iProX: an integrated proteome resource

Supplementary File

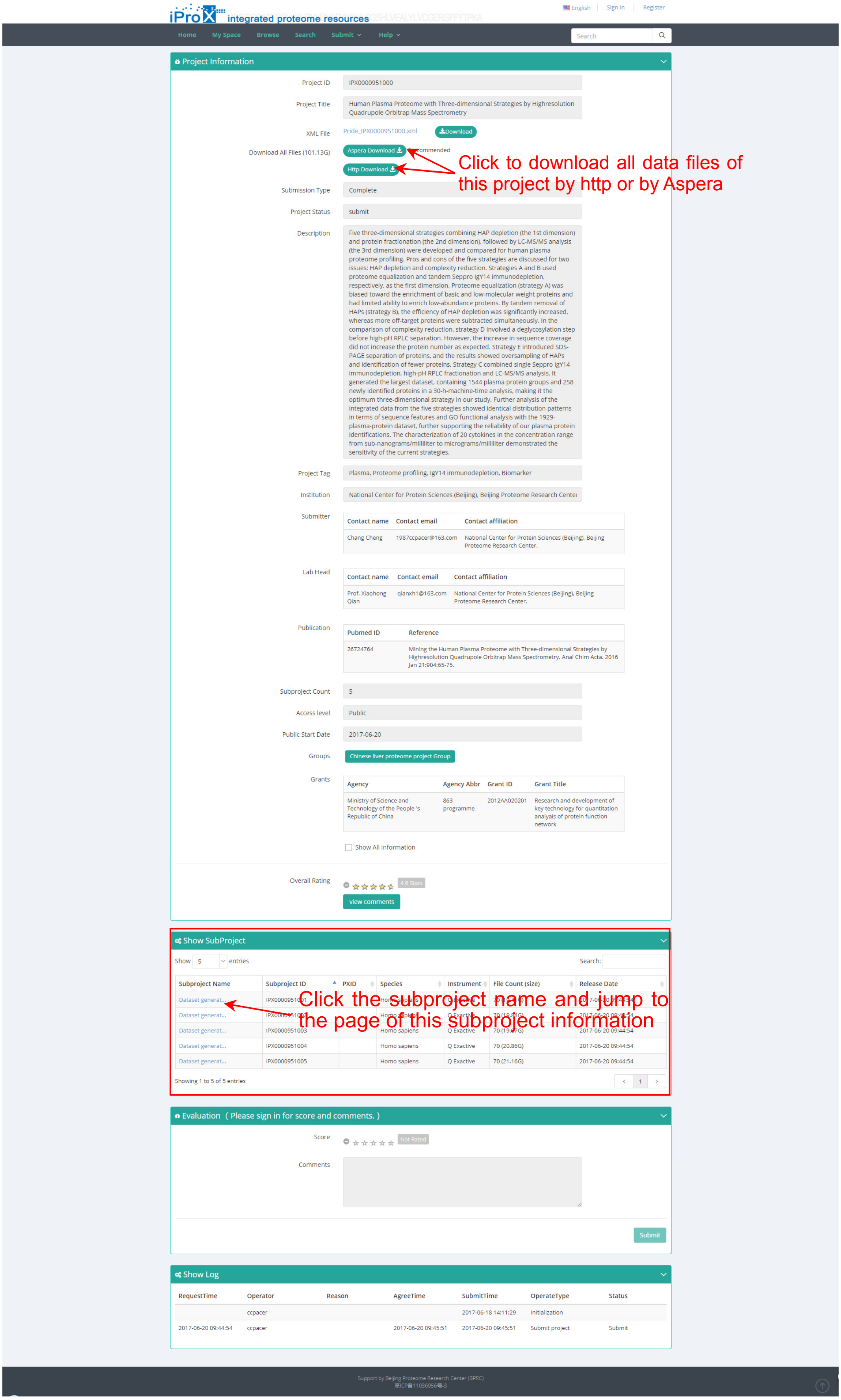
1. An example dataset at iProX

Please refer to project IPX0000951000 as an example of complete submission dataset at iProX, which is composed of the raw data and analysis results of the published paper (1).

The project URL is http://www.iprox.org/page/PDV014.html?projectId=IPX0000951000, and the details can also be found in the example dataset link in iProX (http://www.iprox.org/page/exampleDataset.html).

In this study, five analysis strategies were developed and compared for human plasma proteome profiling, and five sub-datasets were generated. The data from each sub-dataset is composed of a subproject in IPX0000951000. Figure 1 shows the overview information of this project. All data files of this project can be downloaded by clicking the "Aspera Download" or "Http download" button on this page. Five subprojects are shown at the bottom of this page (red rectangle in Figure 1). Taking the first subproject IPX0000951001 as an example, click the subproject name and jump to the page of subproject information (http://www.iprox.org/page/SDV015.html?subprojectId=IPX0000951001).

Figure 2 shows the overview information of this subproject. All data files of this subproject are shown in the bottom of this page (red rectangle in Figure 2A). Select one or several files and click the "Http" or "Aspera" button for downloading (Figure 2B); the http download pages may be blocked by the browser, please configure your web browser to allow pop-ups from iProX. By clicking the "View identification results" button on this page or clicking the 'view' button beside each standard format result file (Figure 2C), the protein and peptide identifications of the result files with standard format can be viewed in iProX (Figure 2D).



Project Information

Project ID	IPX0000951000
Project Title	Human Plasma Proteome with Three-dimensional Strategies by Highresolution Quadrupole Orbitrap Mass Spectrometry
XML File	Pride_IPX0000951000.xml Download
Download All Files (101.13G)	Aspera Download Recommended Http Download
Submission Type	Complete
Project Status	submit
Description	Five three-dimensional strategies combining HAP depletion (the 1st dimension) and protein fractionation (the 2nd dimension), followed by LC-MS/MS analysis (the 3rd dimension) were developed and compared for human plasma proteome profiling. Pros and cons of the five strategies are discussed for two issues: HAP depletion and complexity reduction. Strategies A and B used proteome equalization and tandem Seppro IgY14 immunodepletion, respectively, as the first dimension. Proteome equalization (strategy A) was biased toward the enrichment of basic and low-molecular weight proteins and had limited ability to enrich low-abundance proteins. By tandem removal of HAPs (strategy B), the efficiency of HAP depletion was significantly increased, whereas more off-target proteins were subtracted simultaneously. In the comparison of complexity reduction, strategy D involved a deglycosylation step before high-pH RPLC separation. However, the increase in sequence coverage did not increase the protein number as expected. Strategy E introduced SDS-PAGE separation of proteins, and the results showed oversampling of HAPs and identification of fewer proteins. Strategy C combined single Seppro IgY14 immunodepletion, high-pH RPLC fractionation and LC-MS/MS analysis. It generated the largest dataset, containing 1544 plasma protein groups and 258 newly identified proteins in a 30-h-machine-time analysis, making it the optimum three-dimensional strategy in our study. Further analysis of the integrated data from the five strategies showed identical distribution patterns in terms of sequence features and GO functional analysis with the 1929-plasma-protein dataset, further supporting the reliability of our plasma protein identifications. The characterization of 20 cytokines in the concentration range from sub-nanograms/milliliter to micrograms/milliliter demonstrated the sensitivity of the current strategies.
Project Tag	Plasma, Proteome profiling, IgY14 immunodepletion, Biomarker
Institution	National Center for Protein Sciences (Beijing), Beijing Proteome Research Cente

Click to download all data files of this project by http or by Aspera

Submitter

Contact name	Contact email	Contact affiliation
Chang Cheng	1987ccpacer@163.com	National Center for Protein Sciences (Beijing), Beijing Proteome Research Center.

Lab Head

Contact name	Contact email	Contact affiliation
Prof. Xiaohong Qian	qianxh1@163.com	National Center for Protein Sciences (Beijing), Beijing Proteome Research Center.

Publication

Pubmed ID	Reference
26724764	Mining the Human Plasma Proteome with Three-dimensional Strategies by Highresolution Quadrupole Orbitrap Mass Spectrometry. Anal Chim Acta. 2016 Jan 21;904:65-75.

Subproject Count	5
Access level	Public
Public Start Date	2017-06-20
Groups	Chinese liver proteome project Group

Grants

Agency	Agency Abbr	Grant ID	Grant Title
Ministry of Science and Technology of the People 's Republic of China	863 programme	2012AA020201	Research and development of key technology for quantitation analyais of protein function network

☐ Show All Information

Overall Rating ☆☆☆☆☆ 4.6 Stars

view comments

Show SubProject

Show 5 entries Search:

Subproject Name	Subproject ID	PXID	Species	Instrument	File Count (size)	Release Date
Dataset generat...	IPX0000951001		Homo sapiens	Q Exactive	70 ([illegible])	[illegible]
Dataset generat...	IPX0000951002		Homo sapiens	Q Exactive	70 (19.84G)	2017-06-20 09:44:54
Dataset generat...	IPX0000951003		Homo sapiens	Q Exactive	70 (19.[illegible]7G)	2017-06-20 09:44:54
Dataset generat...	IPX0000951004		Homo sapiens	Q Exactive	70 (20.86G)	2017-06-20 09:44:54
Dataset generat...	IPX0000951005		Homo sapiens	Q Exactive	70 (21.16G)	2017-06-20 09:44:54

Showing 1 to 5 of 5 entries

Click the subproject name and jump to the page of this subproject information

Evaluation （Please sign in for score and comments.）

Score ☆☆☆☆☆ Not Rated

Comments

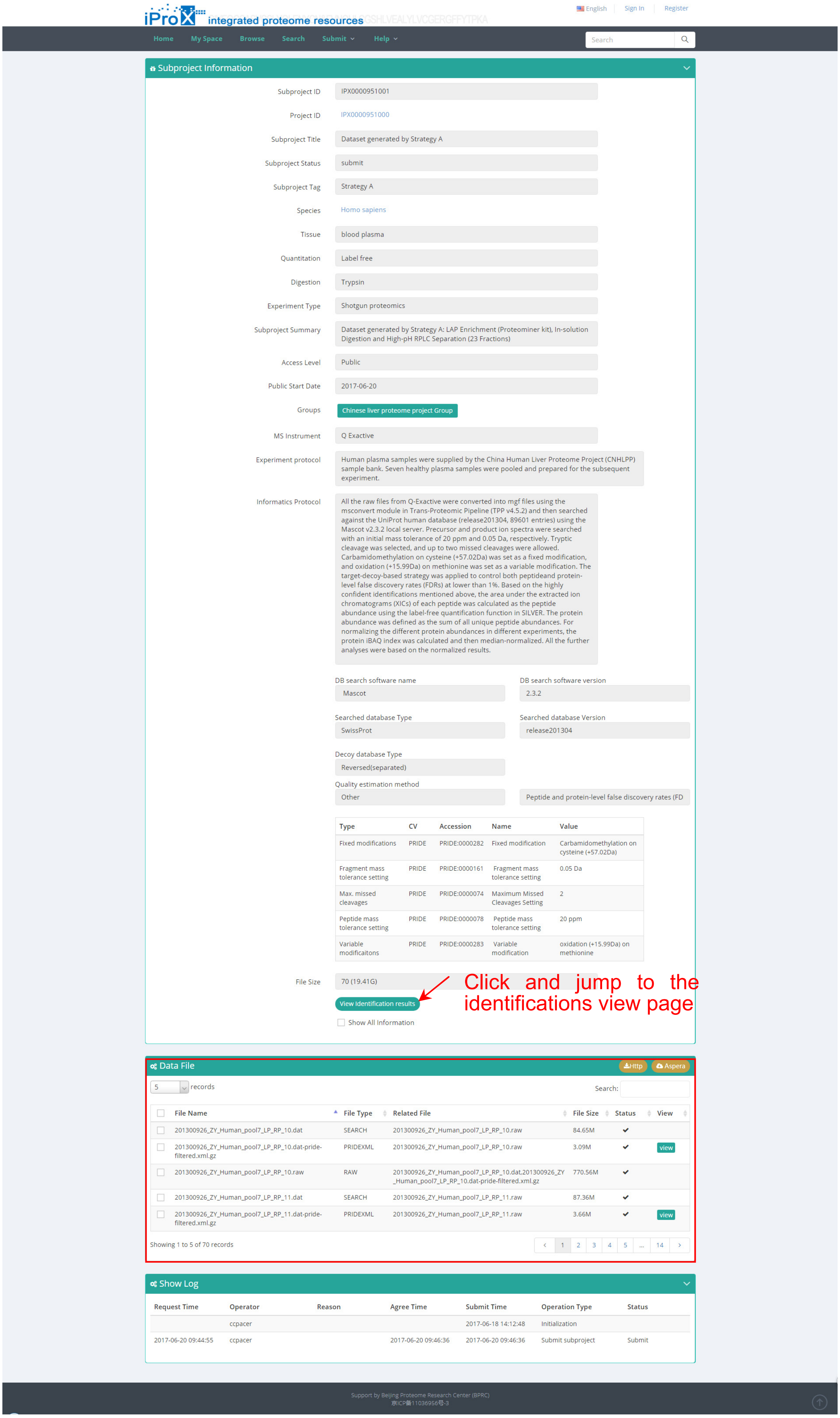
Submit

Show Log

RequestTime	Operator	Reason	AgreeTime	SubmitTime	OperateType	Status
	ccpacer			2017-06-18 14:11:29	Initialization	
2017-06-20 09:44:54	ccpacer		2017-06-20 09:45:51	2017-06-20 09:45:51	Submit project	Submit

Support by Beijing Proteome Research Center (BPRC)
京ICP备11036956号-3

Figure 1. Overview of the example project IPX0000951000 in iProX.



Subproject Information

Subproject ID: IPX0000951001

Project ID: IPX0000951000

Subproject Title: Dataset generated by Strategy A

Subproject Status: submit

Subproject Tag: Strategy A

Species: Homo sapiens

Tissue: blood plasma

Quantitation: Label free

Digestion: Trypsin

Experiment Type: Shotgun proteomics

Subproject Summary: Dataset generated by Strategy A: LAP Enrichment (Proteominer kit), In-solution Digestion and High-pH RPLC Separation (23 Fractions)

Access Level: Public

Public Start Date: 2017-06-20

Groups: Chinese liver proteome project Group

MS Instrument: Q Exactive

Experiment protocol: Human plasma samples were supplied by the China Human Liver Proteome Project (CNHLPP) sample bank. Seven healthy plasma samples were pooled and prepared for the subsequent experiment.

Informatics Protocol: All the raw files from Q-Exactive were converted into mgf files using the msconvert module in Trans-Proteomic Pipeline (TPP v4.5.2) and then searched against the UniProt human database (release201304, 89601 entries) using the Mascot v2.3.2 local server. Precursor and product ion spectra were searched with an initial mass tolerance of 20 ppm and 0.05 Da, respectively. Tryptic cleavage was selected, and up to two missed cleavages were allowed. Carbamidomethylation on cysteine (+57.02Da) was set as a fixed modification, and oxidation (+15.99Da) on methionine was set as a variable modification. The target-decoy-based strategy was applied to control both peptideand protein-level false discovery rates (FDRs) at lower than 1%. Based on the highly confident identifications mentioned above, the area under the extracted ion chromatograms (XICs) of each peptide was calculated as the peptide abundance using the label-free quantification function in SILVER. The protein abundance was defined as the sum of all unique peptide abundances. For normalizing the different protein abundances in different experiments, the protein iBAQ index was calculated and then median-normalized. All the further analyses were based on the normalized results.

DB search software name: Mascot

DB search software version: 2.3.2

Searched database Type: SwissProt

Searched database Version: release201304

Decoy database Type: Reversed(separated)

Quality estimation method: Other

Peptide and protein-level false discovery rates (FD

Type	CV	Accession	Name	Value
Fixed modifications	PRIDE	PRIDE:0000282	Fixed modification	Carbamidomethylation on cysteine (+57.02Da)
Fragment mass tolerance setting	PRIDE	PRIDE:0000161	Fragment mass tolerance setting	0.05 Da
Max. missed cleavages	PRIDE	PRIDE:0000074	Maximum Missed Cleavages Setting	2
Peptide mass tolerance setting	PRIDE	PRIDE:0000078	Peptide mass tolerance setting	20 ppm
Variable modificaitons	PRIDE	PRIDE:0000283	Variable modification	oxidation (+15.99Da) on methionine

File Size: 70 (19.41G)

View Identification results

☐ Show All Information

Click and jump to the identifications view page

Data File

Http Aspera

5 records

Search:

☐	File Name	File Type	Related File	File Size	Status	View
☐	201300926_ZY_Human_pool7_LP_RP_10.dat	SEARCH	201300926_ZY_Human_pool7_LP_RP_10.raw	84.65M	✓	
☐	201300926_ZY_Human_pool7_LP_RP_10.dat-pride-filtered.xml.gz	PRIDEXML	201300926_ZY_Human_pool7_LP_RP_10.raw	3.09M	✓	view
☐	201300926_ZY_Human_pool7_LP_RP_10.raw	RAW	201300926_ZY_Human_pool7_LP_RP_10.dat,201300926_ZY_Human_pool7_LP_RP_10.dat-pride-filtered.xml.gz	770.56M	✓	
☐	201300926_ZY_Human_pool7_LP_RP_11.dat	SEARCH	201300926_ZY_Human_pool7_LP_RP_11.raw	87.36M	✓	
☐	201300926_ZY_Human_pool7_LP_RP_11.dat-pride-filtered.xml.gz	PRIDEXML	201300926_ZY_Human_pool7_LP_RP_11.raw	3.66M	✓	view

Showing 1 to 5 of 70 records

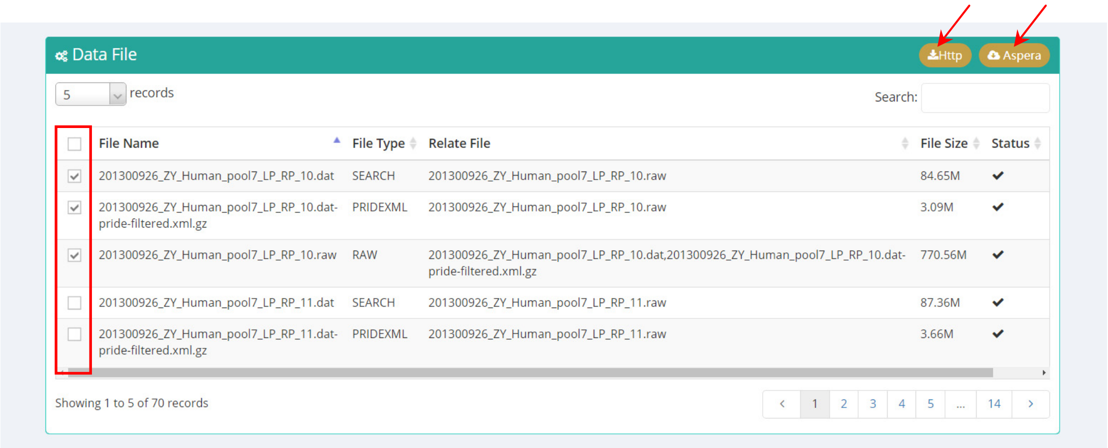
‹ 1 2 3 4 5 ... 14 ›

Show Log

Request Time	Operator	Reason	Agree Time	Submit Time	Operation Type	Status
	ccpacer			2017-06-18 14:12:48	Initialization	
2017-06-20 09:44:55	ccpacer		2017-06-20 09:46:36	2017-06-20 09:46:36	Submit subproject	Submit

Support by Beijing Proteome Research Center (BPRC)
京ICP备11036956号-3

(A)



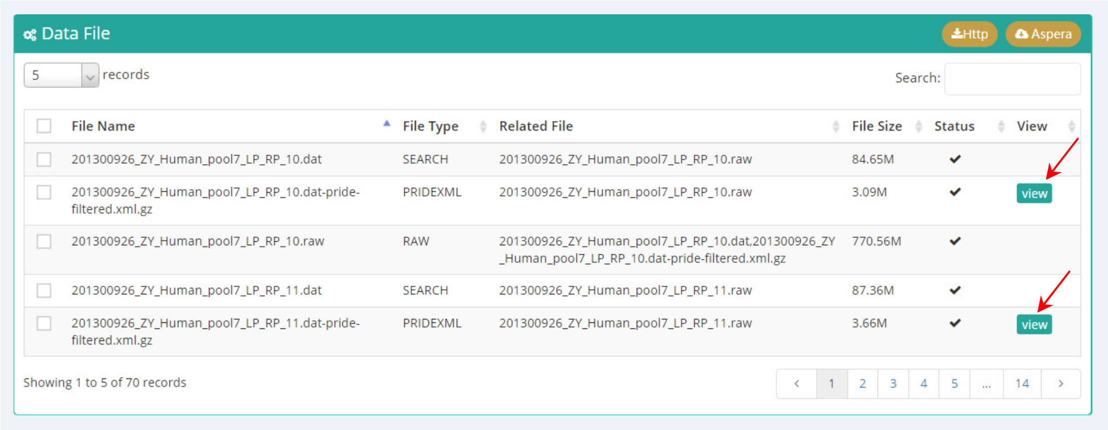
5 records

Search:

☐	File Name	File Type	Relate File	File Size	Status
☑	201300926_ZY_Human_pool7_LP_RP_10.dat	SEARCH	201300926_ZY_Human_pool7_LP_RP_10.raw	84.65M	✓
☑	201300926_ZY_Human_pool7_LP_RP_10.dat-pride-filtered.xml.gz	PRIDEXML	201300926_ZY_Human_pool7_LP_RP_10.raw	3.09M	✓
☑	201300926_ZY_Human_pool7_LP_RP_10.raw	RAW	201300926_ZY_Human_pool7_LP_RP_10.dat,201300926_ZY_Human_pool7_LP_RP_10.dat-pride-filtered.xml.gz	770.56M	✓
☐	201300926_ZY_Human_pool7_LP_RP_11.dat	SEARCH	201300926_ZY_Human_pool7_LP_RP_11.raw	87.36M	✓
☐	201300926_ZY_Human_pool7_LP_RP_11.dat-pride-filtered.xml.gz	PRIDEXML	201300926_ZY_Human_pool7_LP_RP_11.raw	3.66M	✓

Showing 1 to 5 of 70 records

(B)



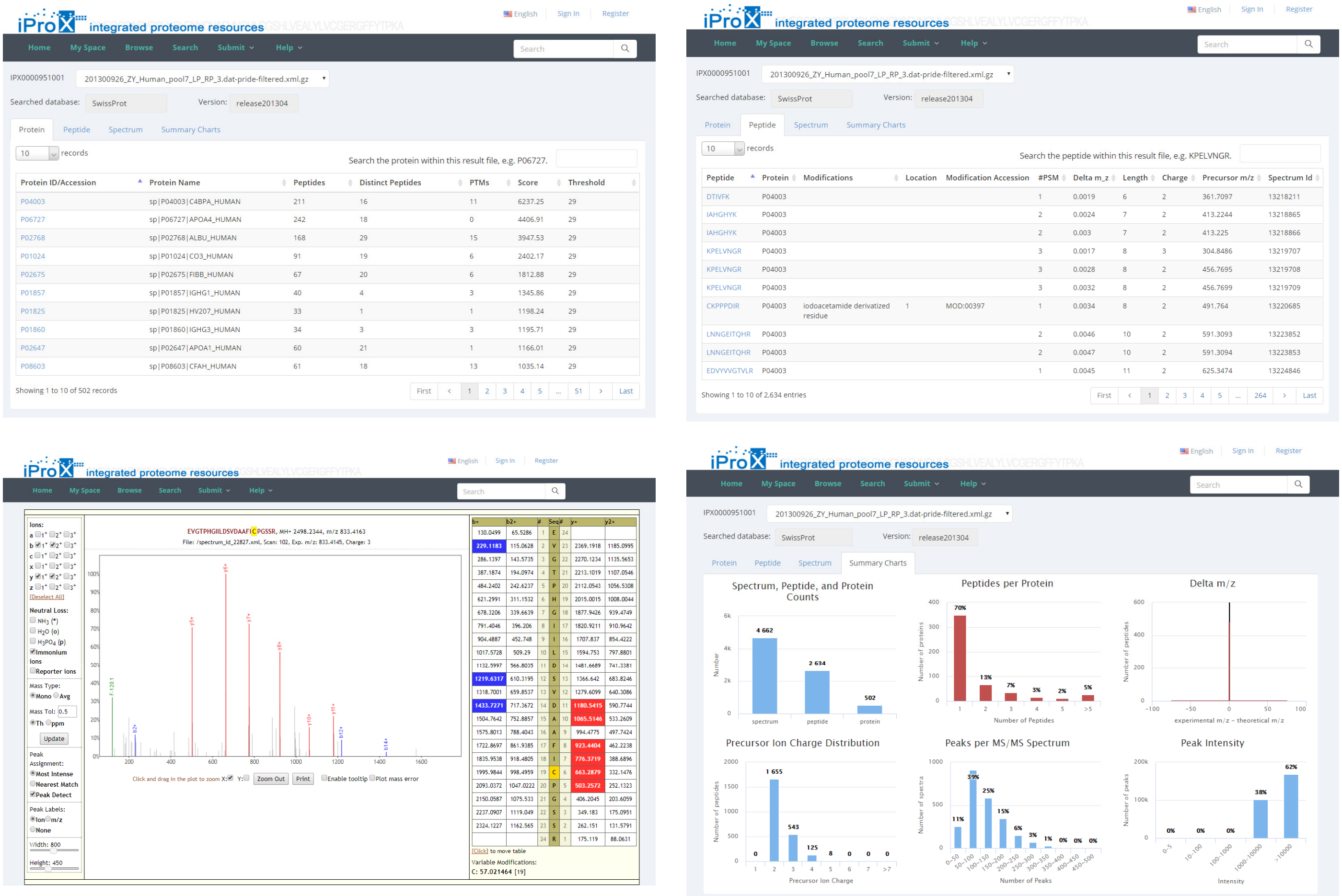
5 records

Search:

☐	File Name	File Type	Related File	File Size	Status	View
☐	201300926_ZY_Human_pool7_LP_RP_10.dat	SEARCH	201300926_ZY_Human_pool7_LP_RP_10.raw	84.65M	✓	
☐	201300926_ZY_Human_pool7_LP_RP_10.dat-pride-filtered.xml.gz	PRIDEXML	201300926_ZY_Human_pool7_LP_RP_10.raw	3.09M	✓	view
☐	201300926_ZY_Human_pool7_LP_RP_10.raw	RAW	201300926_ZY_Human_pool7_LP_RP_10.dat,201300926_ZY_Human_pool7_LP_RP_10.dat-pride-filtered.xml.gz	770.56M	✓	
☐	201300926_ZY_Human_pool7_LP_RP_11.dat	SEARCH	201300926_ZY_Human_pool7_LP_RP_11.raw	87.36M	✓	
☐	201300926_ZY_Human_pool7_LP_RP_11.dat-pride-filtered.xml.gz	PRIDEXML	201300926_ZY_Human_pool7_LP_RP_11.raw	3.66M	✓	view

Showing 1 to 5 of 70 records

(C)



IPX0000951001 201300926_ZY_Human_pool7_LP_RP_3.dat-pride-filtered.xml.gz

Searched database: SwissProt Version: release201304

10 records

Search the protein within this result file, e.g. P06727.

Protein ID/Accession	Protein Name	Peptides	Distinct Peptides	PTMs	Score	Threshold
P04003	sp|P04003|C4BPA_HUMAN	211	16	11	6237.25	29
P06727	sp|P06727|APOA4_HUMAN	242	18	0	4406.91	29
P02768	sp|P02768|ALBU_HUMAN	168	29	15	3947.53	29
P01024	sp|P01024|CO3_HUMAN	91	19	6	2402.17	29
P02675	sp|P02675|FIBB_HUMAN	67	20	6	1812.88	29
P01857	sp|P01857|IGHG1_HUMAN	40	4	3	1345.86	29
P01825	sp|P01825|HV207_HUMAN	33	1	1	1198.24	29
P01860	sp|P01860|IGHG3_HUMAN	34	3	3	1195.71	29
P02647	sp|P02647|APOA1_HUMAN	60	21	1	1166.01	29
P08603	sp|P08603|CFAH_HUMAN	61	18	13	1035.14	29

Showing 1 to 10 of 502 records

IPX0000951001 201300926_ZY_Human_pool7_LP_RP_3.dat-pride-filtered.xml.gz

Searched database: SwissProt Version: release201304

10 records

Search the peptide within this result file, e.g. KPELVNGR.

Peptide	Protein	Modifications	Location	Modification Accession	#PSM	Delta m_z	Length	Charge	Precursor m/z	Spectrum Id
DTIVFK	P04003				1	0.0019	6	2	361.7097	13218211
IAHGHYK	P04003				2	0.0024	7	2	413.2244	13218865
IAHGHYK	P04003				2	0.003	7	2	413.225	13218866
KPELVNGR	P04003				3	0.0017	8	3	304.8486	13219707
KPELVNGR	P04003				3	0.0028	8	2	456.7695	13219708
KPELVNGR	P04003				3	0.0032	8	2	456.7699	13219709
CKPPPDIR	P04003	iodoacetamide derivatized residue	1	MOD:00397	1	0.0034	8	2	491.764	13220685
LNNGEITQHR	P04003				2	0.0046	10	2	591.3093	13223852
LNNGEITQHR	P04003				2	0.0047	10	2	591.3094	13223853
EDVYVVGTVLR	P04003				1	0.0045	11	2	625.3474	13224846

Showing 1 to 10 of 2,634 entries

Ions:
a ☐1+ ☐2+ ☐3+
b ☑1+ ☑2+ ☐3+
c ☐1+ ☐2+ ☐3+
x ☐1+ ☐2+ ☐3+
y ☑1+ ☑2+ ☐3+
z ☐1+ ☐2+ ☐3+
[Deselect All]

Neutral Loss:
☐ NH_3 (*)
☐ H_2O (o)
☐ H_3PO_4 (p)
☑ Immonium ions
☐ Reporter ions

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

● Th ○ ppm

Update

Peak Assignment:
● Most Intense
○ Nearest Match
☑ Peak Detect

Peak Labels:
● Ion ○ m/z
○ None

Width: 800

Height: 450

EVGTPHGIILDSVDAAFICPGSSR, MH+ 2498.2344, m/z 833.4163

File: /spectrum_id_22827.xml, Scan: 102, Exp. m/z: 833.4145, Charge: 3

Click and drag in the plot to zoom X:☑ Y:☐ Zoom Out Print ☐Enable tooltip ☐Plot mass error

b+	b2+	#	Seq	#	y+	y2+
130.0499	65.5286	1	E	24		
229.1183	115.0628	2	V	23	2369.1918	1185.0995
286.1397	143.5735	3	G	22	2270.1234	1135.5653
387.1874	194.0974	4	T	21	2213.1019	1107.0546
484.2402	242.6237	5	P	20	2112.0543	1056.5308
621.2991	311.1532	6	H	19	2015.0015	1008.0044
678.3206	339.6639	7	G	18	1877.9426	939.4749
791.4046	396.206	8	I	17	1820.9211	910.9642
904.4887	452.748	9	I	16	1707.837	854.4222
1017.5728	509.29	10	L	15	1594.753	797.8801
1132.5997	566.8035	11	D	14	1481.6689	741.3381
1219.6317	610.3195	12	S	13	1366.642	683.8246
1318.7001	659.8537	13	V	12	1279.6099	640.3086
1433.7271	717.3672	14	D	11	1180.5415	590.7744
1504.7642	752.8857	15	A	10	1065.5146	533.2609
1575.8013	788.4043	16	A	9	994.4775	497.7424
1722.8697	861.9385	17	F	8	923.4404	462.2238
1835.9538	918.4805	18	I	7	776.3719	388.6896
1995.9844	998.4959	19	C	6	663.2879	332.1476
2093.0372	1047.0222	20	P	5	503.2572	252.1323
2150.0587	1075.533	21	G	4	406.2045	203.6059
2237.0907	1119.049	22	S	3	349.183	175.0951
2324.1227	1162.565	23	S	2	262.151	131.5791
		24	R	1	175.119	88.0631

[Click] to move table

Variable Modifications:
C: 57.021464 [19]

IPX0000951001 201300926_ZY_Human_pool7_LP_RP_3.dat-pride-filtered.xml.gz

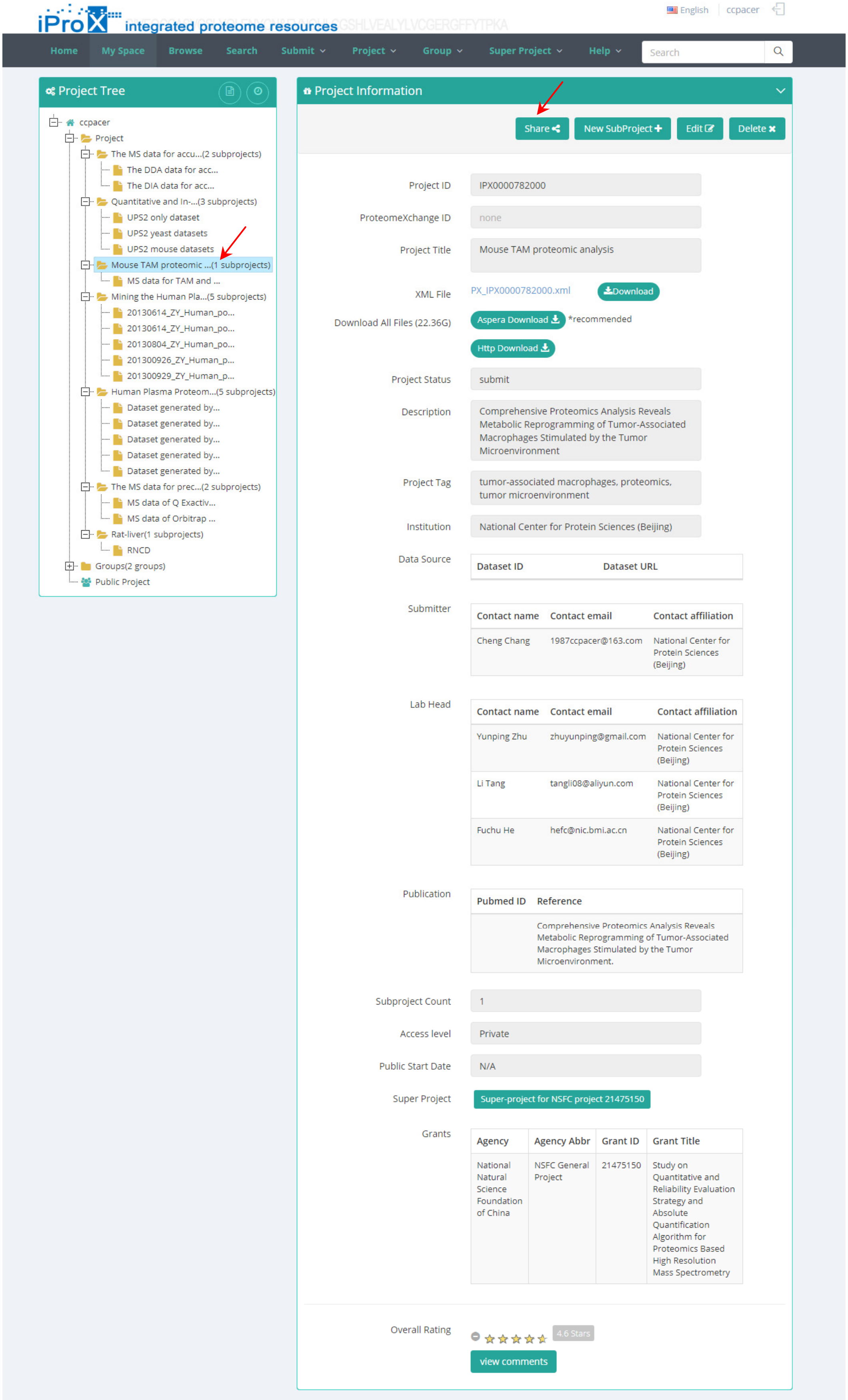
Searched database: SwissProt Version: release201304

(D)

Figure 2. Overview of the example subproject IPX0000951001 in iProX.

2. Access of the shared dataset in iProX

In iProX, submitters can create a sharing URL with a password for peer-review for their private datasets, the validity is limited to 30 days, 90 days, 180 days or 360 days. As shown in Figure 3A, choose the private project in "My Space" ("Project Tree" of the user) and click the "Share" button. Then, a share URL with its password is generated in the pop-up box, and user can also select the valid period of the share link in this box (Figure 3B). Copy and paste the link into the browser (Figure 4A), enter the password, and you will see the shared project (Figure 4B). All data files can be downloaded on this page (red box in Figure 4B). Then click the subproject title and the subproject information is shown (Figure 4C).



- ccpacer
  - Project
    - The MS data for accu...(2 subprojects)
      - The DDA data for acc...
      - The DIA data for acc...
    - Quantitative and in-...(3 subprojects)
      - UPS2 only dataset
      - UPS2 yeast datasets
      - UPS2 mouse datasets
    - Mouse TAM proteomic ...(1 subprojects)
      - MS data for TAM and ...
    - Mining the Human Pla...(5 subprojects)
      - 20130614_ZY_Human_po...
      - 20130614_ZY_Human_po...
      - 20130804_ZY_Human_po...
      - 201300926_ZY_Human_p...
      - 201300929_ZY_Human_p...
    - Human Plasma Proteom...(5 subprojects)
      - Dataset generated by...
      - Dataset generated by...
      - Dataset generated by...
      - Dataset generated by...
      - Dataset generated by...
    - The MS data for prec...(2 subprojects)
      - MS data of Q Exactiv...
      - MS data of Orbitrap ...
    - Rat-liver(1 subprojects)
      - RNCD
  - Groups(2 groups)
  - Public Project

Project ID: IPX0000782000

ProteomeXchange ID: none

Project Title: Mouse TAM proteomic analysis

XML File: PX_IPX0000782000.xml

Download All Files (22.36G): *recommended

Project Status: submit

Description: Comprehensive Proteomics Analysis Reveals Metabolic Reprogramming of Tumor-Associated Macrophages Stimulated by the Tumor Microenvironment

Project Tag: tumor-associated macrophages, proteomics, tumor microenvironment

Institution: National Center for Protein Sciences (Beijing)

Data Source

Dataset ID	Dataset URL

Submitter

Contact name	Contact email	Contact affiliation
Cheng Chang	1987ccpacer@163.com	National Center for Protein Sciences (Beijing)

Lab Head

Contact name	Contact email	Contact affiliation
Yunping Zhu	zhuyunping@gmail.com	National Center for Protein Sciences (Beijing)
Li Tang	tangli08@aliyun.com	National Center for Protein Sciences (Beijing)
Fuchu He	hefc@nic.bmi.ac.cn	National Center for Protein Sciences (Beijing)

Publication

Pubmed ID	Reference
	Comprehensive Proteomics Analysis Reveals Metabolic Reprogramming of Tumor-Associated Macrophages Stimulated by the Tumor Microenvironment.

Subproject Count: 1

Access level: Private

Public Start Date: N/A

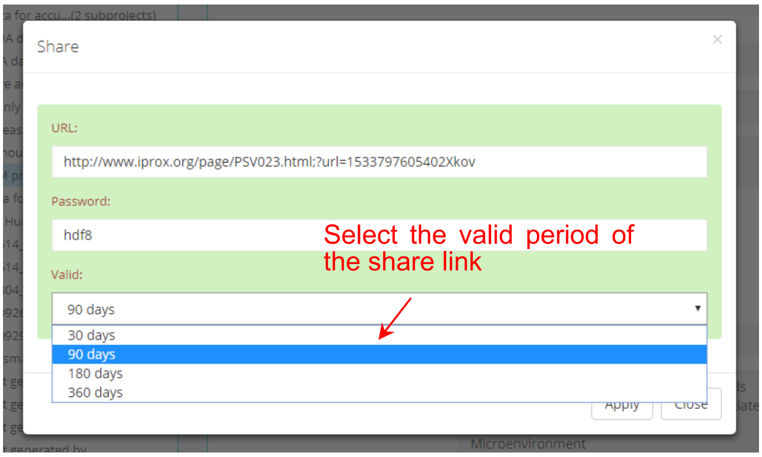
Super Project: Super-project for NSFC project 21475150

Grants

Agency	Agency Abbr	Grant ID	Grant Title
National Natural Science Foundation of China	NSFC General Project	21475150	Study on Quantitative and Reliability Evaluation Strategy and Absolute Quantification Algorithm for Proteomics Based High Resolution Mass Spectrometry

Overall Rating: ☆☆☆☆☆ 4.6 Stars

(A)



URL:

http://www.iprox.org/page/PSV023.html;?url=1533797605402Xkov

Password:

hdf8

Valid:

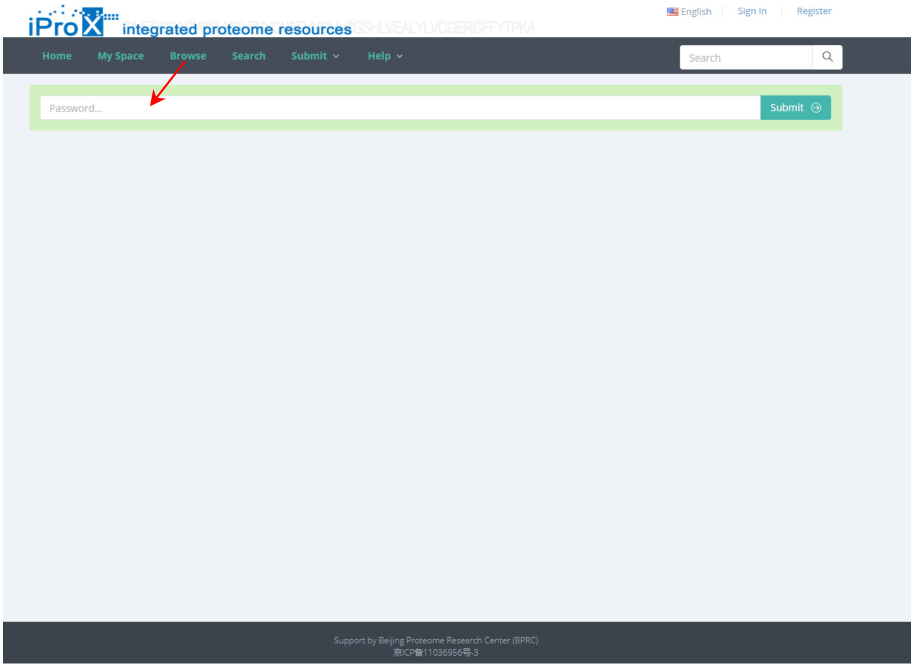
90 days

- 30 days
- 90 days
- 180 days
- 360 days

Select the valid period of the share link

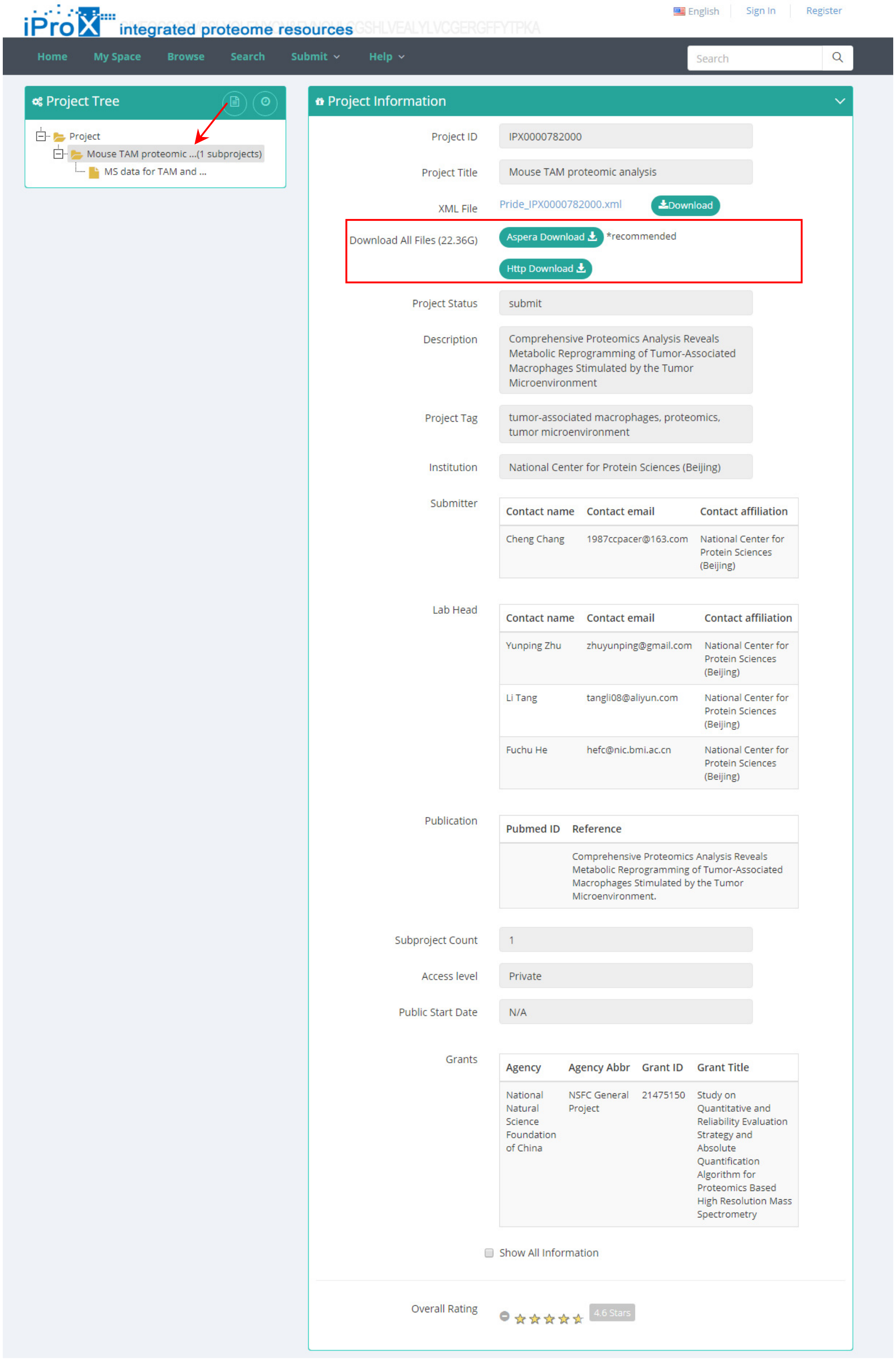
(B)

Figure 3. Creating a share URL for peer-review for the private dataset in iProX.



Support by Beijing Proteome Research Center (BPRC)
京ICP备11036956号-3

(A)



Project Tree

- Project
  - Mouse TAM proteomic ...(1 subprojects)
    - MS data for TAM and ...

Project Information

Project ID: IPX0000782000

Project Title: Mouse TAM proteomic analysis

XML File: Pride_IPX0000782000.xml Download

Download All Files (22.36G): Aspera Download *recommended Http Download

Project Status: submit

Description: Comprehensive Proteomics Analysis Reveals Metabolic Reprogramming of Tumor-Associated Macrophages Stimulated by the Tumor Microenvironment

Project Tag: tumor-associated macrophages, proteomics, tumor microenvironment

Institution: National Center for Protein Sciences (Beijing)

Submitter

Contact name	Contact email	Contact affiliation
Cheng Chang	1987ccpacer@163.com	National Center for Protein Sciences (Beijing)

Lab Head

Contact name	Contact email	Contact affiliation
Yunping Zhu	zhuyunping@gmail.com	National Center for Protein Sciences (Beijing)
Li Tang	tangli08@aliyun.com	National Center for Protein Sciences (Beijing)
Fuchu He	hefc@nic.bmi.ac.cn	National Center for Protein Sciences (Beijing)

Publication

Pubmed ID	Reference
	Comprehensive Proteomics Analysis Reveals Metabolic Reprogramming of Tumor-Associated Macrophages Stimulated by the Tumor Microenvironment.

Subproject Count: 1

Access level: Private

Public Start Date: N/A

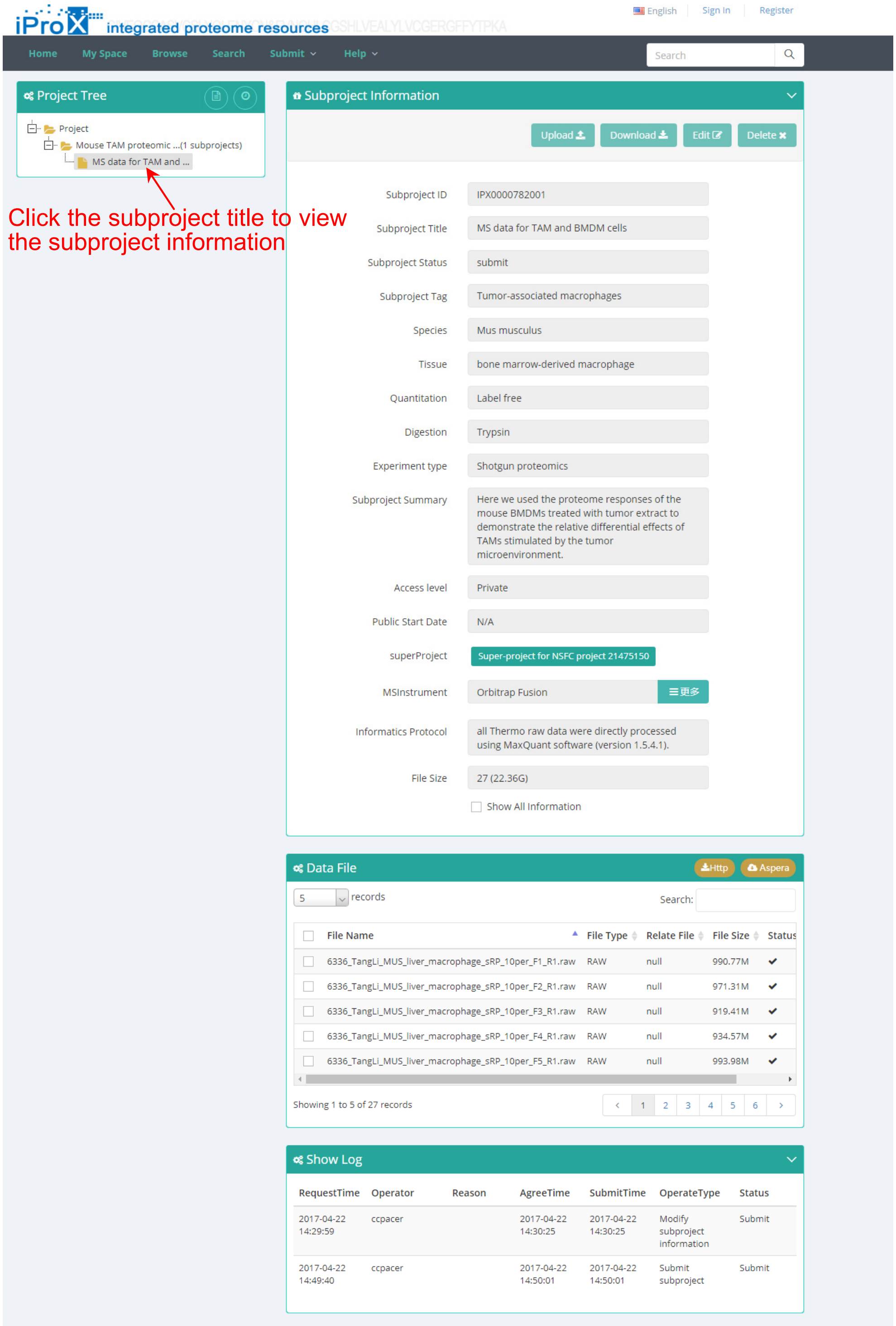
Grants

Agency	Agency Abbr	Grant ID	Grant Title
National Natural Science Foundation of China	NSFC General Project	21475150	Study on Quantitative and Reliability Evaluation Strategy and Absolute Quantification Algorithm for Proteomics Based High Resolution Mass Spectrometry

☐ Show All Information

Overall Rating: ☆☆☆☆☆ 4.6 Stars

(B)



Click the subproject title to view the subproject information

Subproject ID	IPX0000782001
Subproject Title	MS data for TAM and BMDM cells
Subproject Status	submit
Subproject Tag	Tumor-associated macrophages
Species	Mus musculus
Tissue	bone marrow-derived macrophage
Quantitation	Label free
Digestion	Trypsin
Experiment type	Shotgun proteomics
Subproject Summary	Here we used the proteome responses of the mouse BMDMs treated with tumor extract to demonstrate the relative differential effects of TAMs stimulated by the tumor microenvironment.
Access level	Private
Public Start Date	N/A
superProject	Super-project for NSFC project 21475150
MSInstrument	Orbitrap Fusion ☰更多
Informatics Protocol	all Thermo raw data were directly processed using MaxQuant software (version 1.5.4.1).
File Size	27 (22.36G)

☐ Show All Information

5 records

Search:

☐	File Name	File Type	Relate File	File Size	Status
☐	6336_TangLi_MUS_liver_macrophage_sRP_10per_F1_R1.raw	RAW	null	990.77M	✓
☐	6336_TangLi_MUS_liver_macrophage_sRP_10per_F2_R1.raw	RAW	null	971.31M	✓
☐	6336_TangLi_MUS_liver_macrophage_sRP_10per_F3_R1.raw	RAW	null	919.41M	✓
☐	6336_TangLi_MUS_liver_macrophage_sRP_10per_F4_R1.raw	RAW	null	934.57M	✓
☐	6336_TangLi_MUS_liver_macrophage_sRP_10per_F5_R1.raw	RAW	null	993.98M	✓

Showing 1 to 5 of 27 records

‹ 1 2 3 4 5 6 ›

RequestTime	Operator	Reason	AgreeTime	SubmitTime	OperateType	Status
2017-04-22 14:29:59	ccpacer		2017-04-22 14:30:25	2017-04-22 14:30:25	Modify subproject information	Submit
2017-04-22 14:49:40	ccpacer		2017-04-22 14:50:01	2017-04-22 14:50:01	Submit subproject	Submit

(C)

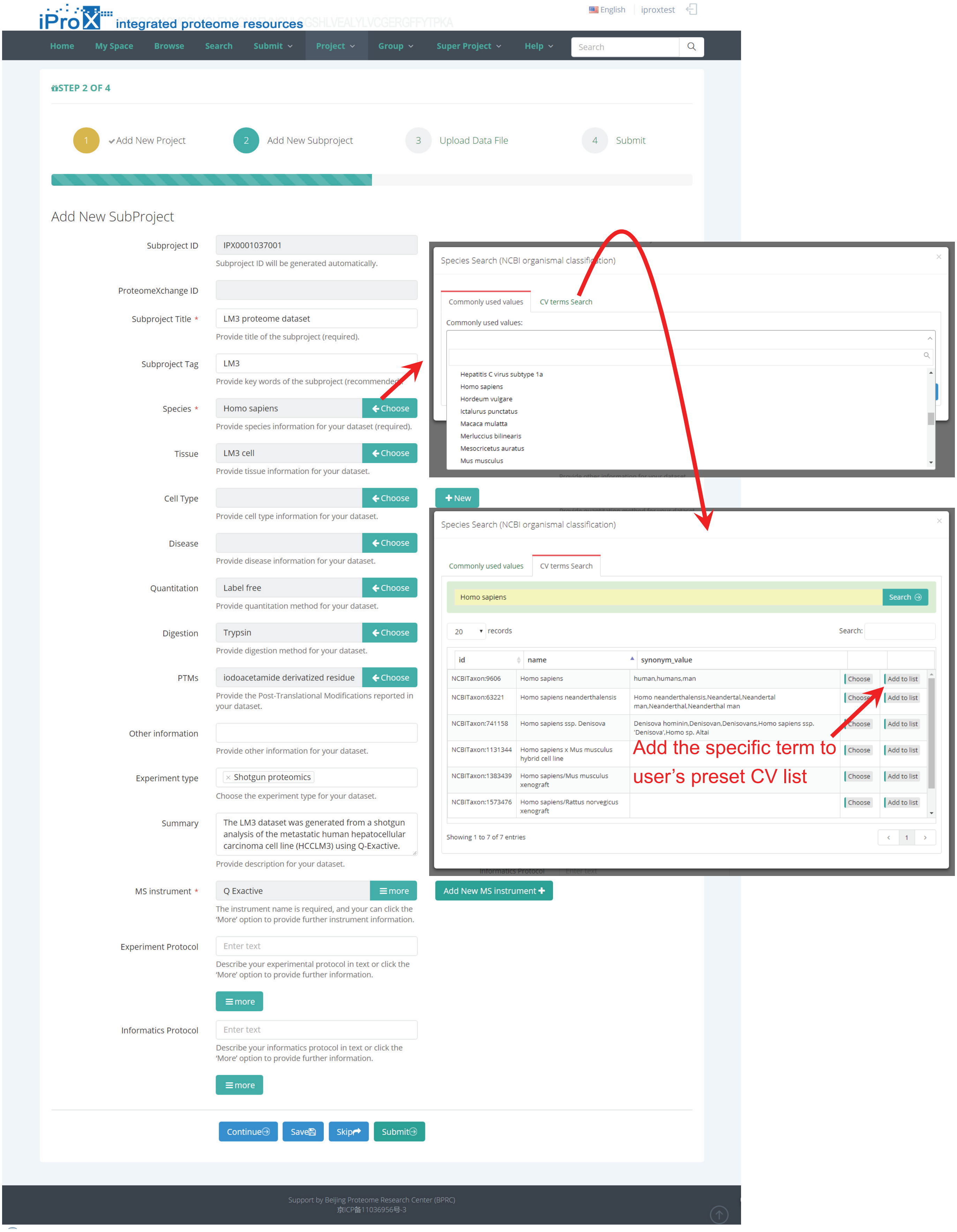
Figure 4. Access to the shared dataset in iProX.

References

1. Zhao, Y., Chang, C., Qin, P., Cao, Q., Tian, F., Jiang, J., Li, X., Yu, W., Zhu, Y., He, F. *et al.* (2016) Mining the human plasma proteome with three-dimensional strategies by high-resolution Quadrupole Orbitrap Mass Spectrometry. *Anal Chim Acta*, **904**, 65-75.

Supplementary Figures

Supplementary Figure S1. The iProX controlled vocabulary viewer. This tool enables data submitters to browse or search for relevant ontology terms directly on the website. Several common values are provided as defaults. Also, users can search and preset their specific CV terms, which can be reused in different data submissions with similar experimental settings.



STEP 2 OF 4

1 ✓Add New Project — 2 Add New Subproject — 3 Upload Data File — 4 Submit

Add New SubProject

Subproject ID: IPX0001037001
Subproject ID will be generated automatically.

ProteomeXchange ID:

Subproject Title *: LM3 proteome dataset
Provide title of the subproject (required).

Subproject Tag: LM3
Provide key words of the subproject (recommended).

Species *: Homo sapiens
Provide species information for your dataset (required).

Tissue: LM3 cell
Provide tissue information for your dataset.

Cell Type:
Provide cell type information for your dataset.

Disease:
Provide disease information for your dataset.

Quantitation: Label free
Provide quantitation method for your dataset.

Digestion: Trypsin
Provide digestion method for your dataset.

PTMs: iodoacetamide derivatized residue
Provide the Post-Translational Modifications reported in your dataset.

Other information:
Provide other information for your dataset.

Experiment type: × Shotgun proteomics
Choose the experiment type for your dataset.

Summary: The LM3 dataset was generated from a shotgun analysis of the metastatic human hepatocellular carcinoma cell line (HCCLM3) using Q-Exactive.
Provide description for your dataset.

MS instrument *: Q Exactive
The instrument name is required, and your can click the 'More' option to provide further instrument information.

Experiment Protocol: Enter text
Describe your experimental protocol in text or click the 'More' option to provide further information.

Informatics Protocol: Enter text
Describe your informatics protocol in text or click the 'More' option to provide further information.

Support by Beijing Proteome Research Center (BPRC)
京ICP备11036956号-3

Species Search (NCBI organismal classification)

Commonly used values | CV terms Search

Commonly used values:

- Hepatitis C virus subtype 1a
- Homo sapiens
- Hordeum vulgare
- Ictalurus punctatus
- Macaca mulatta
- Merluccius bilinearis
- Mesocricetus auratus
- Mus musculus

Species Search (NCBI organismal classification)

Commonly used values | CV terms Search

Homo sapiens

20 records   Search:

id	name	synonym_value		
NCBITaxon:9606	Homo sapiens	human,humans,man	Choose	Add to list
NCBITaxon:63221	Homo sapiens neanderthalensis	Homo neanderthalensis,Neandertal,Neandertal man,Neanderthal,Neanderthal man	Choose	Add to list
NCBITaxon:741158	Homo sapiens ssp. Denisova	Denisova hominin,Denisovan,Denisovans,Homo sapiens ssp. 'Denisova',Homo sp. Altai	Choose	Add to list
NCBITaxon:1131344	Homo sapiens x Mus musculus hybrid cell line		Choose	Add to list
NCBITaxon:1383439	Homo sapiens/Mus musculus xenograft		Choose	Add to list
NCBITaxon:1573476	Homo sapiens/Rattus norvegicus xenograft		Choose	Add to list

Showing 1 to 7 of 7 entries

Add the specific term to user's preset CV list