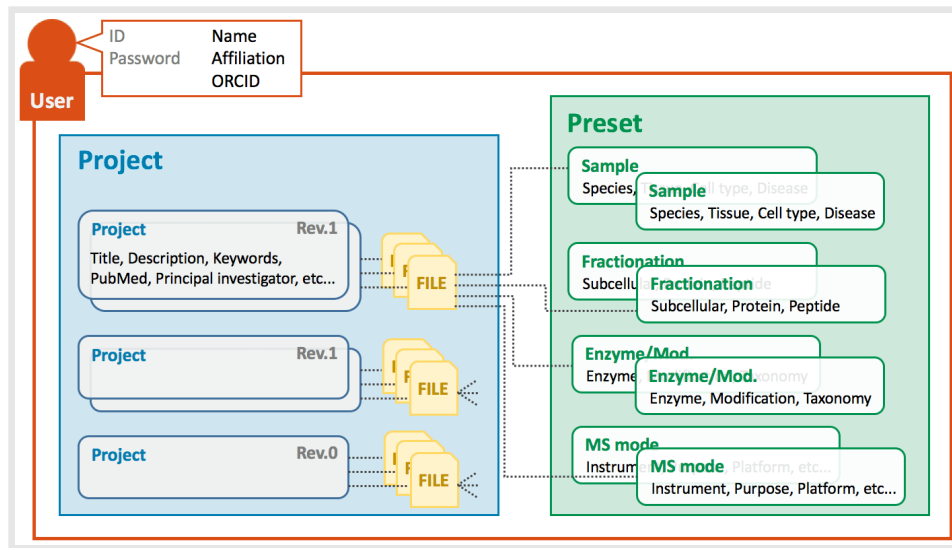
## Our submission tool outline

Our submission procedure has two major steps - "Project and file(PROJECT)" and "Preset experimental procedure(PRESET)."

If you have a group of files for one paper, you should create a project and upload files for it. Files always belong to one project.

In the PRESET step, input the information about experimental procedure and then assign them to files in the PROJECT section.

Preset profiles don't belong to a particular project but to a user, so that you can reuse them if you use the same experimental procedure in another project.

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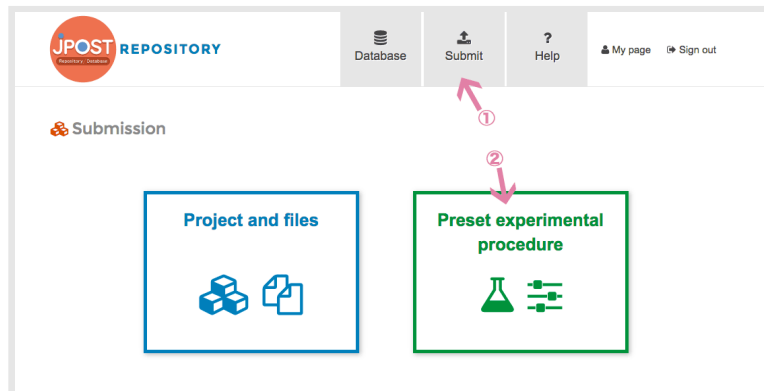
**Search announced data**

- Free word search
- Ontology search

**FAQ**

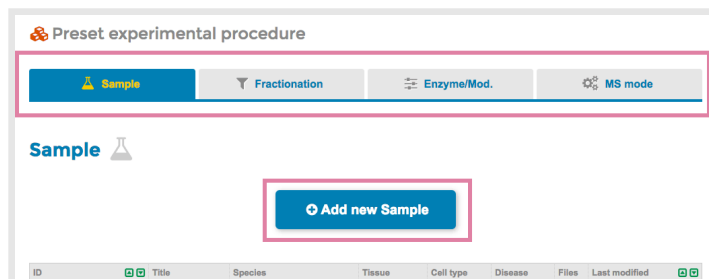
## Preset experimental procedure

You can click "Submit" button on the menu and then click "Preset experimental procedure" button to configure your presets.



PRESET section has four categories - "Sample", "Fractionation", "Enzyme/Mod.", "MS mode."

Each category is independent and can freely be combined and assigned to a file from the PROJECT section later.



## Sample preset

To create a new PRESET profile for sample, click the "Add new Sample" button and fill out the forms.

New Sample profile

Title\*

MOCK-FLAG-IP  
PC12 NF1 minus 24h

Species\*

(select)  
Looking for more items

Homo sapiens (Human)  
Rattus norvegicus (Rat)

Tissue

(select)  
Looking for more items

HeLa cell  
pheochromocytoma 12 cell

Cell type

(select)  
Looking for more items

oocyte  
pheochromocyte

Disease

(select)  
Looking for more items

ovarian cancer  
neural tissue disease

Note

Confirm →

Cancel editing Sample.

If you can't find the appropriate item in the list, click "Looking for more items" and you can search the whole ontology list or you can input the free-form texts.

New Sample profile

Title\*

MOCK-FLAG-IP

Species\*

Arabidopsis thaliana (Mouse-ear cress)  
Looking for more items

Tissue

(select)  
Looking for more items

Search from EBI Ontology Lookup Service

or Enter free word

Enter

Close

(select)  
Looking for more items

You don't need to fill out all of the items, but some are required. A warning message will be shown if a required item is left empty when you click "Confirm" button.

New Sample profile

Confirm:

⚠ Species is required.

Title	MOCK-FLAG-IP
Species	
Tissue	flower
Cell type	oocyte
Disease	disease free
Note	

← Back

Submit Sample →

Note that you cannot edit or remove the PRESET profile after the assigned file is displayed.

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## Fractionation preset

To create a new PRESET profile for fractionation, select "Fractionation" tab and click the "Add new Fractionation" button and fill out the forms. There are three categories about fractionation processes such as "Subcellular", "Protein", and "Peptide". In each subprocess, you can input the number of fractions and replicates.

**New Fractionation profile**

Title\*  SCX fraction

Subcellular (select)  Whole

Replicate:

Protein  SDS-PAGE (5-12.5 %), OFFGEL, Anti-FLAG immunoprecipitation, Phostag-affinity purification

Fraction:  Replicate:  [Add Protein](#)

Peptide  Cation exchange, Anion exchange, Reverse phase at acidic pH, OFFGEL, Fe-IMAC, TIO2

Fraction:  Replicate:  [Add Peptide](#)

Note

[Confirm](#) [Cancel editing Fractionation](#)

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## Fractionation examples

**Example1**

- Cells were solubilized with 2% SDS in 100 mM Tris-HCl, pH8.8
- Sonication for 30 sec
- Centrifuge for 10 min at 19,000 g
- 20 µg proteins were applied to SDS-PAGE (5-14% gradient gel)
- Staining with CBB
- Cut the gel into 12 slices
- In-gel digestion
- LC-MS/MS analysis

Title\*  Whole proteome analysis by GeLC-MS

Subcellular  Whole

Replicate:  1

Protein  SDS-PAGE (5-14% gradient gel)

Fraction:  12 Replicate:  2 [Add Protein](#)

Peptide

Fraction:  Replicate:  [Add Peptide](#)

Note  Proteins were separated with SDS-PAGE (5-14% gradient gel) and stained with CBB. The gel was cut into 12 slices.

Example1: Whole proteome analysis by GeLC-MS

**Example2**

- Cells were solubilized with 2% SDS in 100 mM Tris-HCl, pH8.8
- Sonication for 30 sec
- Centrifuge for 10 min at 19,000 g
- Acetone precipitation (100 µg protein)
- Suspend in 100 mM ammonium bicarbonate
- Sonication
- Add trypsin (2 µg) and incubate for 4 h at 37°C
- Add trypsin (2 µg) and incubate for overnight at 37°C
- Separation by reverse-phase chromatography (high pH, 16 fractions)
- LC-MS/MS analysis

Title\*  Whole proteome analysis with 2D-LC-MS/MS

Subcellular  Whole

Replicate:  1

Protein

Fraction:  Replicate:  [Add Protein](#)

Peptide  SCX fractionation

Fraction:  16 Replicate:  [Add Peptide](#)

Note  Proteins were extracted by 2 % SDS/100 mM ammonium bicarbonate. 100 g proteins were digested with trypsin and subjected to RP-chromatography at pH9.0 to obtain 16-fractions. Each fraction was subjected to LC-MS/MS analysis.

## Example2: Whole proteome analysis with 2D-LC-MS/MS

**Example3**

- HeLa cells were incubated in hypotonic buffer
- Add NP-40 to 0.1%
- Collect nuclear pellet
- High-salt extraction
- Acetone precipitation
- Digestion
- LC-MS/MS analysis

**Title\***  
Nuclear proteome analysis in single-shot LC-MS/MS

**Subcellular**  
Nucleus  
Replicate: 3

**Protein**  
Fraction: Replicate:  
[+ Add Protein](#)

**Peptide**  
Fraction: Replicate:  
[+ Add Peptide](#)

**Note**  
Nuclear proteins were extracted by 1 M NaCl.

## Example3: Nuclear proteome analysis in single-shot LC-MS/MS

**Example4**

- Protein extraction with Trizol from HeLa cell
- Digestion by trypsin
- Desalting
- Fe-IMAC purification
- IMAC-bound fraction
- Anti-PY affinity purification
- Bound and flow-through fraction
- LC-MS/MS analysis

**Title\***  
Phosphoproteome analysis by IMAC-based/anti-PY tandem enrichment

**Subcellular**  
Whole  
Replicate: 3

**Protein**  
Fraction: Replicate:  
[+ Add Protein](#)

**Peptide**  
Fe-IMAC  
Fraction: 1 Replicate: 1  
Anti-PY antibody affinity purification  
Fraction: 2 Replicate: 1  
[+ Add Peptide](#)

**Note**  
Finally, we obtained two fractions (anti-PY bound and flow-through fraction). Each fraction was subjected to LC-MS/MS analysis.

## Example4: Phosphoproteome analysis by IMAC-based/anti-PY tandem enrichment

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## Enzyme/Mod. preset

To create a new PRESET profile for the enzyme, select "Enzyme/Mod." tab and click the "Add new Enzyme/Mod." button and fill out the forms.

New Enzyme/Mod. profile

Title\*

Enzyme

(select)

Looking for more items

Trypsin

+ Add Enzyme

Fixed modification\*

(Select from below)

Acetyl (K)  
Acetyl (N-term)  
Acetyl (Protein N-term)  
Amidated (C-term)  
Amidated (Protein C-term)  
Biotin (K)  
Biotin (N-term)  
Carbamidomethyl (C)

Looking for more items

acetylated residue  
L-homoarginine

Variable modification\*

(Select from below)

Acetyl (K)  
Acetyl (N-term)  
Acetyl (Protein N-term)  
Amidated (C-term)  
Amidated (Protein C-term)  
Biotin (K)  
Biotin (N-term)  
Carbamidomethyl (C)

Looking for more items

acetylated residue  
L-homoarginine

Taxonomy

(select)

Looking for more items

Homo sapiens (Human)  
Rattus norvegicus (Rat)

Note

Confirm →

Cancel editing Enzyme/Mod.

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MS mode preset

To create a new PRESET profile for MS mode, select "MS mode" tab and click the "Add new MS mode" button and fill out the forms.

New MS mode profile

Title\*

Instrument\*

(select)

Looking for more items

LTQ  
QSTAR

Instrument mode

(select)

Looking for more items

DDA-low res.

Purpose

(select)

Looking for more items

Relative quantification

Quantification platform

(select)

Looking for more items

Spectra count  
Product ion (reporter quantification)

Plex

-

Label

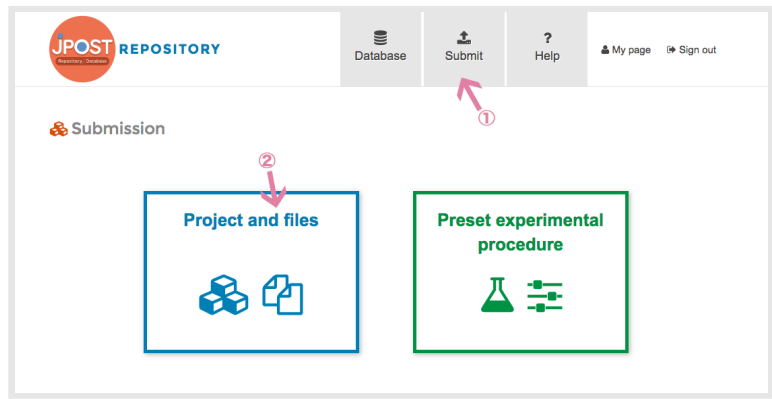
Note

Confirm →

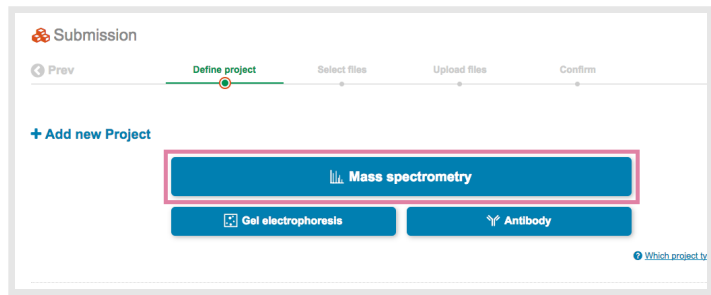
Cancel editing MS mode.

Project and file

When you deposit your data, you can create your project for the data. Every project must have an announcement date and at that time it will be publicly available.



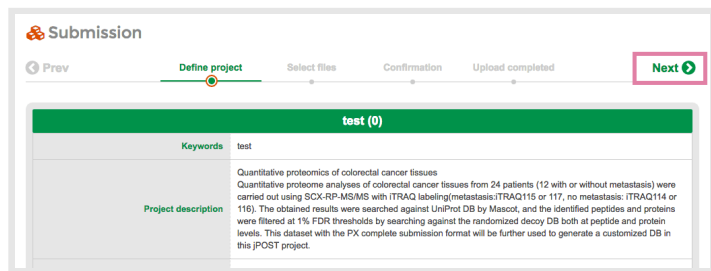
You can create a new project by clicking one of three project type buttons or edit your ongoing project from "Select" button on the project table.



The project type and mode are designed as follows:

Project type	Mass spectrometry		Gel electrophoresis	Antibody
Project mode	Complete submission	Partial submission		
When to use	Projects that include mass spectrometric data. If the project is related to the <a href="#">Human Proteome Project</a> , you <b>must</b> submit as a complete submission.	Projects that include mass spectrometric data but doesn't satisfy complete submission requirements.	Project with gel electrophoresis analysis (but without mass spectrometric data).	Project with antibody analysis (but without mass spectrometric data).
Deposit files	<b>Required</b> Raw, Peak (MGF or mzML), Result (mzTab or mzIdentML) <b>Optional</b> Others	<b>Required</b> Raw, Result (any format) <b>Optional</b> Peak, Others	<b>Required</b> Image, Result (any format) <b>Optional</b> Others	
Experiment procedure preset	<b>Required</b> Sample, Enzyme/Mod., MS mode <b>Optional</b> Fractionation		<b>Required</b> Sample <b>Optional</b> Fractionation	

First, input the information about your project. Then go to "Select files" step.



In the "Select files" section, you can apply your registered presets to files you want to upload. The uploaded files are applied to the presets in four categories such as "Raw data", "Peak list", "Search results", and "Others".

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Raw dataPeak listSearch resultsOthers

Sample

Fractionation

Enzyme/Mod.

MS mode

Search profile...

SortModified date newer

S0000000003

S0000000002

TitleTest sample 2

SpeciesRattus norvegicus (Rat)

Tissueblood platelet

Cell typedendritic cell

Diseasedisease free

Note

TitleMOCK-FLAG-IP

SpeciesArachis hypogaea (Peanut)

Tissueblood serum

Cell typeerythrocyte

Diseasebronchitis

Note

Sample

Fractionation

Enzyme/Mod.

MS mode

(Not selected)

(Not selected)

(Not selected)

(Not selected)

Raw data

When you apply "Raw data" files, go to the following steps.  
Select PRESET profile from each PRESET categories (Sample, Fractionation, Enzyme/Mod., MS mode). Selected profiles are applied to files by dropping below.

Select profiles for files

Sample

Fractionation

Enzyme/Mod.

MS mode

Search profile...

SortModified date newer

Prev 12 items

S0000000002

MOCK-FLAG-IP

Rattus norvegicus (Rat)

embryonic stem cell

breast cancer

SELECTED

Sample

Fractionation

Enzyme/Mod.

MS mode

S0000000002

MOCK-FLAG-IP

Rattus norvegicus (Rat)

bone marrow

embryonic stem cell

breast cancer

Note

F0000000002

SCX fraction

SubcellularSCX Fraction=1

Replicate=1/2

ProteinFLAG-IP Fraction=1

Replicate=1/2

PeptideSCX 40 fraction Fraction=1

Replicate=1/4

Note

E0000000002

test data

EnzymeAsp-N\_ambic

Fixed modificationAcetyl (K)

Variable modificationDIART6plex (K)

TaxonomyBombyx mori (Silk moth)

Note

M0000000002

Test mode

InstrumentLTQ Orbitrap Velos

Instrument modeDIA

PurposeQualification

QuantificationSpectra count

Platform

Plex2

Label113: label1

114: label2

Select files for the project from your computer.  
You can drag and drop files into the box or click the box and select from dialog (Our system is not able to process the directory).

Drop files here or click to upload.

13122018-HILIC-monolith-4h-10p-11p

13122018-HILIC-monolith-4h-10p-21p

13122018-HILIC-monolith-4h-10p-31p

13122018-HILIC-monolith-4h-10p-41p

13122018-HILIC-monolith-4h-10p-51p

13122018-HILIC-monolith-4h-10p-61p

13122018-HILIC-monolith-4h-10p-71p

13122018-HILIC-monolith-4h-10p-81p

13122018-HILIC-monolith-4h-10p-91p

13122018-RP-monolith-5h-11p

13122018-RP-monolith-5h-21p

13122018-RP-monolith-5h-31p

13122018-RP-monolith-5h-41p

13122018-RP-monolith-5h-51p

13122018-RP-monolith-5h-61p

13122018-RP-monolith-5h-71p

13122018-RP-monolith-5h-81p

13122018-RP-monolith-5h-91p

File list

13122018-HILIC-monolith-4h-10p-11p

13122018-HILIC-monolith-4h-10p-21p

13122018-HILIC-monolith-4h-10p-31p

13122018-HILIC-monolith-4h-10p-41p

13122018-HILIC-monolith-4h-10p-51p

13122018-HILIC-monolith-4h-10p-61p

13122018-HILIC-monolith-4h-10p-71p

13122018-HILIC-monolith-4h-10p-81p

13122018-HILIC-monolith-4h-10p-91p

13122018-RP-monolith-5h-11p

13122018-RP-monolith-5h-21p

13122018-RP-monolith-5h-31p

13122018-RP-monolith-5h-41p

13122018-RP-monolith-5h-51p

13122018-RP-monolith-5h-61p

13122018-RP-monolith-5h-71p

13122018-RP-monolith-5h-81p

13122018-RP-monolith-5h-91p

Search / Filter

SearchFile name

File typeAll

Clear

Selection

Select all files in this page

Select all files in entire list

Selected: 0 file

Action

Apply profile

Add profile

Remove selected

Reset

You can edit file profiles from the list at the bottom. Select target file(s) and apply, add profile information or remove the file. If you want to remove all the files from the project, click the "Reset" button.

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https://repository.jpostdb.org/help8/18



**File list**

**Search / Filter**

Search  File type

**Selection**

☒ Select all files in this page ☐ Select all files in entire list Selected: 3 files

**Action**

☒ Apply profile

20 per page 1 - 16 / 16 1

Select	File Name	Software	Experimental preset (Sample, Fractionation, Enzyme/Mod., MS mode)	Location
<input checked="" type="checkbox"/>	131228k-HILIC-monolith-4h-1ug-1.txt	<input type="button" value="Add"/>	<input type="button" value="S"/> Comparative Transcriptomics and Proteomics on PI Depleted Arabidopsis Roots <input type="button" value="F"/> Comparative Transcriptomics and Proteomics on PI Depleted Arabidopsis Roots [1] <input type="button" value="E"/> Comparative Transcriptomics and Proteomics on PI Depleted Arabidopsis Roots <input type="button" value="M"/> Comparative Transcriptomics and Proteomics on PI Depleted Arabidopsis Roots <input type="button" value="S"/> Comparative Transcriptomics and Proteomics on PI Depleted Arabidopsis Roots	Local

## Peak list ("Mass spectrometry" type only)

When you apply "Peak list" files, first you can select the file format of files you apply. Then you can drag and drop your files into the box or click the box to select files.

**Format:**

☐ mzML ☐ MGF ☐ Other

Drop files here or click to upload.

## Search results

When you apply "Search results" files, you need to select a software name created your files. Additionally, you can select the file format of the files you apply (this is needed for the complete submission). Then, you can drag and drop your files into the box or click the box to select files.

**Software:**

No software selected

Byonic  
Comet  
Mascot  
MaxQuant  
MS-GF+  
Myrimatch  
OMSSA

**Format:**

☐ mzIdentML ☐ mzTab ☐ Other

**Software setting:**

Drop files here or click to upload.

You can also provide details of software settings as an option. This additional software settings include information such as used software, used precursor, fragment tolerance, etc. in addition to the detailed workflows and FDR values.

**Software setting:**

Current setting: Vertebrates\_EST; Asp-N; Oxidation (M); ITRAQ4plex (N-term), ITRAQ4plex (K); ...

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New Software setting profile

Database

(select)

Input free text

Enzyme

(select)

Looking for more items

Trypsin

+ Add Enzyme

Allow up to

0-9

Quantification

(select)

Input free text

Taxonomy

(select)

Looking for more items

Homo sapiens (Human), Mus musculus (Mouse)

Fixed modification

(Select from below)

Carbamidomethyl (C)  
Carboxymethyl (C)  
Cation:Na (C-term)  
iTRAQ4plex (K)  
iTRAQ4plex (N-term)  
iTRAQ8plex (K)  
iTRAQ8plex (N-term)  
Label:13C(6) (K)

Looking for more items

Carbamidomethyl (C)

Variable modification

(Select from below)

Acetyl (K)  
Acetyl (N-term)  
Gln->pyro-Glu (Q)  
Glu->pyro-Glu (E)  
Label:13C(6) (K)  
Label:13C(6) (R)  
Label:13C(6)15N(2) (K)  
Label:13C(6)15N(4) (R)

Looking for more items

Oxidation (M), Phospho (S), Phospho (T)

Peptide tol. ±

Da

#<sup>13</sup>C

(select)

0-2

MS/MS tol. ±

Da

FDR

PSM %

Protein %

Peptide %

Note for workflow

Confirm →

Cancel editing Software setting.

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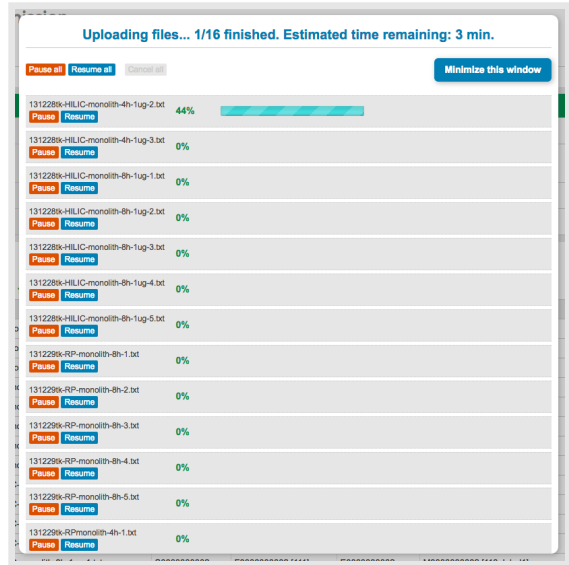
Search announced data

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File upload

Go to the "Upload files" menu, you can upload your files to the jPOST server. It may take a while in the case of uploading a large quantities of files.



Note that you are not able to edit or remove the any part of the project after the announcement date.

Confirmation

To complete the submission process, go to "Confirmation" menu. If your uploaded files and applied presets passed our check, you can submit your project to the jPOST server and then you can obtain the project ID. If the uploaded files and applied presets don't pass the check, you need to modify them to go back to the previous processes.

This checking procedure is performed based on the PX partial submission process.  
Your project must have:

- At least one search result file.
- At least one raw file.
- Information of species, modifications and instruments.

Confirm project

Can't submit this project.

No search result file is found.

No raw file is found.

0 species is found in this project.

0 instrument is found in this project.

0 modification is found in this project.

This project will be announced right after the submission finished.

Partial submission

Complete submission

Input additional information for complete submission

After submission, you are not able to edit this project any more with the exception of PubMed ID and Announcement date. Please check carefully and confirm your project.

How to cite jPOST Repository

jPOSTrepo: an international standard data repository for proteomes

Shujiro Okuda; Yu Watanabe; Yuki Moriya; Shin Kawano; Tadashi Yamamoto; Masaki Matsumoto; Tomoyo Takami; Daiski Kobayashi; Norie Araki; Akiyasu C. Yoshizawa; Tsuyoshi Tabata; Naoyuki Sugiyama; Susumu Goto; Yasushi Ishihama

Nucleic Acids Research 45 (D1): D1107-D1111 (2017).

doi: 10.1093/nar/gkw1080

Copy citation text

Submit project

Recommended browsers

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- Preparing for submission
- Our submission tool outline

Preset experimental procedure

- Sample preset
- Fractionation preset
- Enzyme/Mod. preset
- MS mode preset

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Multiplex case

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- Raw file

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- Free word search
- Ontology search

FAQ

https://repository.jpostdb.org/help

11/18

**Confirm project**

**All checks have passed.**

- ✓ Project has at least one search result file.
- ✓ Project has at least one raw file.
- ✓ 1 species is found in this project.
- ✓ 1 instrument is found in this project.
- ✓ 3 modifications are found in this project.

**The announcement date is temporarily set to 2017-05-20, but you can edit it later.**  
\*We will notice you by e-mail on 1 week prior to the announcement date.

☒ **Partial submission**    ☐ **Complete submission**  
☒ Input additional information for complete submission

After submission, **you are not able to edit this project any more** with the exception of PubMed ID and Announcement date. Please check carefully and confirm your project.

**How to cite jPOST Repository**

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 Shujiro Okuda; Yu Watanabe; Yuki Moriya; Shin Kawano; Tadashi Yamamoto; Masaki Matsumoto; Tomoyo Takami; Daiki Kobayashi; Norie Araki; Akiyasu C. Yoshizawa; Tsuyoshi Tabata; Naoyuki Sugiyama; Susumu Goto; Yasushi Ishihama  
 Nucleic Acids Research 45 (D1): D1107-D1111 (2017).  
 doi: 10.1093/nar/gkw1080

[Copy citation text](#)

**Submit project**

After the submission, the jPOST server validates your files and prepares your project page. Any change of the project data is not allowed while validation is in progress.

In general, this process finishes within a few minute.

## Multiplex case

### Sample preset

In the case of multiplex quantification analysis, the "Sample profile" preset should be set for each sample labelled with each multiplex reagent, such as iTRAQ or TMT.

For example, if each 4 sample is labelled with iTRAQ 4-plex (114-117), 4 "Sample profile" presets have to be set.

**New Sample profile**

**Title \***  
 HeLa EGF 30 min    MOCK-FLAG-IP, PC12 NF1 minus 24h

**Species \***  
 Homo sapiens (Human)    Homo sapiens (Human), Mus musculus (Mouse)  
Looking for more items

**Tissue**  
 HeLa cell    HeLa cell, pheochromocytoma 12 cell  
Looking for more items

**Cell type**  
 cultured cell    oocyte, pheochromocytoma  
Looking for more items

**Disease**  
 cervical cancer    ovarian cancer, neural tissue disease  
Looking for more items

**Note**

**Confirm** →

Cancel editing Sample.

### MS mode preset

"Purpose" - In the case of multiplex relative quantification, such as iTRAQ or TMT, select "Relative quantification".

"Quantification platform" - In the case of multiplex relative quantification, such as iTRAQ or TMT, select "Product ion (reporter quantification)".

### Recommended browsers

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#### FAQ

New MS mode profile

Title\*

ITRAQ 4-plex

Instrument\*

QSTAR

Looking for more items

LTQ, QSTAR

Instrument mode

DDA-high res.

Looking for more items

DDA-low res.

Purpose

Relative quantification

Looking for more items

Relative quantification

Quantification platform

Product ion (reporter quantification)

Looking for more items

Spectra count, Product ion (reporter quantification)

Plex

"Plex" - If iTRAQ 4-plex was used, select "4".  
If "Plex" is select as "4", 4 columns (each column for each plex) are appeared in "Label" below.  
Enter each label name, such as "iTRAQ 114, iTRAQ 115, iTRAQ 116, iTRAQ 117" for iTRAQ 4-plex.

Plex

4

Label

ITRAQ 114

ITRAQ 115

ITRAQ 116

ITRAQ 117

Raw file

Select the preset of sample which is labelled with multiplex reagent such as iTRAQ/TMT.  
Select the "MS mode" preset for multiplex experiment.

Raw dataPeak listSearch resultsOthers

SampleFractionationEnzyme/Mod.MS mode

S0000000005

TitleHeLa EGF 30 min

SpeciesHomo sapiens (Human)

Tissuehuman lens epithelial cell

Cell typecultured cell

Diseasecervical cancer

Note

S0000000004

TitleHuman sample

SpeciesHomo sapiens (Human)

Tissueblood

Cell typeblood cell

Diseasedisease free

Note

S0000000003

TitleTest sample 2

SpeciesRattus norvegicus (Rat)

Tissueblood platelet

Cell typedendritic cell

Diseasedisease free

Note

S0000000002

TitleMOCK-FLAG-IP

SpeciesArachis hypogaea (Peanut)

Tissueblood serum

Cell typeerythrocyte

Diseasebronchitis

Note

SampleFractionationEnzyme/Mod.MS mode

S0000000005

TitleHeLa EGF 30 min

SpeciesHomo sapiens (Human)

Tissuehuman lens epithelial cell line

Cell typecultured cell

Diseasecervical cancer

Note

F0000000010

TitleSCX fraction

SubcellularWhole Replicate:1

Protein

PeptideCation exchange Replicate:1

Note

E0000000004

TitleITRAQ 4-plex human

EnzymeTrypsin

Fixed modificationMethyl/Tris (C), ITRAQ4plex (K), ITRAQ4plex (N-term)

Variable modificationOxidation (M)

TaxonomyHomo sapiens (Human)

Note

(Not selected)

If "MS mode" preset for multiplex experiment is selected, label names set in the preset appears. Select the label name(s) for the selected sample.  
Note that if multiple labels correspond to the same profile, you can select multiple (or all) label names at once. But we recommend you to define detailed profile for each label.

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When the raw data files are set in "File list", selected "Sample" and "MS mode" presets are assigned to the files.

Select the other preset of sample which is labelled with other multiplex reagent.

Repeatedly, select the same "MS mode" preset and select the label name for the selected sample.

Select the all raw files, and click "Add profile". Selected "Sample" and "MS mode" preset are set as the file profiles.

## Recommended browsers

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### FAQ

**File list**

Search / Filter

Search File name  File type **Raw**

Selection

☐ Select all files in this page ☒ **Select all files in entire list** Selected: 10 files

Action

20 per page 1 - 4 / 4 1

Select	File Name	Software	Experimental preset (Sample, Fractionation, Enzyme/Mod., MS mode)	Location
<input checked="" type="checkbox"/>	raw_sample_1.raw		S HeLa EGF 30 min F SCX fraction E ITRAQ 4-plex human M ITRAQ 4-plex (ITRAQ 114)	Local
<input checked="" type="checkbox"/>	raw_sample_2.raw		S HeLa EGF 60 min F SCX fraction E ITRAQ 4-plex human M ITRAQ 4-plex (ITRAQ 114)	Local
<input checked="" type="checkbox"/>	raw_sample_3.raw		S HeLa EGF 30 min F SCX fraction E ITRAQ 4-plex human M ITRAQ 4-plex (ITRAQ 114)	Local
<input checked="" type="checkbox"/>	raw_sample_4.raw		S HeLa EGF 60 min F SCX fraction E ITRAQ 4-plex human M ITRAQ 4-plex (ITRAQ 114)	Local

Repeat the setting of profiles for all multiplex experiments.

## Complete submission

PX provides a complete submission system for more informative data deposit. As the same way, jPOST provides a complete submission as an option. If you want to submit your dataset as a complete submission, you need to upload raw files and the corresponding peak and result files. In addition, you need to input metadata such as species, instruments, and modifications about your experiments. Then, you can select "Complete submission" button in the "Confirm" section. Similarly, you need to select your files separated into "Raw data", "Peak list", and "Search results" sections into one group obtained from one serious process. In this complete submission mode, a file format of "Peak list" files should be "mzML" or "MGF" and also that of "Search results" files should be "mzIdentML" or "mzTab". When all these conditions are validated, you can submit your datasets as a complete submission.

**Confirm project**

☒ **All checks have passed.**

- ✓ Project has at least one search result result file.
- ✓ Project has at least one raw file.
- ✓ 1 species is found in this project.
- ✓ 1 instrument is found in this project.
- ✓ 2 modifications are found in this project.

⚠ This project will be announced right after the submission finished.

☐ Partial submission ☒ **Complete submission**

⚠ After submission, you are not able to edit this project any more with the exception of PubMed ID and Announcement date. Please check carefully and confirm your project.

**How to cite jPOST Repository**

jPOSTrepo: an international standard data repository for proteomes  
Shujiro Okuda; Yu Watarabe; Yuki Moriya; Shin Kawano; Tadashi Yamamoto; Masaki Matsumoto; Tomoyo Takami; Daisi Kobayashi; Norie Araki; Aklyasu C. Yoshizawa; Tsuyoshi Tabata; Naoyuki Sugiyama; Susumu Goto; Yasushi Ishihama  
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### Recommended browsers

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We provide the "Auto relationship detection" function suggesting file relationships from the contents of your files. If your files are in a general format, this may be helpful for defining relationships.

Our validation process for a complete submission may take a few minutes per one peaklist file. You will receive an e-mail when it finishes.

## Recommended browsers

### Before submission

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### Preset experimental procedure

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## My page

An overview of your submission is available at [My page](#).

### Project list

All revisions of all projects are listed in the project table. You can jump to the submission page by clicking the "edit" button if the project is in editing. Project ID in the project list table links to the file list page.

Projects						
Title	Status	Revision	ID	Files	PubMed	Annou date
Sample Project	Editing	2		3		Unfixed
test 0518-2	Complete	Submitted	JPST000008	5		2017-05

### Set Announcement date and PubMed

You can update the announcement date and PubMed ID of submitted project from this list. If the revision is the latest and is submitted, "Date/PubMed" button appears. Textboxes will be appeared by pressing the button.

If the PubMed ID is not set after the announcement, you can input it only once in the same way.



## Revise

If you want to revise submitted project, press the "Revise" button in the project table (this button appears for the latest and submitted revision).

You can set the new announcement date for the next revision during the revise process.

It may take a while to revise the project with large amount of data.

The jPOST ID and PX ID will be taken over from the previous revision.

## Search announced data

We provide two searching functions for announced data.

### Free word search

The default is a search by a free word. All words that inputted by submitters will be searched.

### Ontology search

If you want to search by a controlled vocabulary, click "Search by ontology" and use ontology search mode.

As entering characters to the textbox, candidate vocabularies are shown. You can click the vocabulary (or press enter key) to adopt for searching.

\*Candidate vocabularies will be searched from vocabularies in announced data, not from entire ontology.

In case that more than one vocabulary is chosen, each vocabulary is used as an "AND" search.

Click "Add keyword" if more than three vocabularies are needed.

Click "Search" to execute ontology search.

## FAQ

### Recommended browsers

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#### FAQ

## I want to show my project and files to the reviewer before announcement date.

Click the "Request preview code" button in the project list table in [My page](#).

You can get a temporary URL for your project and a four digit code to access that page for reviewers.

**You cannot request preview code for the revision in editing.**

## How can I confirm if files are correctly uploaded to your server?

Click "Project ID" in the project list table in [My page](#) and go to the file list page.

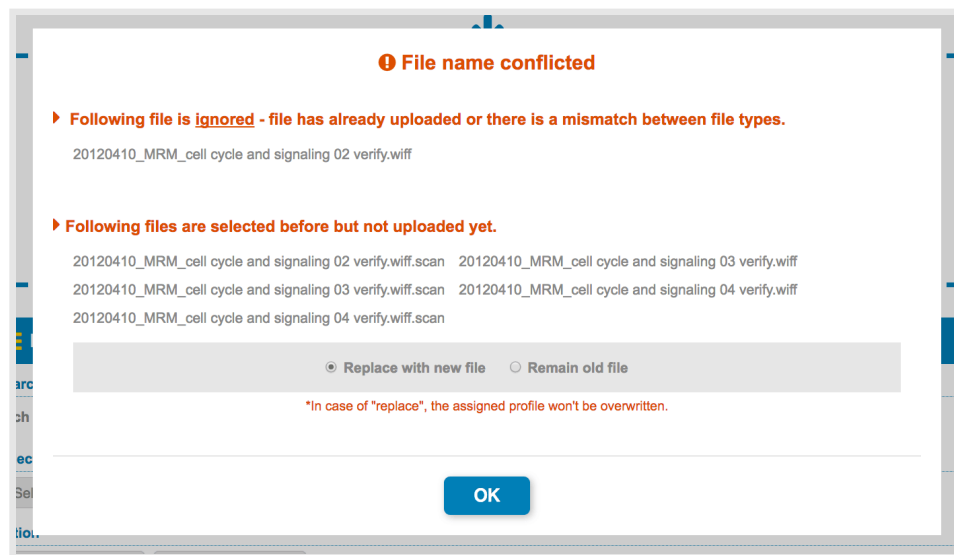
The MD5 checksum of each file is listed there so that you can compare it with the local file's.

**It takes about an hour to calculate MD5 checksum. If you cannot find any list, please visit the corresponding page again later.**

## File upload seems to be stopped. How can I retry?

Reload the browser, then drop files again and select "Replace with new file" in the dialog.

Files not uploaded are replaced with new files and getting into the upload queue.



## My personal information has changed.

You can edit your e-mail address, name, affiliation, ORCID and password from the bottom of [My page](#).

## Cannot edit or remove project, preset, etc.

To edit or remove data already announced is not allowed with the exception of the PubMed ID. If you have any problem with that, please [contact us](#).

## I want to deposit data which is going to publish in proteomics journals.

We strongly recommend to read each guideline of each journal. For instance, if you deposit the data on human proteome project (HPP), we recommend that you follow [the HPP guidelines](#) published by [Deutsch, E. et al . J. Proteome Res. 2016](#). According to the HPP guideline, you can submit your data only as complete submission. Likewise, the major proteomics journals such as Molecular and Cellular Proteomics and Journal of Proteome Research as well as the journals from nature publishing group have their own guidelines.

## Do we obtain the human sample information such as age and gender for deposited data?

Since human samples deposited to jPOSTrepo have unlinked anonymized metadata including age and gender, you can get these information from "Note" in "Sample" preset or "other files".

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