

# AJACSオンライン 10 (20220120)



jPOSTを使って  
プロテオーム解析をする

熊本大学生命科学研究部  
腫瘍医学 荒木令江&  
jPOST TEAM  
(代表 京都大学 石濱泰)

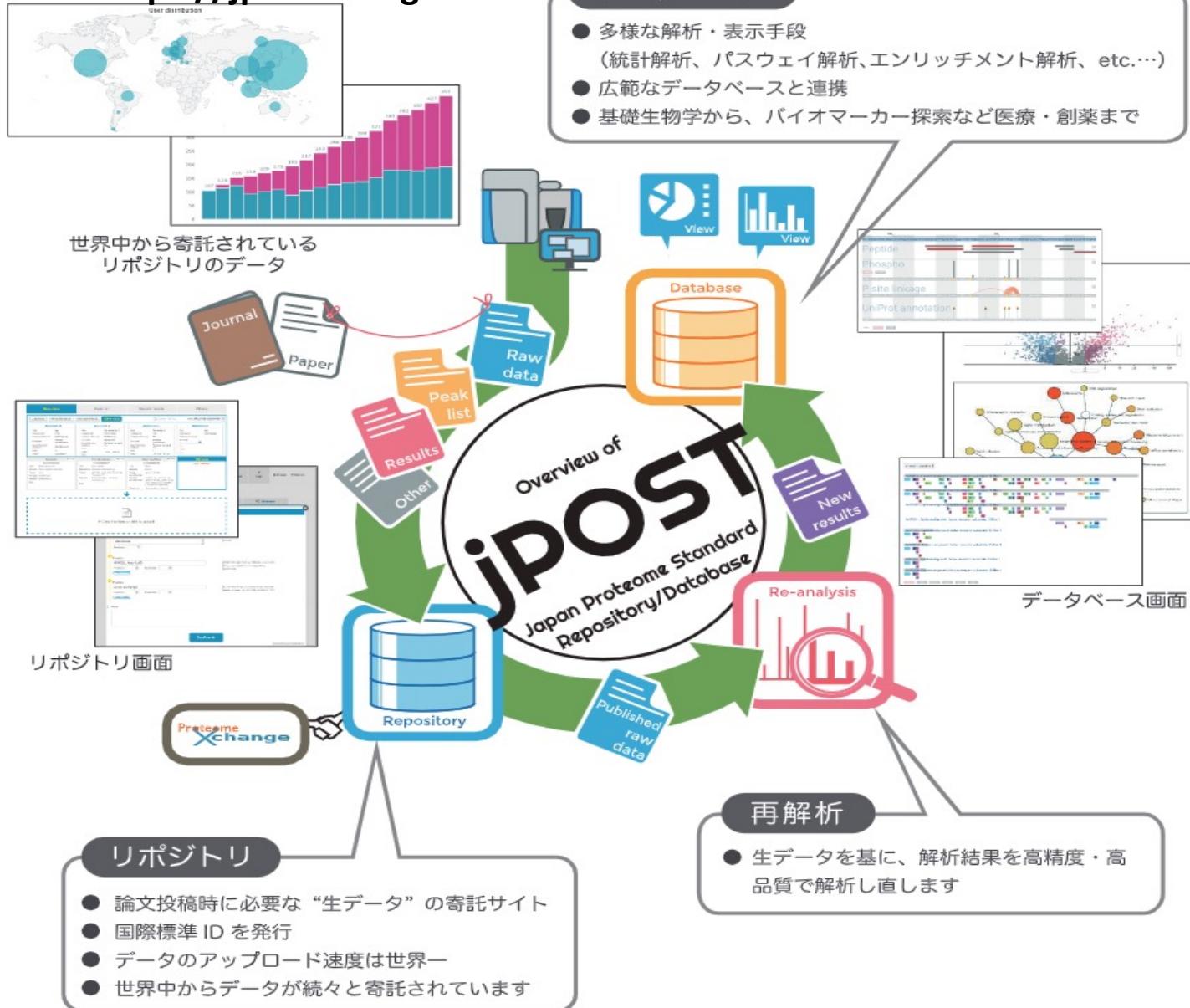


# jPOST とは？



## (Japan Proteome Standard Repository/Database)

<https://jpostdb.org>



# <https://jpostdb.org>

→ ⌂ https://jpostdb.org

The screenshot shows the jPOST website homepage. At the top, there's a navigation bar with links for About, Repository, Database, Workflow, Gadgets, COVID-19, Help, FAQ, and Contact. A search bar is also present. On the left, there's a large orange circular logo with the text "jPOST" and "Repository / Database". Below the logo, it says "Japan Proteome Standard Repository/Database". There's a section for "Recent posts" with a link to a member's co-authored paper about USI. The main content area has six sections: "Repository", "Database", "Workflow", "Gadgets", "COVID-19", and "Help", each with an icon and a brief description.

**jPOST**  
Repository / Database

Japan Proteome Standard  
Repository/Database

Recent posts

[other](#)  
**jPOST member's co-authored  
paper about USI has been  
published.**

⌚ 2021-06-30 jpost

The Universal Spectrum Identifier (USI) is an essential mechanism for the wide use of proteomics data provided by the ProteomeXchange (PX) repositories. It has been discussed for a long time in the HUPO Proteomics Standards Initiative, to which jPOST member Prof. Kawano has contributed greatly. The USI facilitates access to the huge amount of spectral data registered in the PX repositories, and is expected to make proteomics data is more findable, accessible, interoperable, and reusable. We expect that the USI leads to the use of

**About** **Repository** **Database** **Workflow** **Gadgets** **COVID-19** **Help** **FAQ** **Contact**

 **Repository** [Help ▾](#)  
jPOSTrepo is a raw and processed data repository of mass-based proteomics.

 **Database** [Help ▾](#)  
jPOSTdb is a database containing re-analysis results with unified criteria for proteome data from jPOSTrepo.

 **Workflow** [Help ▾](#)  
This provides the re-analysis workflow used in jPOST.

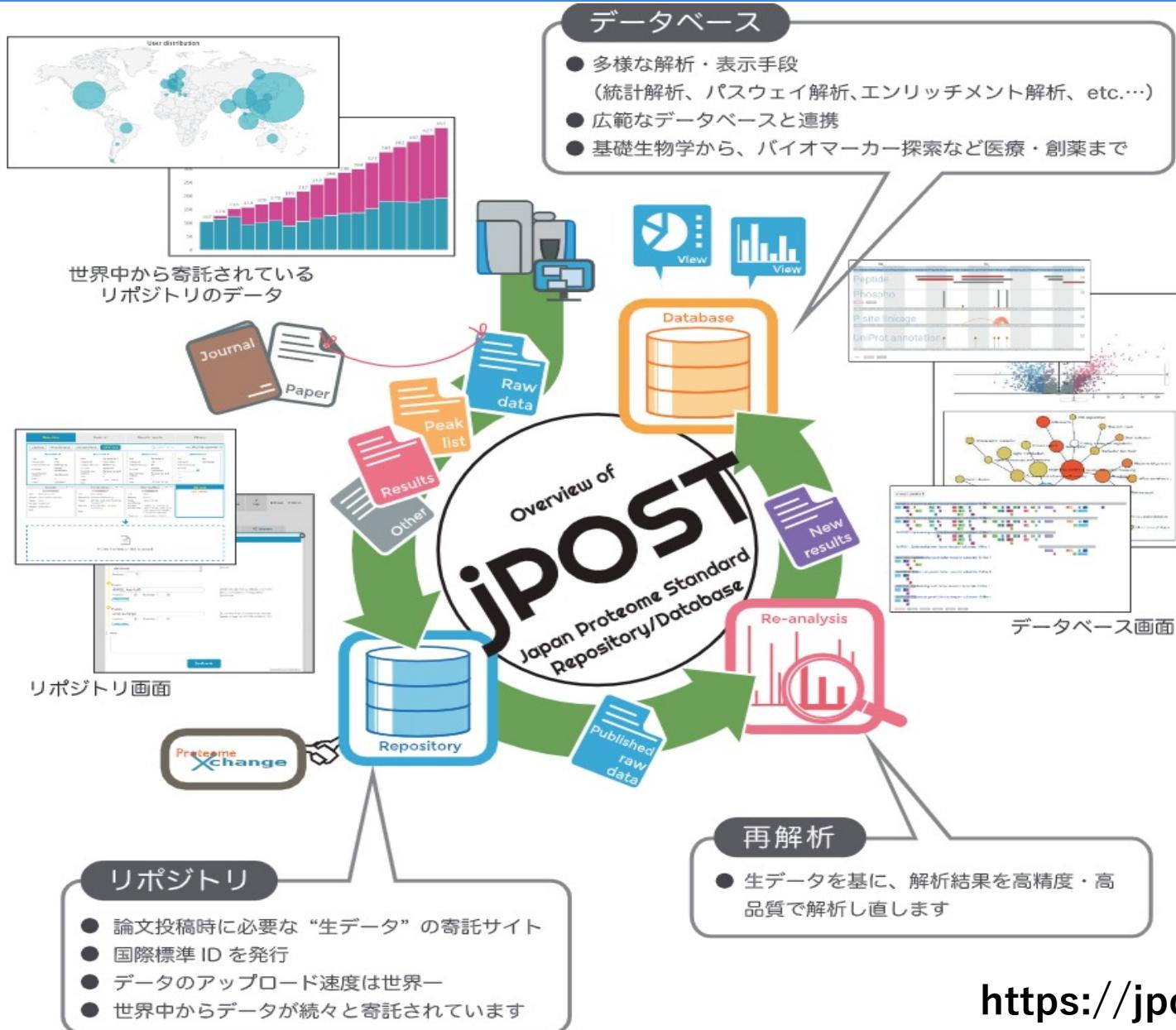
 **Gadgets** [Help ▾](#)  
jPOST gadget is a collection of tools we have developed as well as other commonly used tools for mass spectrometry-based proteomics.

 **COVID-19** [Help ▾](#)  
This is a special page on coronavirus (SARS-CoV-2) and the COVID-19 disease data, where mass-based proteomics data in ProteomeXchange resources are analyzed by the jPOST re-analysis workflow.

 **Help**  
A guide to using the jPOST resources.

# jPOST とは？

(Japan Proteome Standard Repository/Database)



<https://jpostdb.org>

# jPOST とは？



## ProteomeXchange Consortium

Mission: The ProteomeXchange Consortium was established to provide globally coordinated standard data submission and dissemination pipelines involving the main proteomics repositories, and to encourage open data policies in the field. Please review our [Data Submission Guidelines](#), [Guidelines for Reprocessed datasets](#) and [PX Membership Agreement](#). See also the [original Nature Biotechnology publication](#) and the [2017](#) and [2020](#) update papers.

## Proteome: プロテオームとは？

組織や細胞や体液分泌物などの、生体系に存在するタンパク質の総体

例. 肝臓組織に含まれるすべてのタンパク質

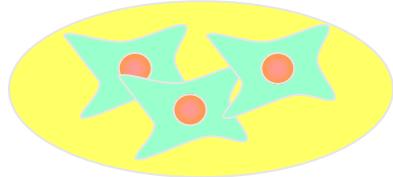
HEK293培養細胞の細胞膜や核や細胞質を構成するすべてのタンパク質等

質量分析(Mass Spectrometry/MS)で  
プロテオームを測定する。

質量分析を用いて、ある生体系に存在している  
すべてのタンパク質を測定する。

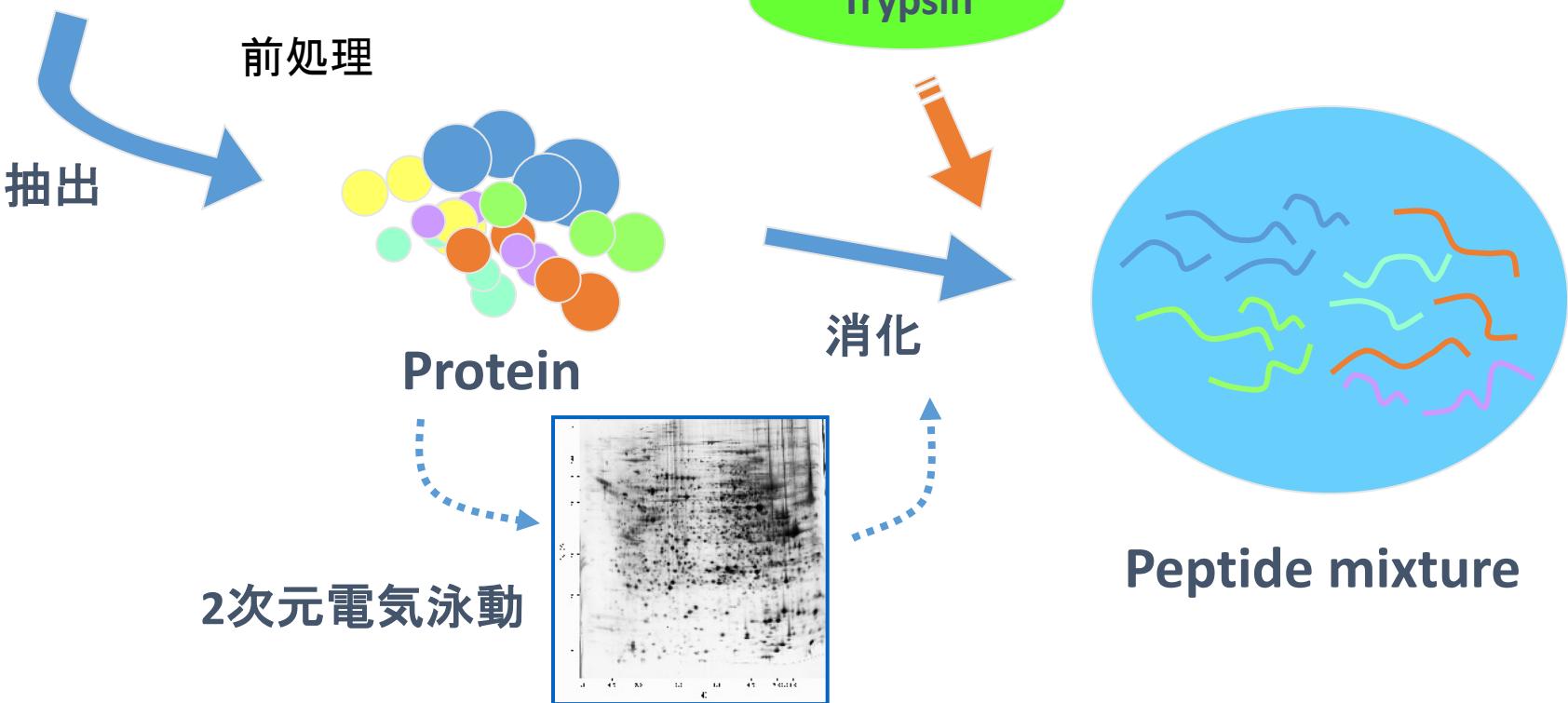
# Proteome Analysis Workflow

## プロテオミクスにおけるタンパク質同定のワークフロー(1) 酵素(Trypsin)による消化



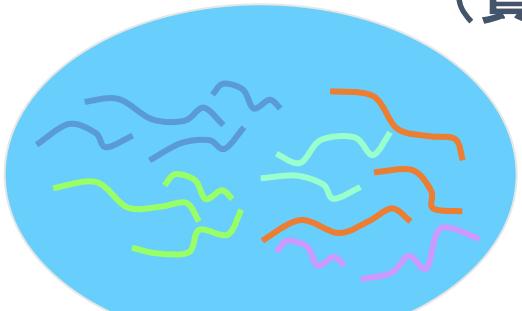
生体試料 (培養細胞、組織、体液、菌など)

Trypsin: Lysine(K)またはArginine(R)の  
C末端側のペプチド結合を加水分解  
する酵素



# Proteome Analysis Workflow

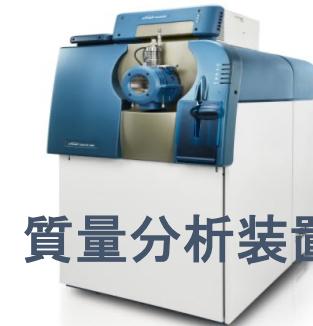
## プロテオミクスにおけるタンパク質同定のワークフロー(2) (質量分析装置による測定)



Peptide mixture

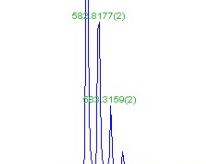
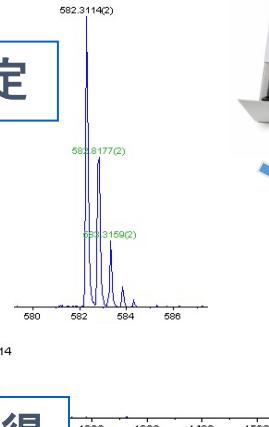


Nano LC  
(ペプチド分離)

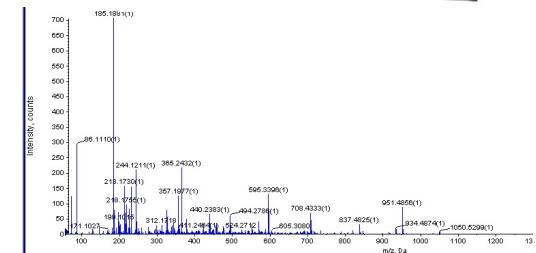
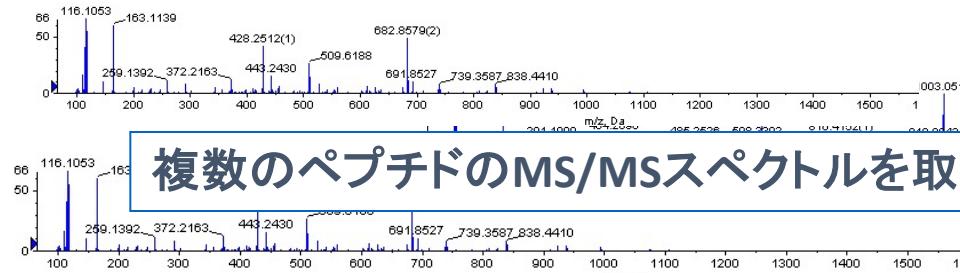


質量分析装置

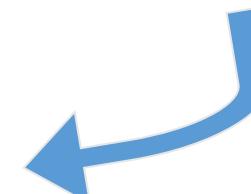
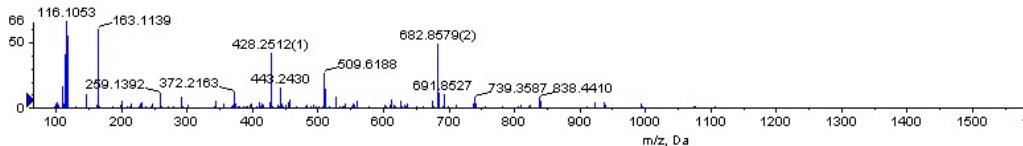
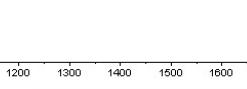
MS測定



複数のペプチドのMS/MSスペクトルを取得



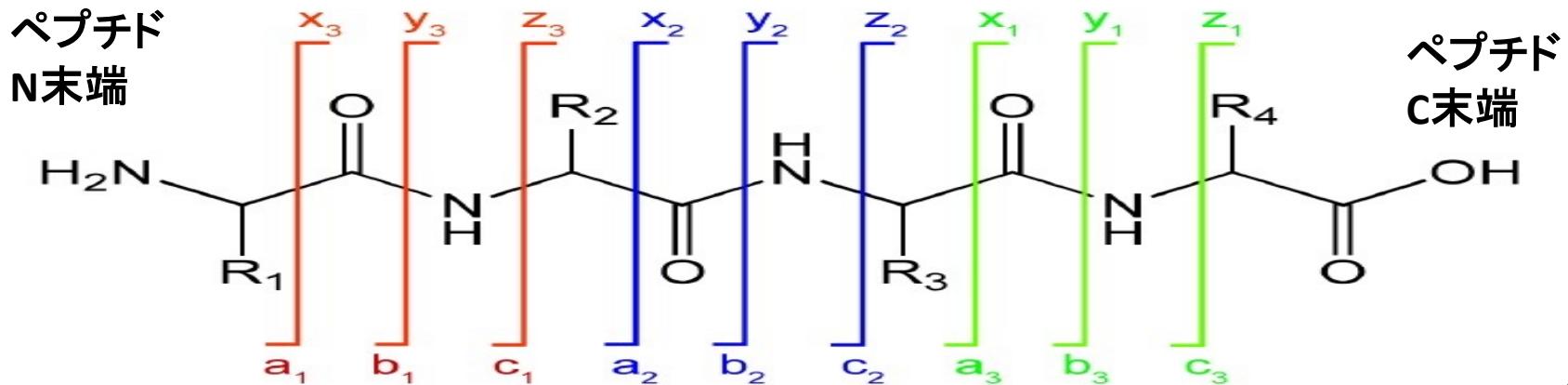
MS/MS測定



# Proteome Analysis Workflow

ペプチドの配列を同定するための質量分析で計測される  
MS/MSスペクトル

## ペプチドのフラグメント化パターン



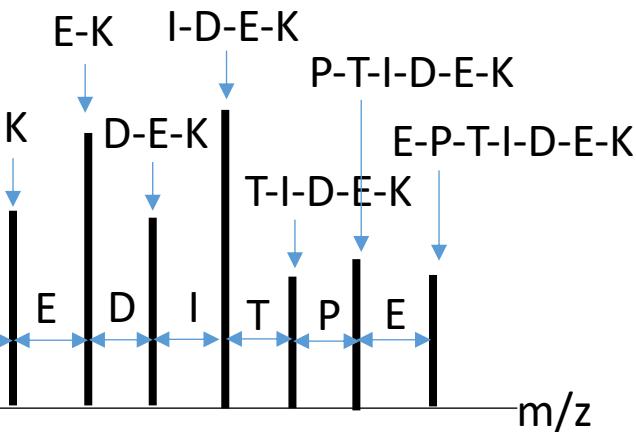
## Collision

### ペプチド

-P--E--P--T--I--D--E--K

-P- -E--P--T--I--D--E--K-  
-P--E- -P--T--I--D--E--K-  
-P--E--P- -T--I--D--E--K-  
-P--E--P--T- -I--D--E--K-  
-P--E--P--T--I- -D--E--K-  
-P--E--P--T--I--D- -E--K-  
-P--E--P--T--I--D--E- -K-

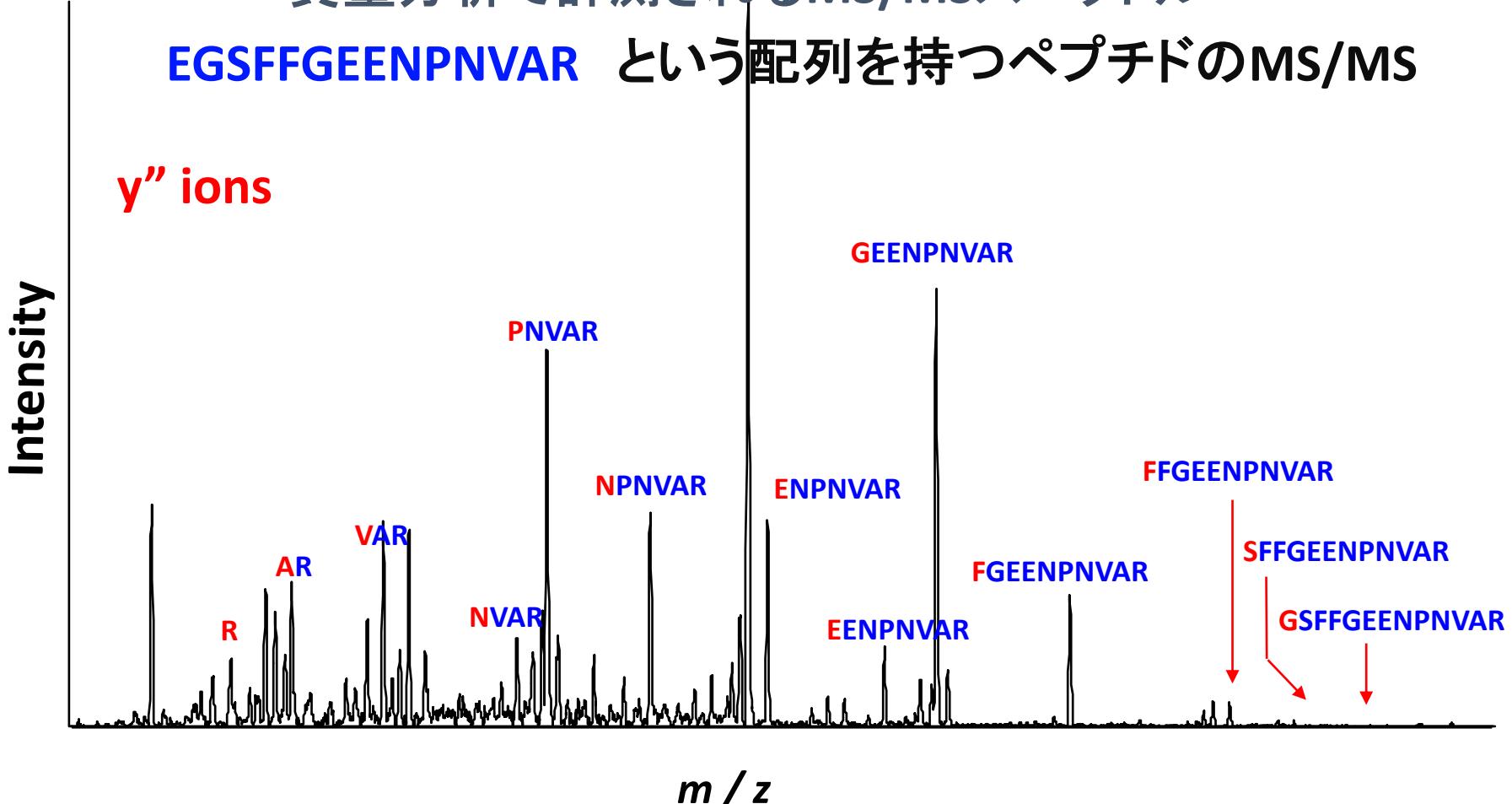
## MS/MS スペクトル



# Proteome Analysis Workflow

ペプチドの配列を同定するための  
質量分析で計測されるMS/MSスペクトル

EGSFFGEENPNVAR という配列を持つペプチドのMS/MS

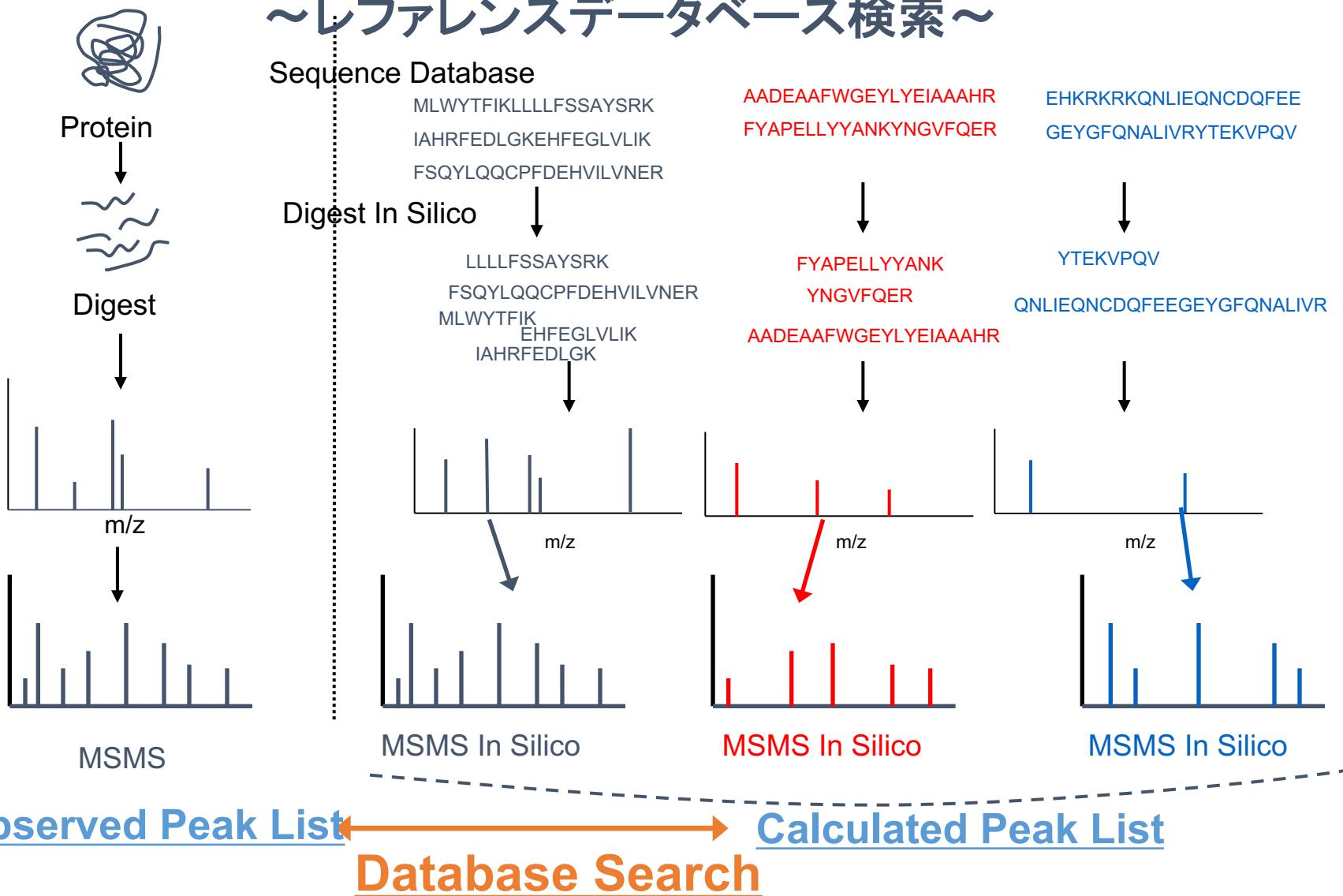


MS/MSによってペプチド断片のスペクトル情報(質量情報)が得られる

# Proteome Analysis Workflow

MS/MSスペクトルからタンパク質を同定する

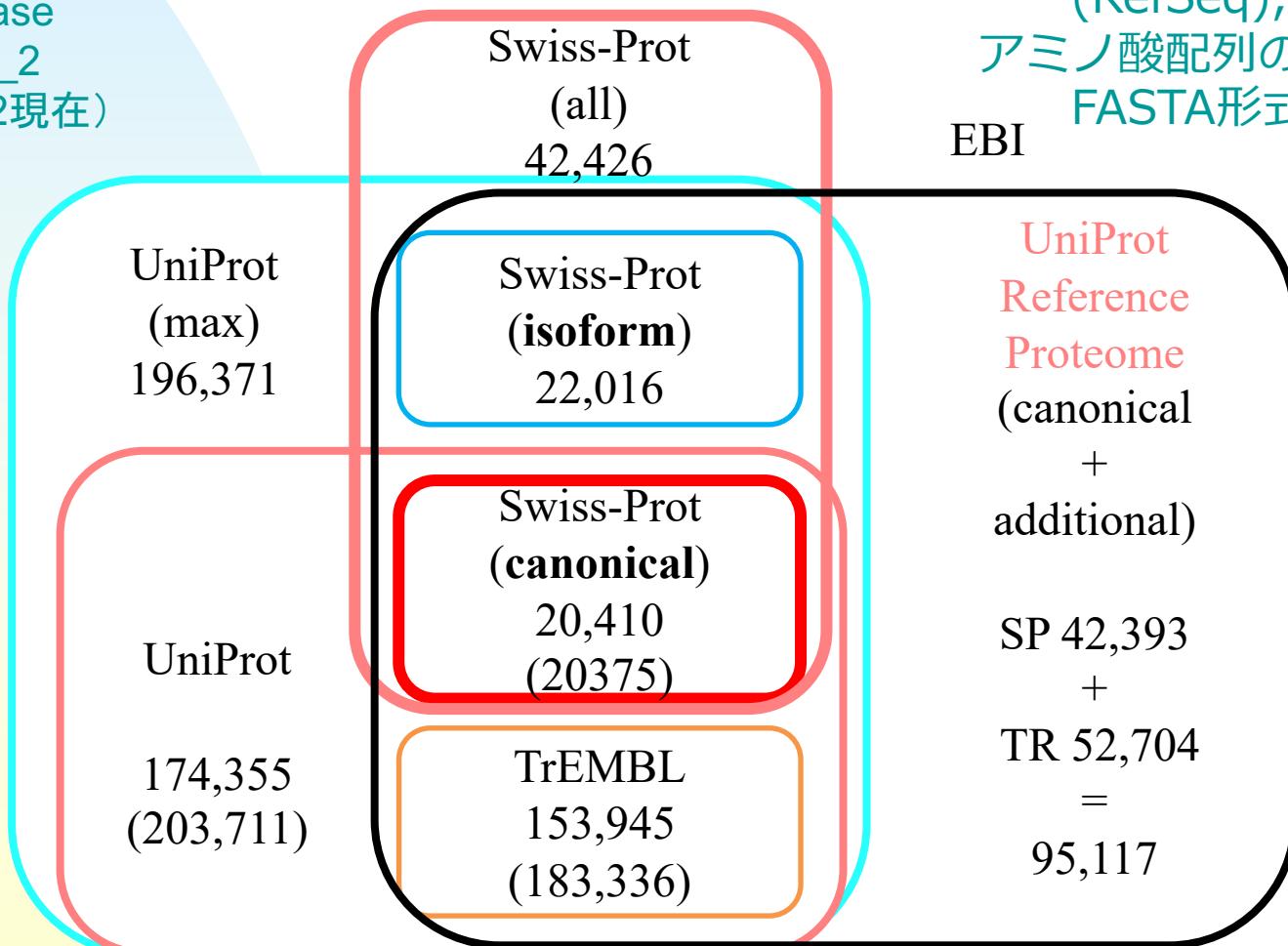
～レファレンスデータベース検索～



# Reference Protein Database Sequence collection

## ヒトの場合

Release  
2018\_2  
(2022現在)



アミノ酸配列コレクション  
amino acid sequence collection  
UniProt, Swiss-Prot  
(RefSeq),(IPI)  
アミノ酸配列の集合  
FASTA形式  
EBI

# MS based proteome analyses

## 質量分析による様々なプロテオーム解析

- ・定性プロテオーム解析(タンパク質の網羅的同定)
- ・定量プロテオーム解析(タンパク質の網羅的発現差異解析)
- ・翻訳後修飾ペプチド・タンパク質の網羅的同定・定量解析
- ・特定の分子(低分子化合物・生体分子)に結合するタンパク質の網羅的同定

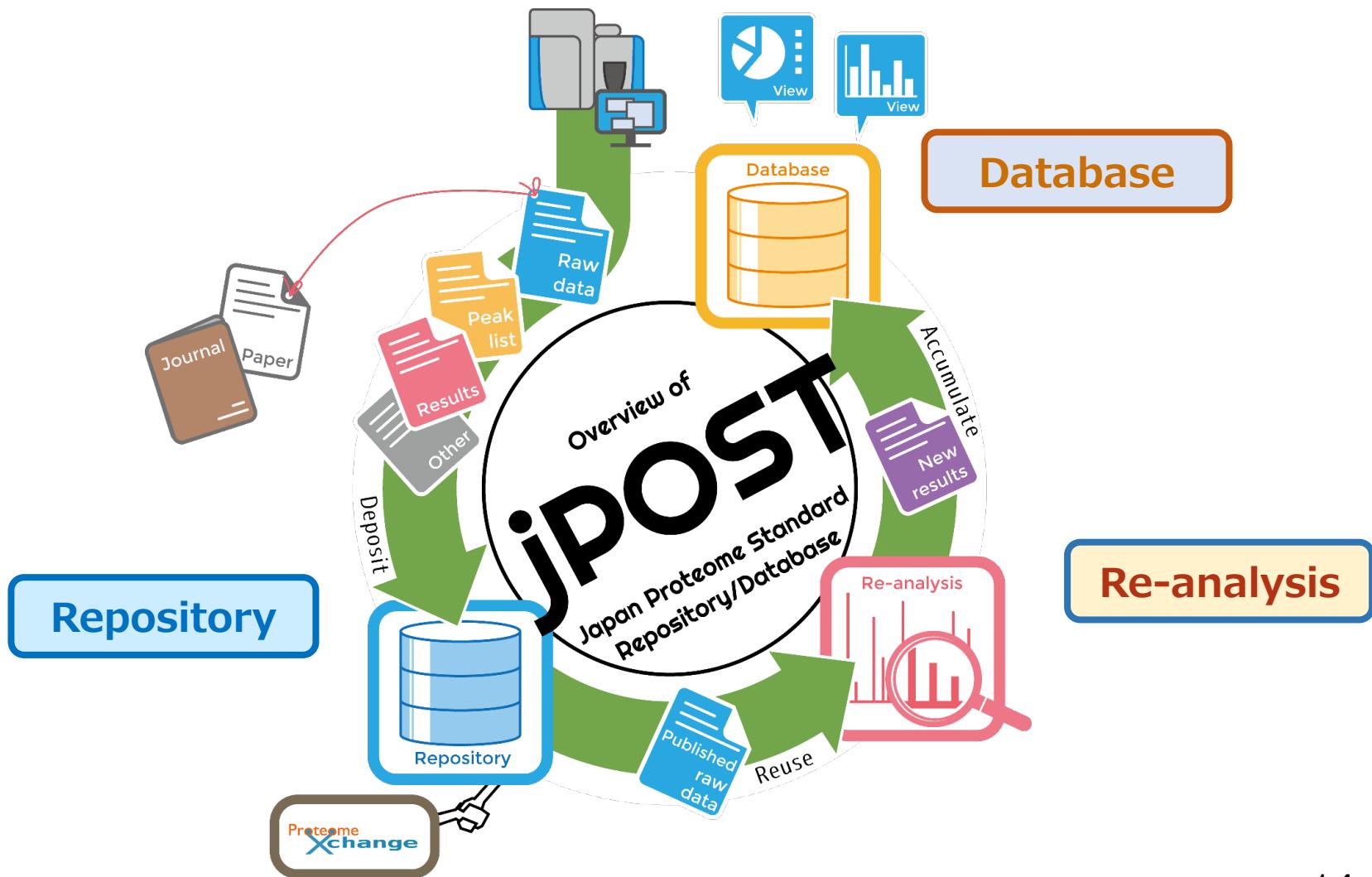
などなど

莫大な質量分析情報がどんどん溜まっていく！→  
これらの情報をまとめて格納し、再利用できるようにする。

→ jPOSTへ

# jPOSTとは

## Data Integration & Sharing in Life Science



# jPOSTの特徴



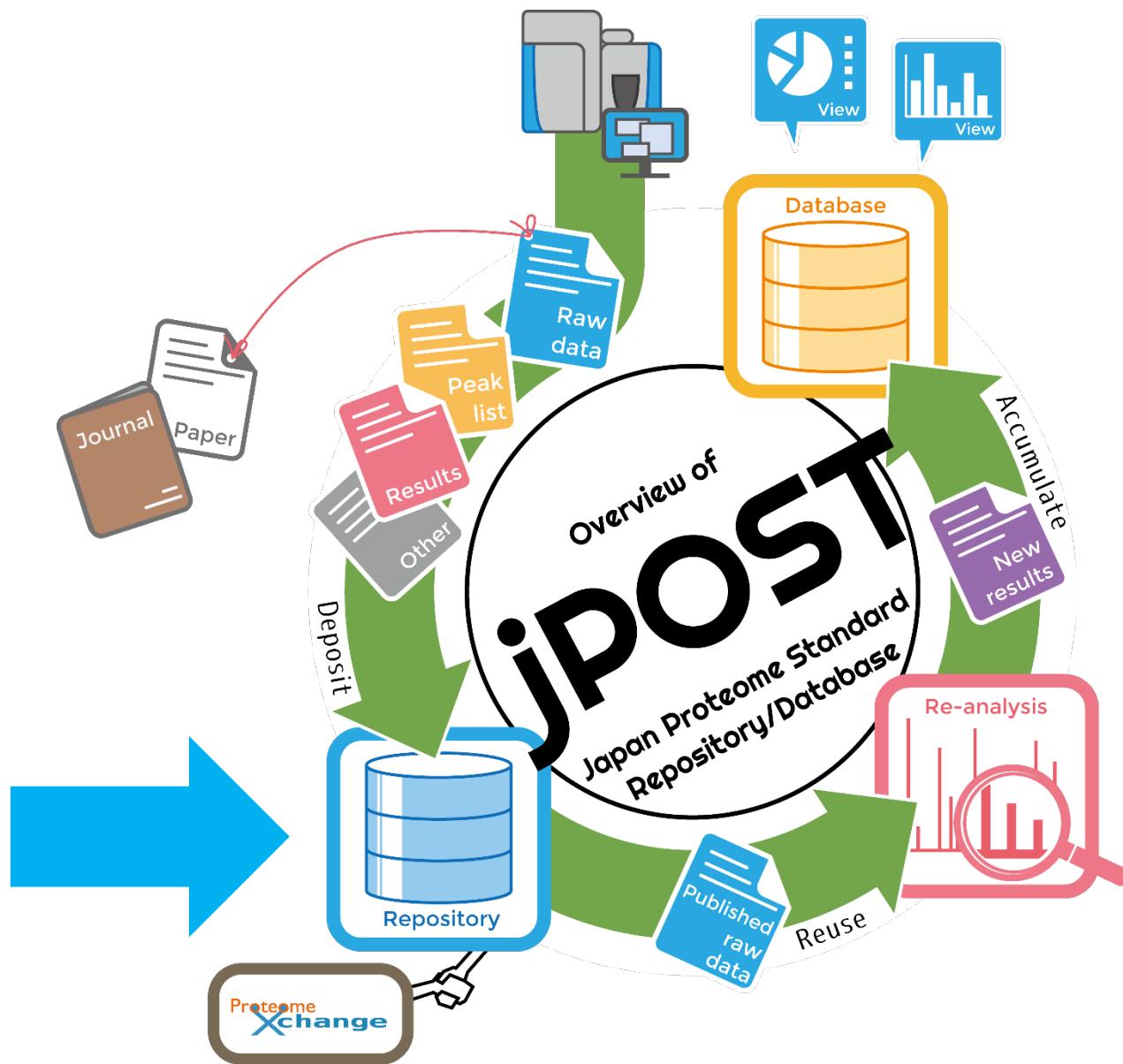
1. フレッシュな生データがどんどん勝手にたまる
2. 再解析により、データの統一化が実現される
3. カスタムDBの作成ツールと可視化ツールの提供

# jPOSTの特徴



1. フレッシュな生データがどんどん勝手にたまる

# jPOST repository



# <https://jpostdb.org>

→ ⌂ 🗃 https://jpostdb.org

The screenshot shows the jPOST website homepage. At the top left is a large orange circular logo with "jPOST" in white and "Repository / Database" below it. To its right is a navigation bar with links: About, Repository, Database, Workflow, Gadgets, COVID-19, Help, FAQ, and Contact. A search bar is located at the top right. Below the navigation bar, there are six main sections, each with an icon and a title: "Repository" (orange box icon), "Database" (orange server icon), "Workflow" (orange process icon), "Gadgets" (orange gear icon), "COVID-19" (orange virus icon), and "Help" (orange question mark icon). Each section has a brief description below its title. On the left side of the page, there is a sidebar with a heading "Recent posts" and a link to a blog post about the Universal Spectrum Identifier (USI). The main content area has a light gray background with horizontal lines.

Japan Proteome Standard  
Repository/Database

## Recent posts

other

[jPOST member's co-authored paper about USI has been published.](#)

⌚ 2021-06-30 🏁 jpost

The Universal Spectrum Identifier (USI) is an essential mechanism for the wide use of proteomics data provided by the ProteomeXchange (PX) repositories. It has been discussed for a long time in the HUPO Proteomics Standards Initiative, to which jPOST member Prof. Kawano has contributed greatly. The USI facilitates access to the huge amount of spectral data registered in the PX repositories, and is expected to make proteomics data is more findable, accessible, interoperable, and reusable. We expect that the USI leads to the use of

About   Repository   Database   Workflow   Gadgets   COVID-19   Help   FAQ   Contact

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### Help

A guide to using the jPOST resources.

# jPOST repository

<https://repository.jpostdb.org>



jPOST repositoryはプロテオームの測定データを寄託・開示するためのWebサイト

The screenshot shows the top navigation bar of the jPOST repository website. It includes the jPOST logo, a "REPOSITORY" button, a "Proteome Xchange" member badge, and links for "Repository", "Submit", "Help", "Sign in", and "Sign up".

## About jPOSTrepo

jPOSTrepo (Japan ProteOme STandard Repository) is a new data repository of sharing MS raw/processed data. It consists of a newly-developed, high-speed file upload process, flexible file management system and easy-to-use interfaces. Users can release their "raw/processed" data via this site with a unique identifier number for the paper publication. Users also can suspend (or "embargo") their data until their paper is published. The file transfer from users' computer to our repository server is very fast (roughly ten times faster than usual file transfer) and uses only web browsers – it does not require installing any additional software.

jPOST is a certificated member of [ProteomeXchange Consortium](#) and jPOSTrepo provides official ProteomeXchange Identifiers to projects stored in our repository.



## Reference

Please cite the following article when using jPOSTrepo:

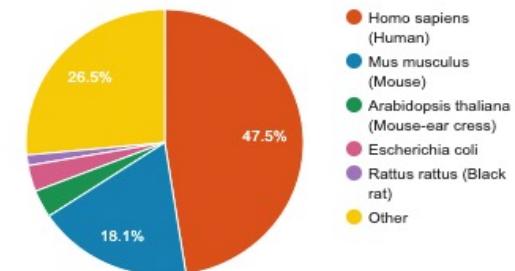
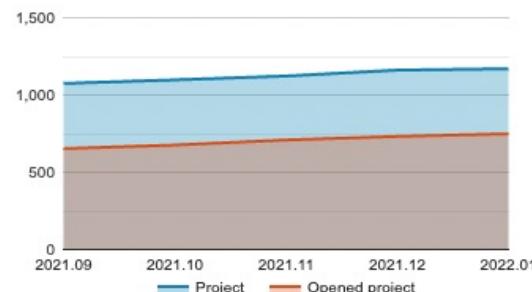
Okuda, S. et al. jPOSTrepo: an international standard data repository for proteomes. Nucl. Acids Res. 45 (D1): D1107-D1111 (2017). doi: [10.1093/nar/gkw1080](https://doi.org/10.1093/nar/gkw1080) [pubmed]

## Statistics

1170 projects are registered. 749 are opened.

87193 files amount to 40.0 TB.

187 species.

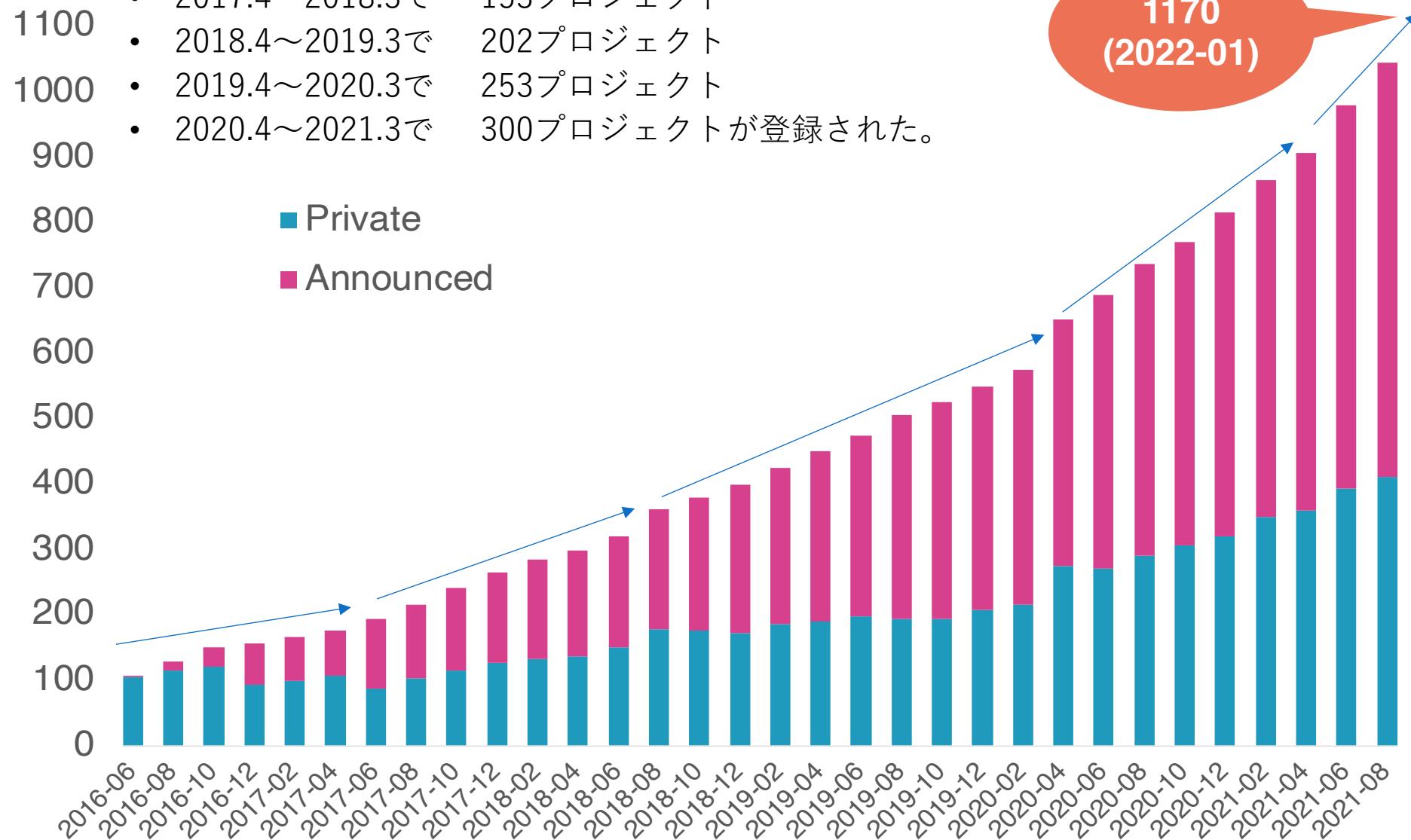


# jPOST repository – Current status

データ登録数は目標としていた年間100プロジェクトを大きく上回り、

- 2017.4～2018.3で 153プロジェクト
- 2018.4～2019.3で 202プロジェクト
- 2019.4～2020.3で 253プロジェクト
- 2020.4～2021.3で 300プロジェクトが登録された。

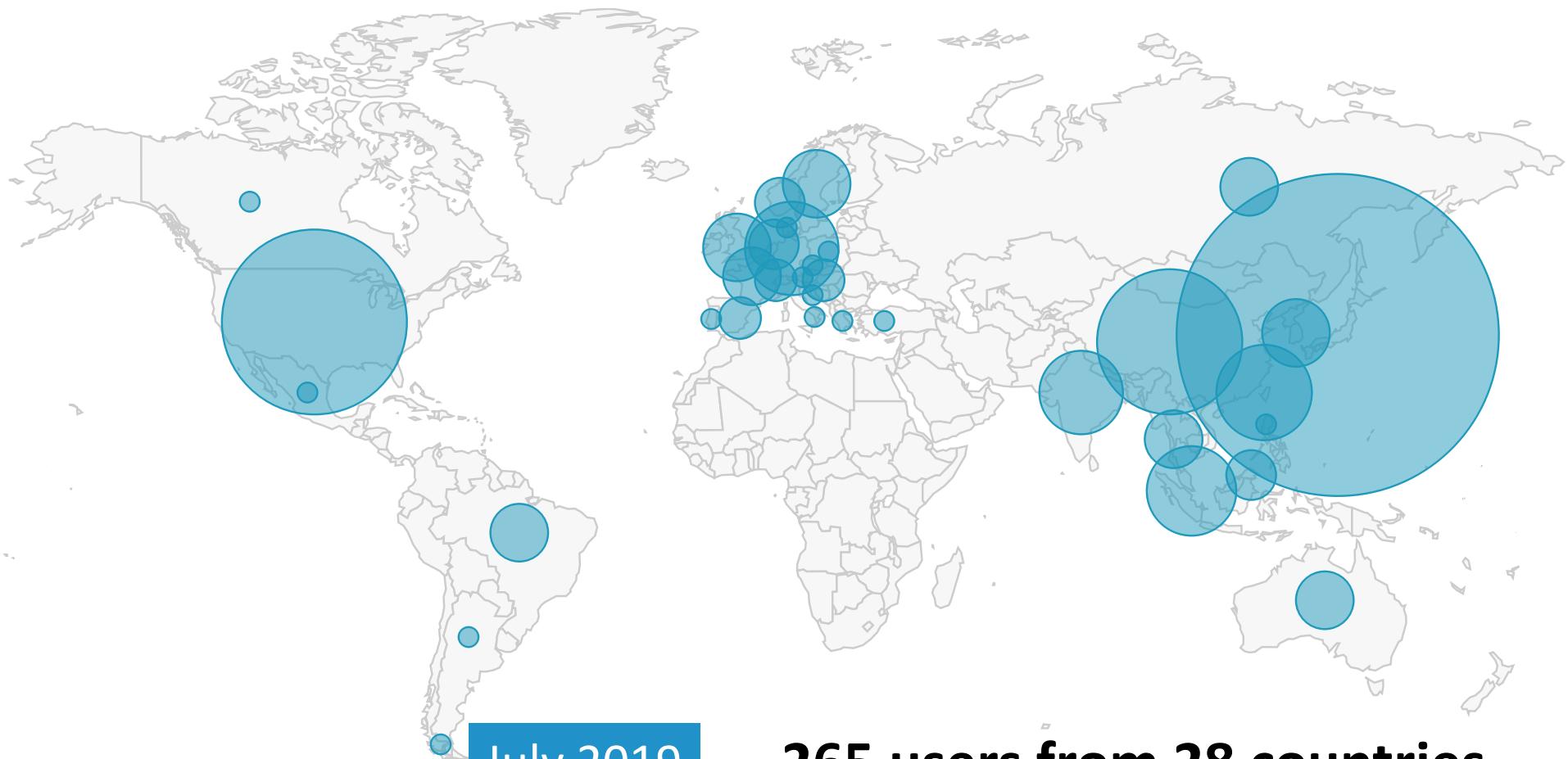
**1170  
(2022-01)**



# jPOST User Distribution



User distribution



July 2019

July 2020

Sep 2021

**265 users from 28 countries**

**391 users from 37 countries**

**543 users from 37 countries**

# Statistics

Nov 2020

798 projects are registered. 479 are opened.

65623 files amount to 26.3 TB.

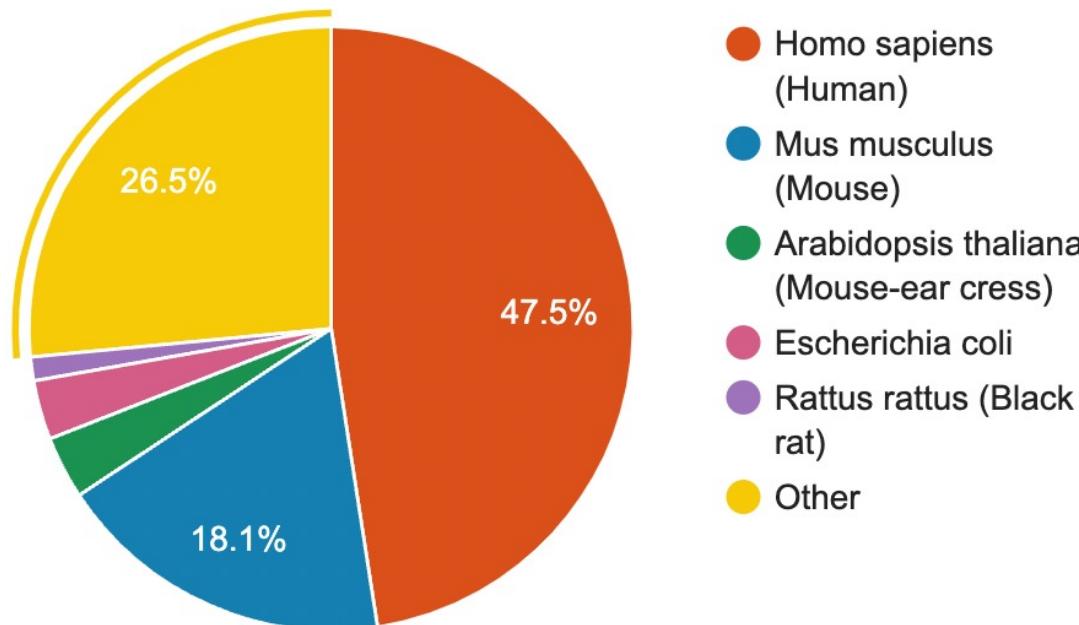
126 species.

Sep 2021

1170 projects are registered. 749 are opened.

87193 files amount to 40.0 TB.

187 species.



# jPOST repositoryへのデータ登録する手順 (Movie)



<https://www.youtube.com/watch?v=qXBFLfsCbBs>

TOGO TV

Proteomeデータリポジトリ、  
jPOSTrepoにデータを登録する

180901版



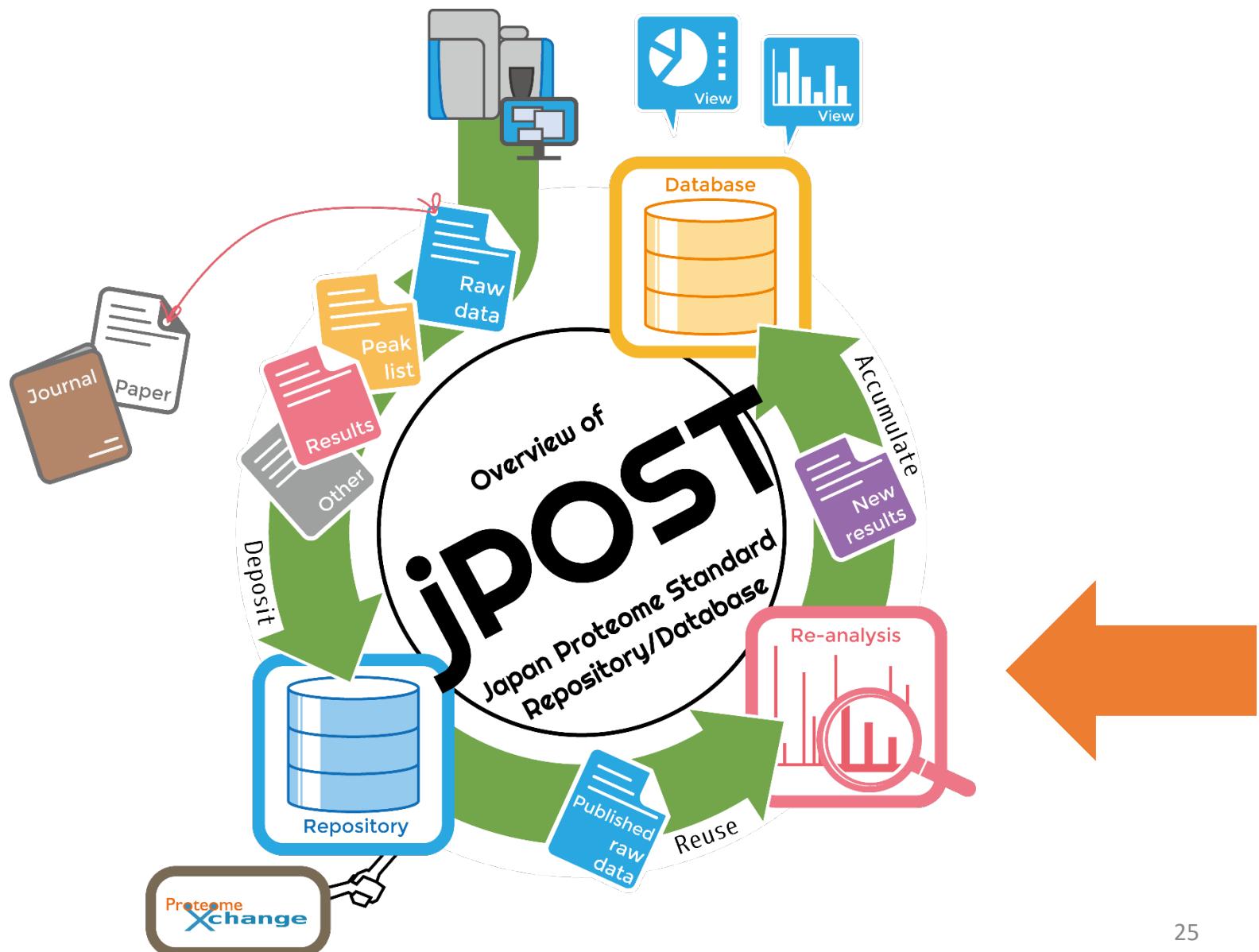
# jPOST repositoryへのデータ登録する



## 注意点

- 1) 一旦、登録されたものが公開されると、取り消しや訂正ができません。
- 2) メタデータを正確にできるだけ詳しく入力していただく必要があります。簡易的に入力しても登録はできますが、その後の再解析やデータベースへの応用が困難になります。アンケートにて後日、その詳細をお聞きすることができます。
- 3) 論文が採択されて公開された場合は、その旨を報告して頂く必要があります。
- 4) 論文にjPOSTに登録されたアクセッショNNO jPSTxxxxxを記載される場合、以下の論文のIDかDOIを登録していただきたい。  
Okuda, S. et al. jPOSTrepo: an international standard data repository for proteomes. Nucl. Acids Res. 45 (D1): D1107-D1111 (2017). [doi: 10.1093/nar/gkw1080](https://doi.org/10.1093/nar/gkw1080) [pubmed]
- 5) リポジトリのデータをダウンロードする際は  
ダウンロード—jPOSTリポジトリ/LSDB Archive、  
<https://dbarchive.biosciencedbc.jp/jp/jpost/download.html>  
からFTPのツールを使えば大量のデータも容易にダウンロードできるようになります。

# jPOST Re-Analysis

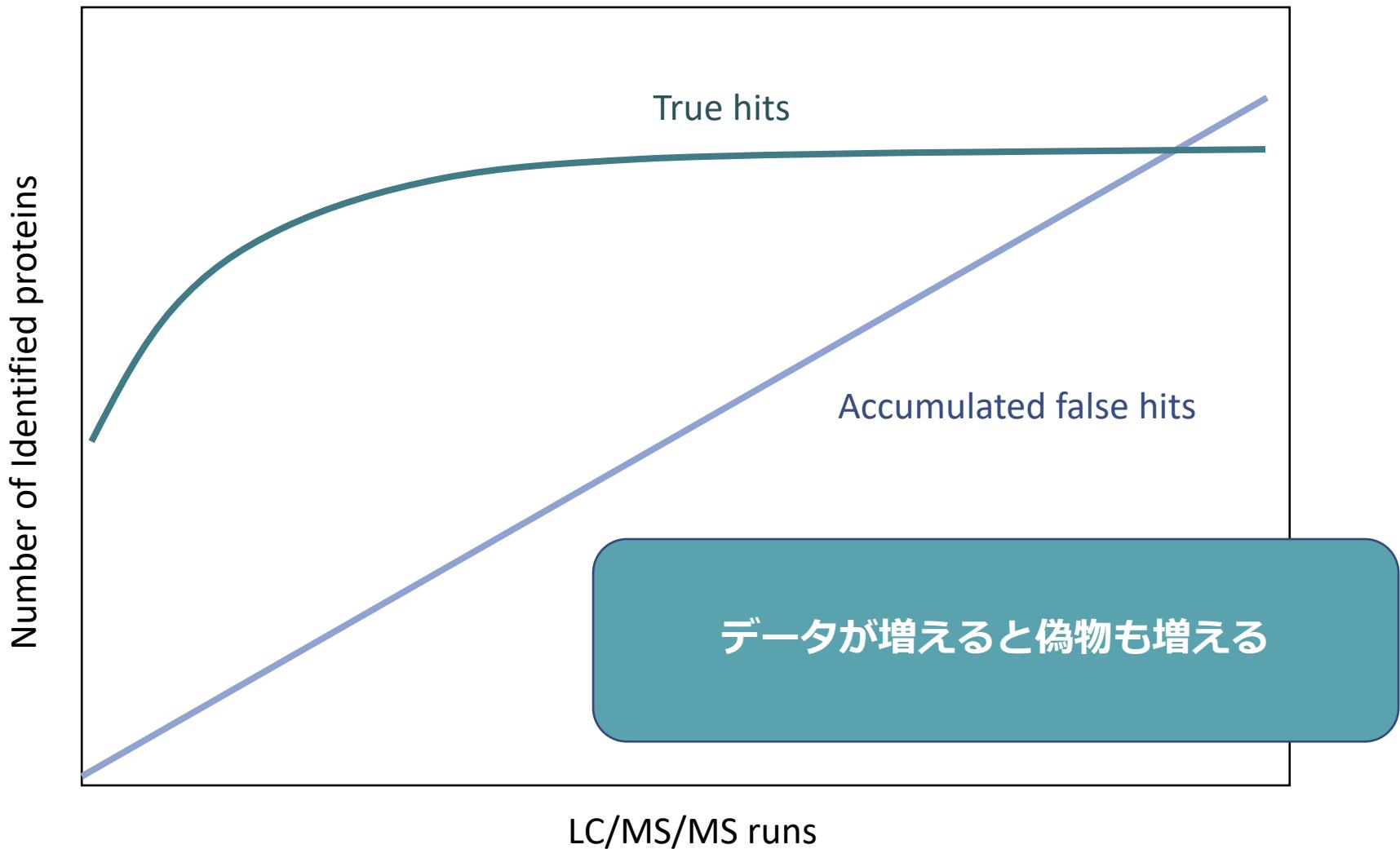


# jPOSTの特徴

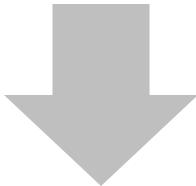


1. フレッシュなデータがどんどん勝手にたまる
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# 偽ヒットのコントロール



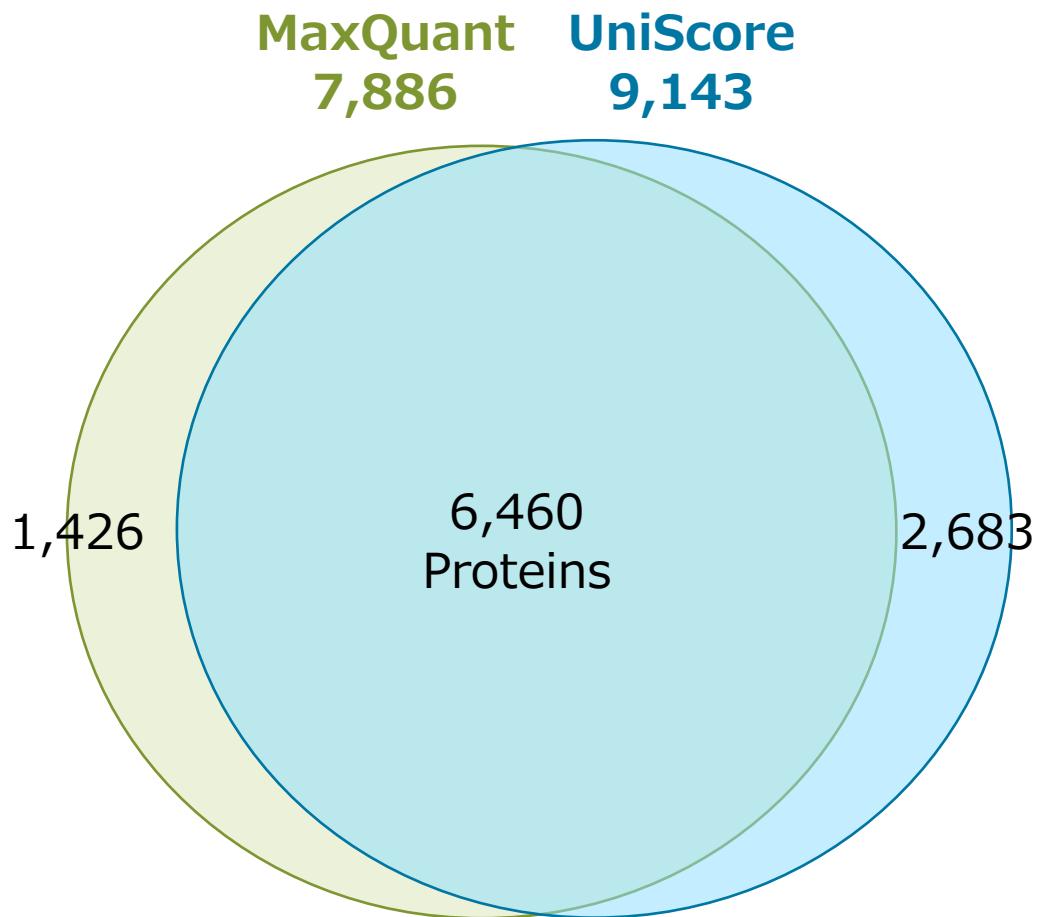
How can we merge the results  
from different sources?



## UniScore

- based on peak annotation in MSMS
- search engine independent
- MS instrument independent
- search DB independent
- can be used as universal threshold  
for peptide identification

# UniScoreによる再解析 (Human Proteome Project)



Dataset:JPST000203 – 206  
Colorectal cancer samples (used in Wilhelm et al Nature 2014)

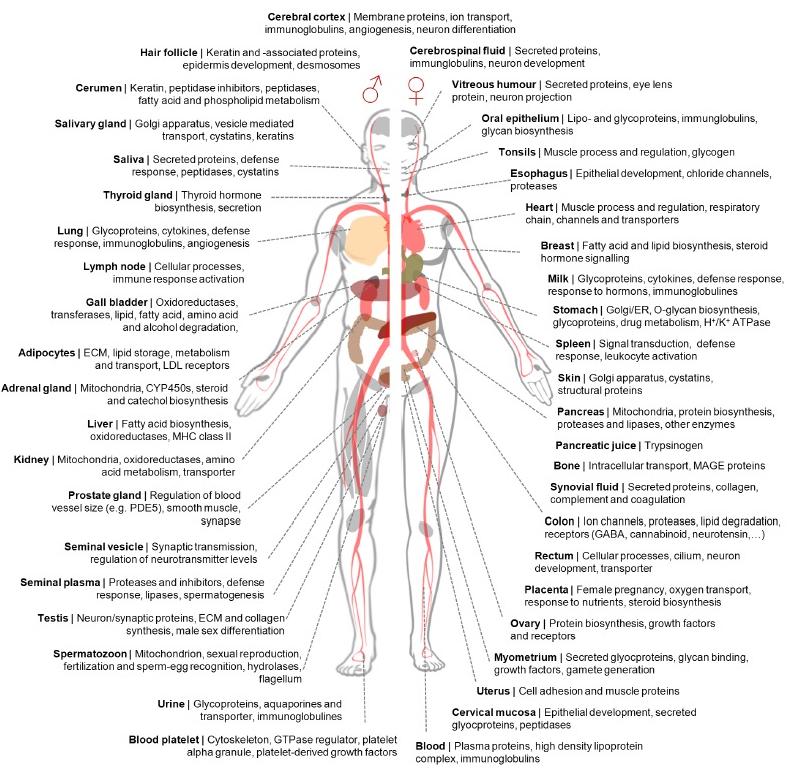
# Re-analysis : Human Proteome 1<sup>st</sup> Draft

582 | NATURE | VOL 509 | 29 MAY 2014

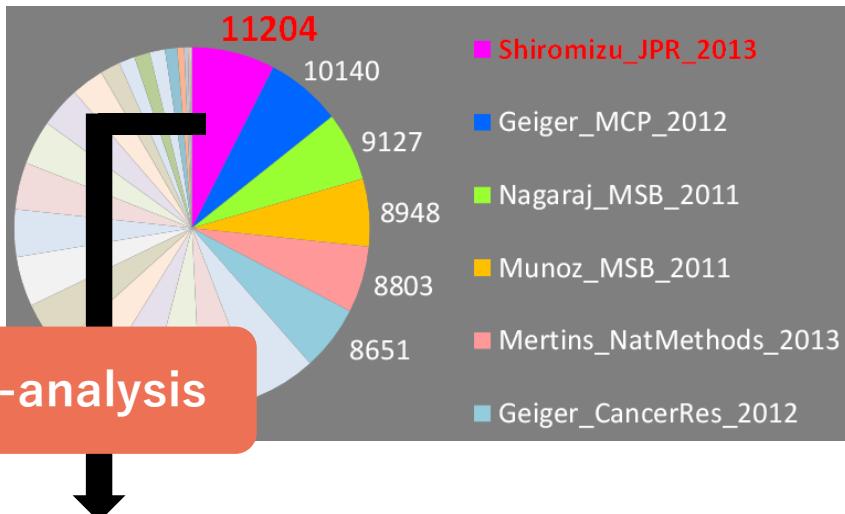
## ARTICLE

doi:10.1038/nature13319

### Mass-spectrometry-based draft of the human proteome

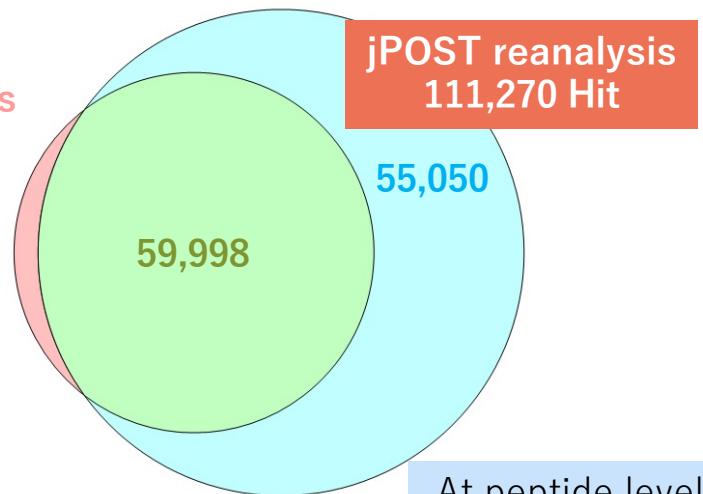


10447 raw files from Proteome Xchange



Re-analysis

Original Results  
63,127 Hit  
3,129



# UniScore for re-analysis of SARS-CoV-2 related publications



https://jpostdb.org/jpost-will-publish-the-re-analyzed-proteome-data-related-to-covid-19/



**jPOST**  
Repository / Database

Japan Proteome Standard  
Repository/Database

Q

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[Database](#)
[Workflow](#)
[Gadgets](#)
[COVID-19](#)
[Help](#)
[FAQ](#)
[Contact](#)
RSS

other

## jPOST will publish the re-analyzed proteome data related to COVID-19

© 2020-07-8 jpost

**Recent posts**

---

other

**jPOST member's co-authored paper about USI has been published.**

⌚ 2021-06-30 jpost

The Universal Spectrum Identifier (USI) is an essential mechanism for the wide use of proteomics data provided by the ProteomeXchange (PX) repositories. It has been discussed for a long time in the HUPO Proteomics Standards Initiative, to which jPOST member Prof. Kawano has contributed greatly. The USI facilitates access to the huge amount of spectral data registered in the PX repositories, and is expected to make proteomics data more findable, accessible, interoperable, and reusable. We expect that the USI leads to the use of jPOST data and contribute to research in the field of life science, including proteome research. Universal Spectrum Identifier for mass spectra. Eric W. Deutsch, Yasset [...]

event

**JCompMS 6th workshop**

⌚ 2021-05-26 jpost

Workshop details in Japanese

other

**jPOST database and repository will be stopped. (on Nov. 27-30)**

⌚ 2020-11-19 jpost

jPOST database and repository server will be unavailable during the time shown below due to a scheduled system maintenance. We thank you for

other

**jPOST will publish the re-analyzed proteome data related to COVID-19**

⌚ 2020-07-8 jpost

jPOST will publish the re-analyzed proteome data related to COVID-19 as soon as possible to support the scientific community for overcoming the world-wide crisis.

Current progress: 100% [ Last modified date: 2021-07-13 ]

**COVID-19 datasets**

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**Analysis target**

- [PXD019113](#) The Global Phosphorylation Landscape of SARS-CoV-2 Infection
- [PXD019645](#) Data, reagents, assays and merits of proteomics for SARS-CoV-2 research and testing
- [PXD019423](#) MS analysis of SARS-CoV2 proteins from patient samples
- [PXD018804](#) Extensive proteomic dataset of Vero E6 cells infected by Italy-INMI1 SARS-CoV-2 virus at Day 4 post-infection
- [PXD018594](#) Shotgun proteomics of Vero E6 cells infected by Italy-INMI1 SARS-CoV-2 virus
- [PXD018357](#) Inhibition of growth factor signaling prevents SARS-CoV-2 replication
- [PXD018117](#) A SARS-CoV-2-Human Protein-Protein Interaction Map Reveals Drug Targets and Potential Drug-Purposing
- [PXD018581](#) Proteomics of SARS-CoV and SARS-CoV-2 infected cells
- [PXD018241](#) Characterisation of the transcriptome and proteome of SARS-CoV-2 using direct RNA sequencing and tandem mass spectrometry reveals evidence for a cell passage induced in-f
- [PXD017710](#) Proteome and Translatome of SARS-CoV-2 infected cells

**Currently analysis pending**

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- [PXD019221](#) Proteomic and Metabolomic Characterization of COVID-19 Patient Sera
- [PXD018970](#) Urine proteomics profiling of the COVID-19

# UniScore for re-analysis of jPOSTrepo datasets



jPOST再解析進行表 ☆ □ ☐  
 ファイル 編集 表示 挿入 表示形式 データ ツール アドオン ヘルプ

On-going: 40 projects/year

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X							
	Project ID	MS	生物種	ダウンロード生種 Taxonomy ID	配列DBのDL日付	データ特徴	データサイズ (GB) (目安)	日付は作業開始日			PSM計算完了	55	196+10=206	26.7%	再解析完了	43	203-3-4-10 projects=	20.9%	P	Q	R	S	T	U	V	W	X				
								interview, マニュアル作業, Sample	Fractionation, 自動後処理	メタデータ作成					PSMメタデータ変換	メタデータベース作成	配列データベース作成	フレーザー	サーチリストランス決定	本サーチ (ピーカピッキング、DBサーチ) -PSM	PSM→ペプチド同定	提出	提出ID	RPXD	ファイル準備, JR-mzTab	submission 作業 (submitモタン直前まで)	Submission to the repository	特記事項			
4	JPST000059.0	LTQ Orbitrap[MS:1000449]	Escherichia	83333	20200318	27	---	DK	DK	5/5	3/18	3/23	4/13	4/13-4/15	4/16	4/16			20200416 JPST000790.0 RPXD018464		2020/09/29										
5	JPST000075.1	Q Exactive[MS:1001911]	Homo sapien	9606	20200318	19	2020/10/01	2020/10/01-	4	---	DK	DK	5/5	3/18	3/18	3/19												CIDデータとHCDデータが混			
6	JPST000091.1	Q Exactive[MS:1001911]	Mus musculus	10090	20200318	4	---	DK	DK	5/5	3/18	3/18	3/25	3/25-3/27	3/31	3/31			20200331 JPST000791.0 RPXD018465		2020/09/29										
7	JPST000096.0	Q Exactive[MS:1001911]	Mus musculus	10090	20200318	4	---	DK	DK	5/5	3/18	3/18	3/25	3/25-3/27	3/31	4/1			20200331 JPST000792.0 RPXD018466		2020/09/29										
8	JPST000097.0	Q Exactive[MS:1001911]	Mus musculus	10090	20200318	4	---	DK	DK	5/5	3/18	3/18	3/25	3/25-3/27	3/31	4/1			20200331 JPST000793.0 RPXD018467		2020/09/29										
9	JPST000100.0	Q Exactive[MS:1001911]	Bacillus subtilis	224308	20200403	10	---	DK	DK	5/5	4/3	4/7	4/8	4/8-4/9	4/16	4/17			20200416 JPST000794.0 RPXD018468		2020/09/29										
10	JPST000101.0	Q Exactive[MS:1001911]	Klebsiella pneumoniae	272620	20200403	14	---	DK	DK	5/5	4/3	4/7	4/8	4/8-4/9	4/16	4/17			20200416 JPST000795.0 RPXD018469		2020/09/29										
11	JPST000111.0	Q Exactive[MS:1001911]	Gallus gallus[9031]	phospho	17	2020/10/01																									
12	JPST000117.0	Q Exactive[MS:1001911]	Homo sapien	9606	20200318	26	---	DK	DK	5/5	3/18	3/18	3/25	3/27-3/30	5/6	5/6			20200506 JPST000796.0 RPXD018470		2020/09/29										
13	JPST000120.0	Q Exactive[MS:1001911]	Homo sapien	9606	20200318	SILAC	20	---	DK	DK	5/5	3/18	3/18	3/25	4/20-4/24	4/24	4/24			20200424 JPST000797.0 RPXD018471		2020/09/29									
14	JPST000123.0	Q Exactive[MS:1001911]	Homo sapien	9606	20200318	SILAC	14	---	DK	DK	5/5	3/18	3/18	3/25	4/20-4/22	4/24	4/24			20200424 JPST000798.0 RPXD018472		2020/09/29									
15	JPST000126.0	Q Exactive[MS:1001911]	Homo sapien	9606	20200318	24	---	DK	DK	5/5	3/18	3/18	4/3	4/3-4/5	4/16	4/17			20200416 JPST000799.0 RPXD018473		2020/09/29										
16	JPST000129.0	Q Exactive[MS:1001911]	Homo sapien	9606	20200318	34	---	DK	DK	5/5	3/18	3/18	4/3	4/3-4/9	4/16	4/17			20200416 JPST000800.0 RPXD018474		2020/09/29										
17	JPST000200.0	Q Exactive[MS:1001911]	Homo sapien	9606	20200318	4	---	DK	DK	5/5	3/18	(2/14)	(2/28)	3/25-3/27	3/31	4/1			20200331 JPST000819.0 RPXD018493		2020/09/29										
18	JPST000201.0	LTQ Orbitrap Velos[MS:100174]	Homo sapien	9606	20200318	18	---	DK	DK	5/5	---	---	---	---	---	---			20200323 JPST000801.0 RPXD018475		2020/05/06	2020/05/27									
19	JPST000203.0	LTQ Orbitrap Velos[MS:100174]	Homo sapien	9606	20200318	15	---	DK	DK	5/5	---	---	---	---	---	---			20200323 JPST000802.0 RPXD018476		2020/05/06	2020/05/27									
20	JPST000204.0	LTQ Orbitrap Velos[MS:100174]	Homo sapien	9606	20200318	13	---	DK	DK	5/5	---	---	---	---	---	---			20200323 JPST000803.0 RPXD018477		2020/05/06	2020/05/27									
21	JPST000205.0	LTQ Orbitrap Velos[MS:100174]	Homo sapien	9606	20200318	17	---	DK	DK	5/5	---	---	---	---	---	---			20200323 JPST000804.0 RPXD018478		2020/05/06	2020/05/27									
22	JPST000206.0	LTQ Orbitrap Velos[MS:100174]	Homo sapien	9606	20200318	17	---	DK	DK	5/5	---	---	---	---	---	---			20200323 JPST000805.0 RPXD018479		2020/05/06	2020/05/27									
23	JPST000207.0	LTQ Orbitrap Velos[MS:100174]	Homo sapien	9606	20200318	72	---	DK	DK	5/5	---	---	---	---	---	---			20200323 JPST000806.0 RPXD018480		2020/05/06	2020/05/27									
24	JPST000208.0	LTQ Orbitrap Velos[MS:100174]	Homo sapien	9606	20200318	10	---	DK	DK	5/5	---	---	---	---	---	---			20200323 JPST000807.0 RPXD018481		2020/05/06	2020/05/27									
25	JPST000210.0	LTQ Orbitrap Velos[MS:100174]	Homo sapien	9606	20200318	54	---	DK	DK	5/5	---	---	---	---	---	---			20200323 JPST000808.0 RPXD018482		2020/05/06	2020/05/27									
26	JPST000267.1	Q Exactive[MS:1001911];TripleTOF Arabidopsis thaliana (Mouse-ear	ファイル分	148	2020/10/01																										
27	JPST000305.0	Q Exactive[MS:1001911]	Brucella abortus[235]			27	2020/10/01																								
28	JPST000369.1	Q Exactive[MS:1001911]	Escherichia coli[562]			16	2020/10/01																								
29	JPST000379.1	Q Exactive[MS:1001911]	Homo sapien	9606	20200318	18	---	DK	DK	5/5	3/18	4/1	6/3	6/3-6/4	6/5	6/5			20200605 JPST000820.0 RPXD018494		2020/09/29										
30	JPST000415.0	Q Exactive[MS:1001911]	Meyeromyza guillermundi[4929]			8	2020/10/01																								
31	JPST000417.0	Q Exactive[MS:1001911]	Meyeromyza guillermundi[4929]			8	2020/10/01																								
32	JPST000670.0	Q STAR[MS:100190]	Rattus rattus	10116	20200403	Sciex	4	---	DK	DK	5/5	4/6	4/8	4/10	4/10-4/13	4/15	4/17			20200416 JPST000809.0 RPXD018483											
33	JPST000811.0	TripleTOF 5600[MS:1000932]	Homo sapien	9606	20200318	Sciex	10	---	DK	DK	5/5	---	---	---	---	---	---			20200323 JPST000810.0 RPXD018484		2020/05/06	2020/06/04	IP							
34	JPST000822.0	TripleTOF 5600[MS:1000932]	Homo sapien	9606	20200318	Sciex	10	---	DK	DK	5/5	---	---	---	---	---	---			20200323 JPST000811.0 RPXD018485		2020/05/06	2020/06/04	IP							
35	JPST000863.0	TripleTOF 5600[MS:1000932]	Homo sapien	9606	20200318	Sciex	10	---	DK	DK	5/5	---	---	---	---	---	---			20200323 JPST000812.0 RPXD018486		2020/05/06	2020/06/04	IP							
36	JPST000865.0	TripleTOF 5600[MS:1000932]	Homo sapien	9606	20200318	Sciex	9	---	DK	DK	5/5	---	---	---	---	---	---			20200323 JPST000813.0 RPXD018487		2020/05/06	2020/06/04	IP							
37	JPST000866.0	TripleTOF 5600[MS:1000932]	Homo sapien	9606	20200318	Sciex	9	---	DK	DK	5/5	---	---	---	---	---	---			20200323 JPST000814.0 RPXD018488		2020/05/06	2020/06/04	IP							
38	JPST000867.0	TripleTOF 5600[MS:1000932]	Homo sapien	9606	20200318	Sciex	10	---	DK	DK	5/5	---	---	---	---	---	---			20200323 JPST000815.0 RPXD018489		2020/05/06	2020/06/04	IP							
39	JPST000868.0	TripleTOF 5600[MS:1000932]	Homo sapien	9606	20200318	Sciex	9	---	DK	DK	5/5	---	---	---	---	---	---			20200323 JPST000816.0 RPXD018490		2020/05/06	2020/06/04	IP							
40	JPST000869.0	TripleTOF 5600[MS:1000932]	Homo sapien	9606	20200318	Sciex	10	---	DK	DK	5/5	---	---	---	---	---	---			20200323 JPST000817.0 RPXD018491		2020/05/06	2020/06/04	IP							
41	JPST000899.0	TripleTOF 5600[MS:1000932]	Escherichia	83333	20200318	Sciex	13	---	DK	DK	5/5	3/18	4/7	4/9	10/4-12/10/20/04/15, 10/2	10/2	2020102 JPST000818.0 RPXD018492		2020/10/01												
42	JPST000100.0	TripleTOF 5600[MS:1000932]	Bacillus subtilis	224308	20200403	Sciex	10	---	DK	DK	5/5	4/3	4/8	4/10	4/10-4/12	4/15	4/17			20200416 JPST000794.0 RPXD018468		2020/10/01									
43	JPST000101.0	TripleTOF 5600[MS:1000932]	Klebsiella pneumoniae	272620	20200403	Sciex	14	---	DK	DK	5/5	4/3	4/8	4/9	4/10-4/12	4/15	4/17			20200416 JPST000795.0 RPXD018469		2020/10/01									
44	JPST000144.0	Q STAR[MS:100190]	Mus musculus	10090	20200318	RAQ4plex I	2	---	DK	DK	5/5	3/18	4/8	4/13	4/13-4/14	4/15	4/17			20200416 JPST000821.0 RPXD018495		2020/10/01									
45	JPST000149.0	TripleTOF 5600[MS:1000932]	Homo sapien	9606	20200318	Sciex	0	---	DK	DK	5/5	3/18	4/7	4/9	4/10-4/12	4/15	4/17			20200416 JPST000822.0 RPXD018496		2020/10/01									
46	JPST000150.1	TripleTOF 5600[MS:1000932]	Homo sapien	9606	20200318	Sciex	15	---	DK	DK	5/5	3/18	4/7	4/9	4/10-4/12	5/6	5/6			20200506 JPST000823.0 RPXD018497		2020/10/01									

# jPOST customizable database 'Slice'



# jPOSTの特徴



1. フレッシュなデータがどんどん勝手にたまる

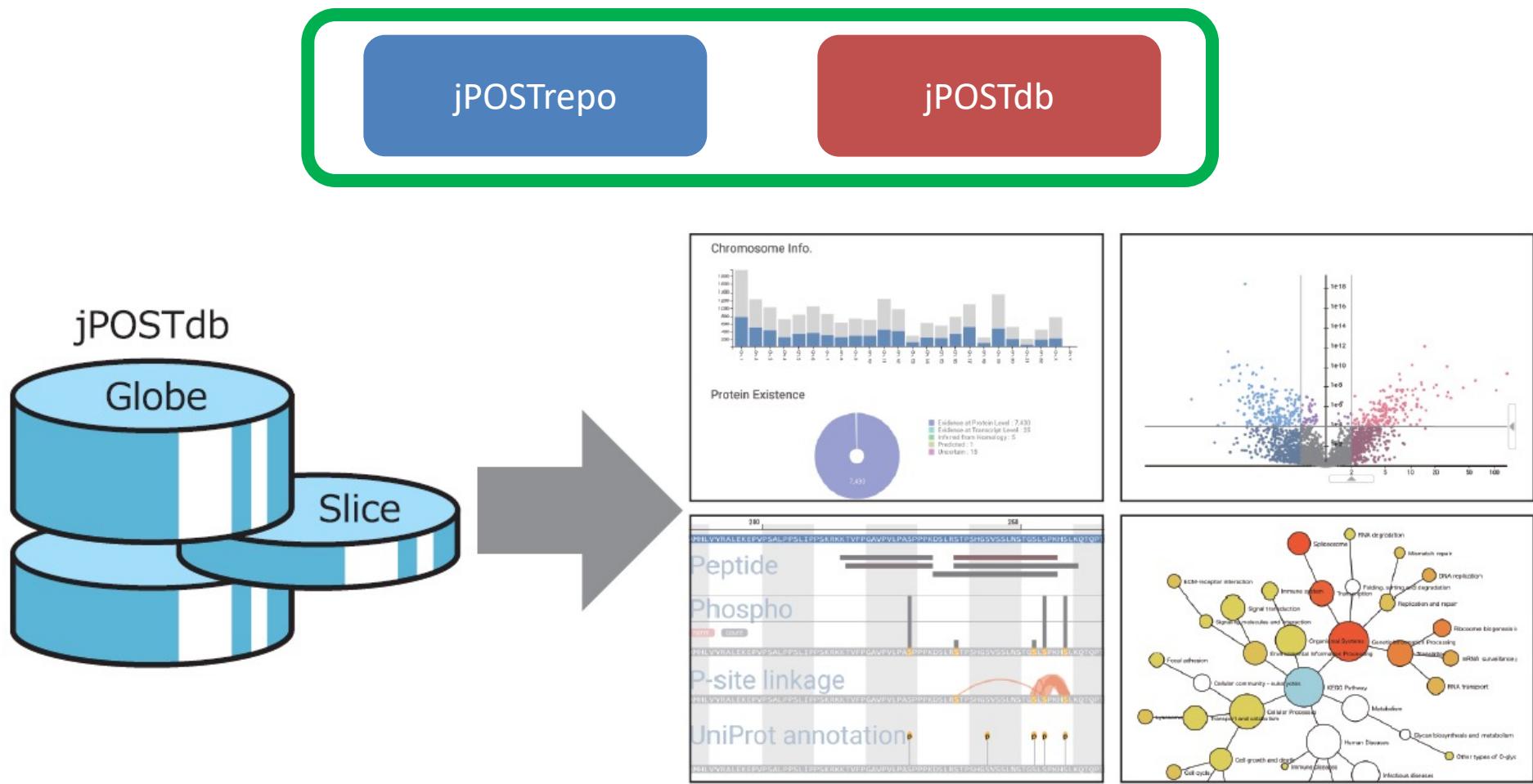
2. 再解析により、データの統一化が実現される

3. カスタムDBの作成ツールと可視化ツールの提供

# The jPOST Environment

The jPOST environment: an integrated proteomics data repository and database

Moriya et al., *Nucleic Acids Res*, 2019 Jan 8;47(D1):D1218-D1224



## Slice Comparison

Slice 1

( Select a slice. )



Slice 2

( Select a slice. )



# UniProtとの連携：

## Cross-references between UniProt and jPOST

**UniProtKB - P40925 (MDHC\_HUMAN)**

**Display**

- Entry
- Publications
- Feature viewer
- Feature table

None

Modified residue<sup>i</sup>: 332 Phosphoserine By similarity  
Modified residue<sup>i</sup>: 333 Phosphoserine Combined sources

Post-translational modification<sup>i</sup>:

- ISGylated: 1 Publication
- Acetylation at Lys-118 dramatically enhances enzymatic activity and promotes adipogenic differentiation. 2 Publications

Keywords - PTM<sup>i</sup>: Acetylation, Methylation, Phosphoprotein, Ubl conjugation

Proteomic databases

EPD <sup>i</sup>	P40925
jPOST <sup>i</sup>	P40925
PaxDb <sup>i</sup>	P40925
PeptideAtlas <sup>i</sup>	P40925
PRIDE <sup>i</sup>	P40925
ProteomicsDB <sup>i</sup>	55384
	55385 [P40925-2]
TopDownProteomics <sup>i</sup>	P40925-1 [P40925-1]

**jPOSTdb** Search Slices Compare Help

**Protein: P40925**

Protein Name: Malate dehydrogenase, cytoplasmic

Protein ID: MDHC\_HUMAN

Gene Name: MDH1

Accession: P40925

Length: 334 aa

Sequence: MSEPIRVLVTGAACGGTAYSLLYSIGNGSVEGKDOPIILVLLDTTPPMQGLDGVLMLQDICALPLKKDVIATDKEDVAFKDQLDVAILVGSMPREGEGRDOLTLGANVKLFRQGRALDKYAKSVKIVIVGNPAVNTETASAPGIPKENFSCLTRLDHNRKADIAALKLGVTAIDVKNVIIWGNHSSTOYPDVNHAKVYKLQGKEVGVEALKDOSWLKGEFVTTTVQORGAAVIKARKLSSAMSAAKAICDINVRD1WFGTPEGEFVSMGVISODGNSYGVPDOLLSFPVVIKNKTWKFVEGLPINDFSREKMDLTAKELTEEKESAFEFLLSSA

Location: Chromosome 2

Statistics:

- # peptides: 42
- # spectra: 1,834
- # unique peptides (UniProt entry level): 31
- # unique peptides (gene name level): 42

for Absolute GenID: 4190

Quantification: search in iMPAQ

**Protein Browser**

Peptide

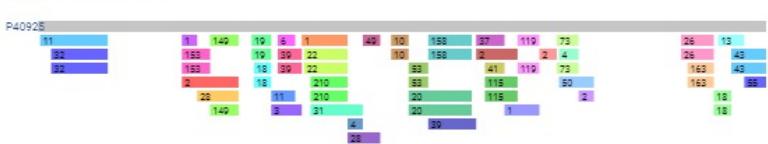
Label:  Peptides  Isoforms

-- Add view --

**Peptide Sharing**

shared in isoforms

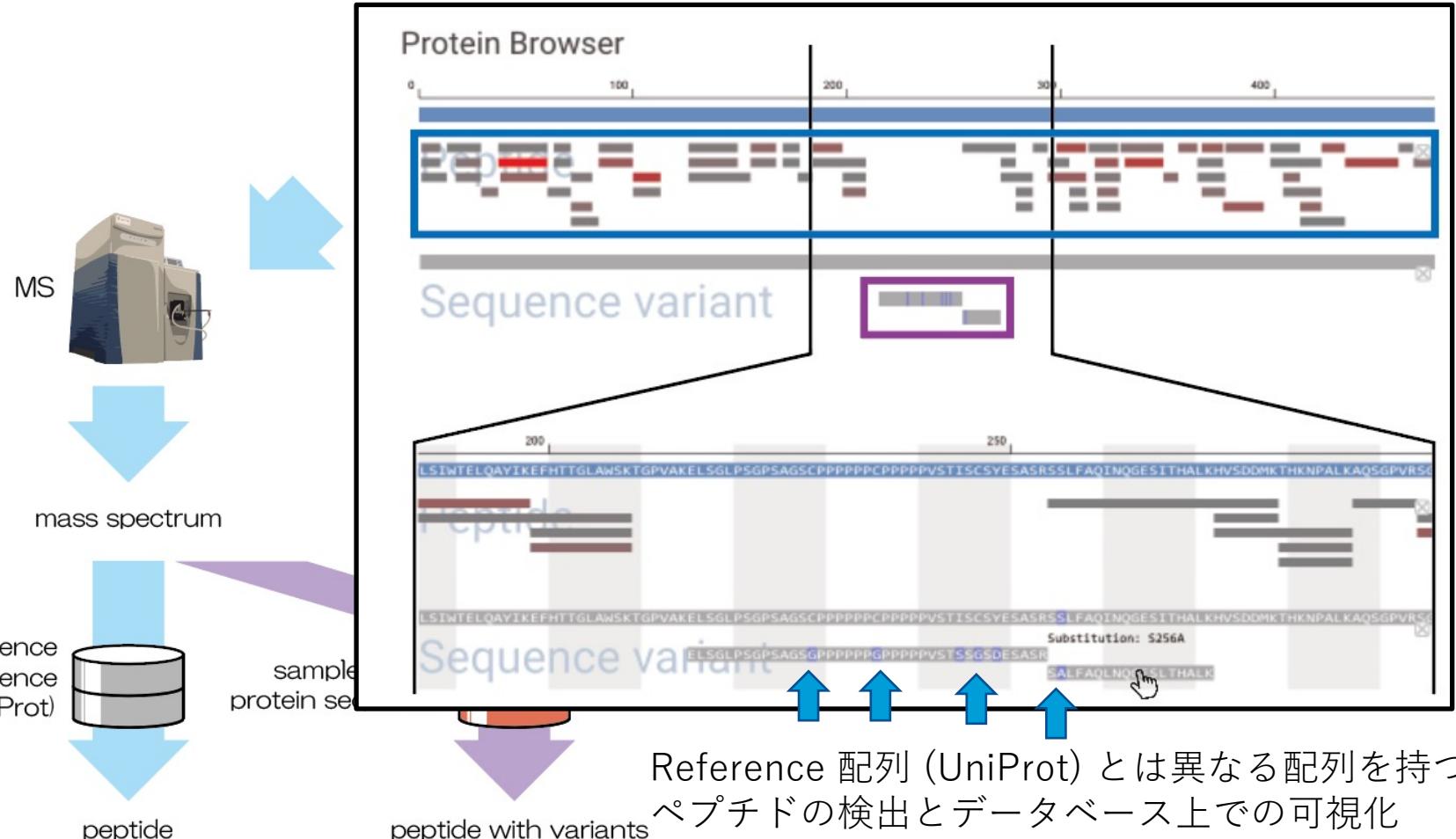
P40925



# プロテオゲノミクス対応

解析プロトコル、データベースのプロテオゲノミクス対応を進めている

## Proteomics



# jPOSTの特徴



1. フレッシュなデータがどんどん勝手にたまる
2. 再解析により、データの統一化が実現される
3. カスタムDBの作成ツールと可視化ツールの提供

# <https://jpostdb.org>

→ ⌂ https://jpostdb.org

The screenshot shows the jPOST website homepage. At the top left is a large orange circular logo with "jPOST" in white and "Repository / Database" below it. To its right is a navigation bar with links: About, Repository, Database, Workflow, Gadgets, COVID-19, Help, FAQ, and Contact. A search bar is located at the top right. Below the navigation, there are six main sections, each with an icon and a title followed by a "Help" link:

- Repository** [Help ▾](#)  
jPOSTrepo is a raw and processed data repository of mass-based proteomics.
- Database** [Help ▾](#)  
jPOSTdb is a database containing re-analysis results with unified criteria for proteome data from jPOSTrepo.
- Workflow** [Help ▾](#)  
This provides the re-analysis workflow used in jPOST.
- Gadgets** [Help ▾](#)  
jPOST gadget is a collection of tools we have developed as well as other commonly used tools for mass spectrometry-based proteomics.
- COVID-19** [Help ▾](#)  
This is a special page on coronavirus (SARS-CoV-2) and the COVID-19 disease data, where mass-based proteomics data in ProteomeXchange resources are analyzed by the jPOST re-analysis workflow.
- Help** [Help ▾](#)  
A guide to using the jPOST resources.

**Recent posts**

**other**

**jPOST member's co-authored paper about USI has been published.**

⌚ 2021-06-30 jpost

The Universal Spectrum Identifier (USI) is an essential mechanism for the wide use of proteomics data provided by the ProteomeXchange (PX) repositories. It has been discussed for a long time in the HUPO Proteomics Standards Initiative, to which jPOST member Prof. Kawano has contributed greatly. The USI facilitates access to the huge amount of spectral data registered in the PX repositories, and is expected to make proteomics data is more findable, accessible, interoperable, and reusable. We expect that the USI leads to the use of

# Molecular Cell

## Growth Factor Receptor Signaling Inhibition Prevents SARS-CoV-2 Replication

other

### jPOST will publish the re-analyz

© 2020-07-8 jpost

jPOST will publish the re-analyzed proteome data related to COVID-19 as

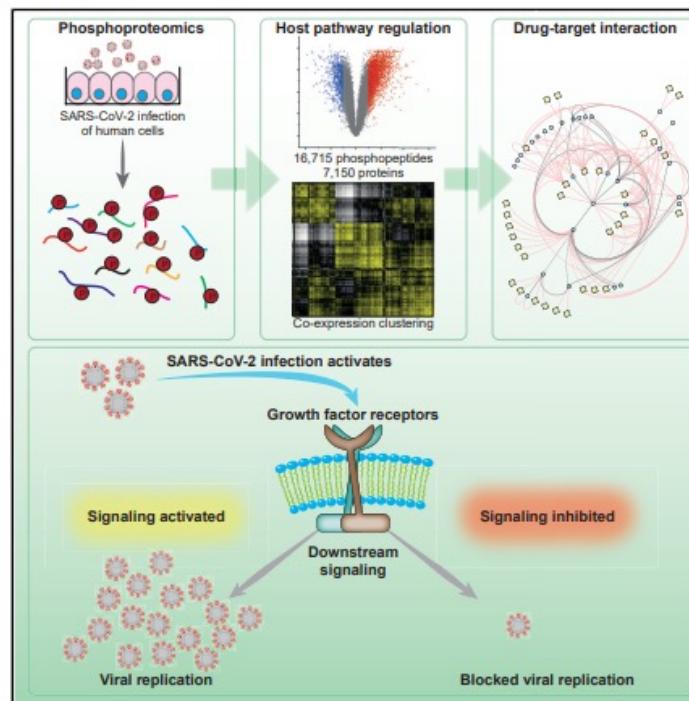
Current progress: 100% [ Last modified date: 2020-07-08 ]

### COVID-19 datasets

#### Analysis target

- PXD019113 The Global Phosphorylation Landscape of SARS-CoV-2 Infection
- PXD019645 Data, reagents, assays and merits of proteomics for SARS-CoV-2
- PXD019423 MS analysis of SARS-CoV2 proteins from patient samples
- PXD018804 Extensive proteomic dataset of Vero E6 cells infected by Italy-II
- PXD018594 Shotgun proteomics of Vero E6 cells infected by Italy-INMI1 SA
- PXD018357 Inhibition of growth factor signaling prevents SARS-CoV-2 replication
- PXD018117 A SARS-CoV-2-Human Protein-Protein Interaction Map Reveals
- PXD018581 Proteomics of SARS-CoV and SARS-CoV-2 infected cells
- PXD018241 Characterisation of the transcriptome and proteome of SARS-CoV-2 frame deletion in the spike glycoprotein that removes the furin
- PXD017710 Proteome and Translatome of SARS-CoV-2 infected cells

### Graphical Abstract



### Authors

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Georg Tascher, Sandra Ciesek,  
Christian Münch, Jindrich Cinatl

### Correspondence

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cinatl@em.uni-frankfurt.de (J.C.)

### In Brief

In this study, Klann et al. dissected the host cell signaling landscape upon infection with SARS-CoV-2. Mapping differential signaling networks identified a number of pathways activated during infection. Drug-target network analysis revealed potential therapeutic targets. Growth factor receptor signaling was highly activated upon infection and its inhibition prevented SARS-CoV-2 replication in cells.

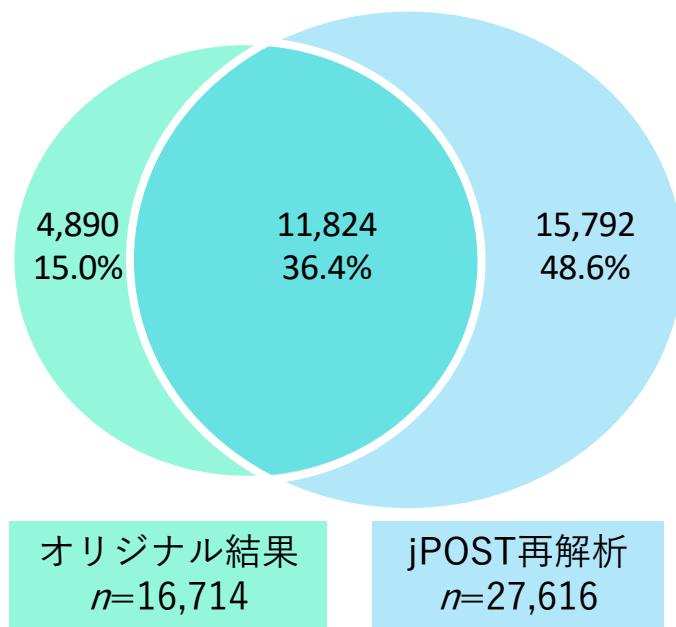
### Highlights

- Phosphoproteomics of SARS-CoV-2-infected cells reveal the signaling landscape
- SARS-CoV-2 proteins are extensively phosphorylated in host cells
- Infection leads to the activation of growth factor receptor signaling
- Drugs inhibiting growth factor receptor signaling prevent viral replication

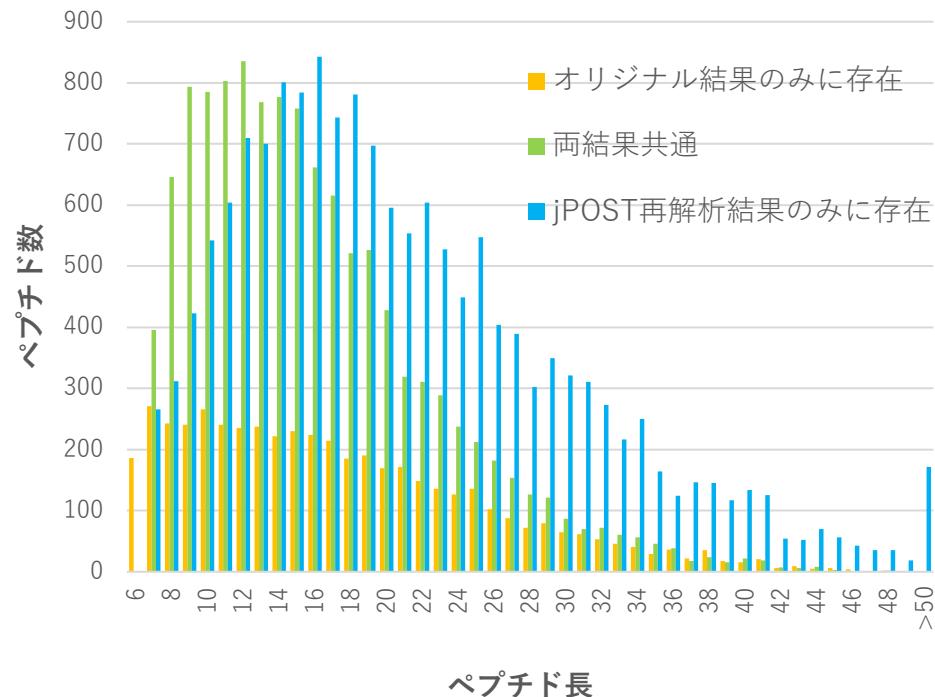
# Re-analysis of COVID-19 paper

Klann *et al.*, *Molecular Cell* **80**, 164 (2020)

## 同定リン酸化ペプチド数の比較



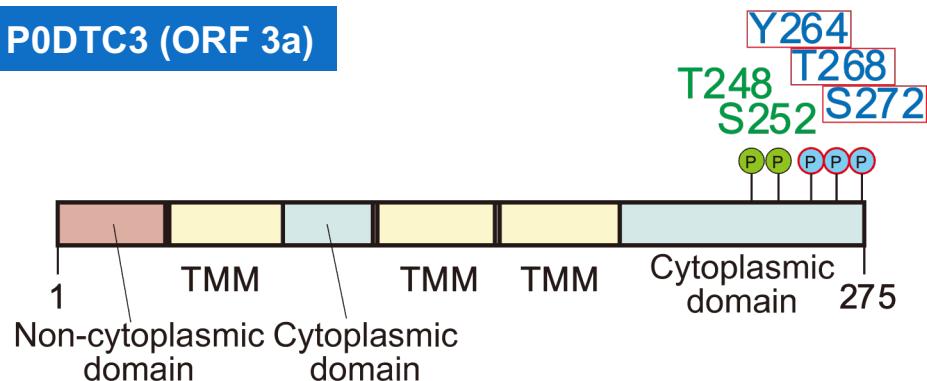
## 両解析結果のペプチド長ごとの比較



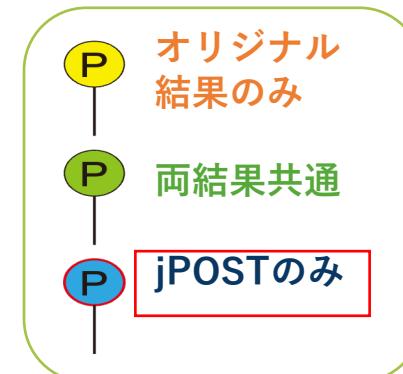
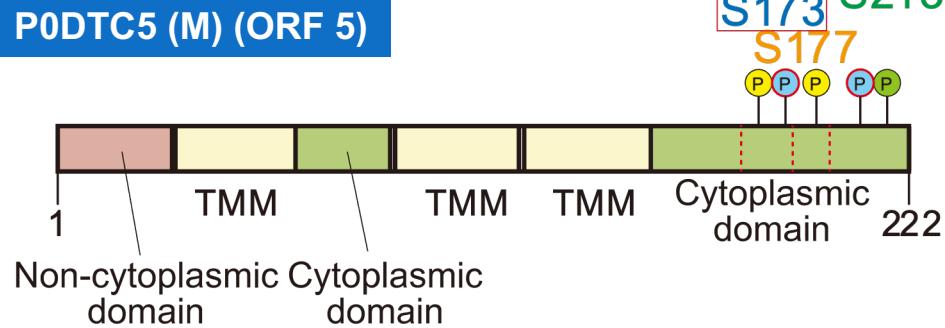
# Phosphorylated sites on SARS-CoV-2 proteins

## 同定されたリン酸化サイトの比較

P0DTc3 (ORF 3a)



P0DTc5 (M) (ORF 5)



b+	#	Seq	#	y+
359.2128	1	E	8	
472.2968	2	I	7	827.4022
573.3445	3	T	6	714.3182
672.4129	4	V	5	613.2705
743.4500	5	A	4	514.2021
844.4977	6	T	3	443.1650
1011.4960	7	S	2	342.1173
	8	R	1	175.1190

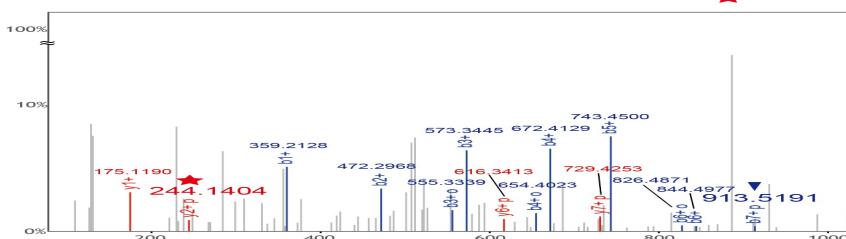
[Click] to move table

Add to N-term: 229.1629

Variable Modifications:

S: 79.9663 [7]

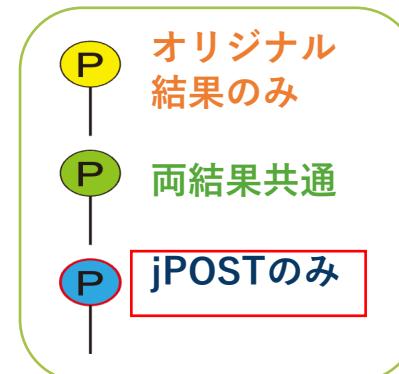
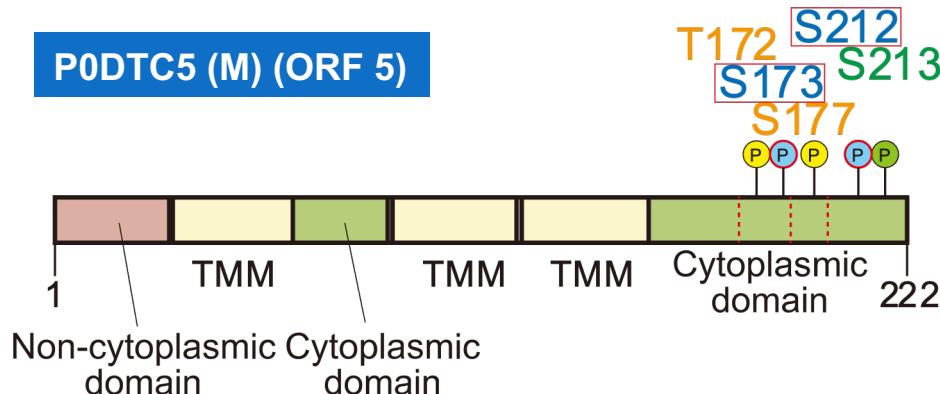
T172 vs S173  
↓  
EITVATSR



# Phosphorylated sites on SARS-CoV-2 proteins

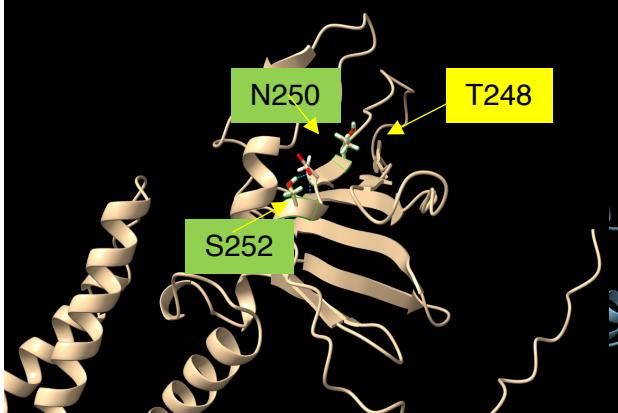
## 同定されたリン酸化サイトの比較

P0DT5 (M) (ORF 5)

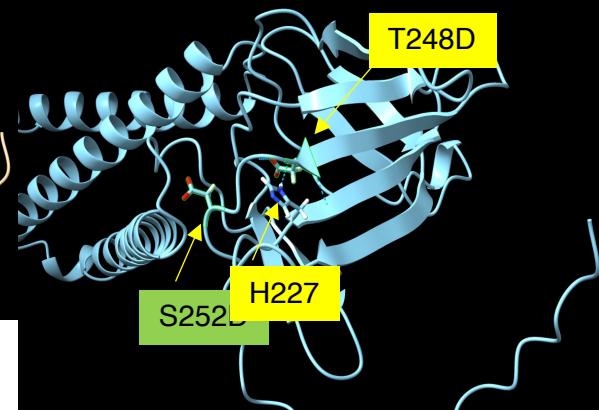


Alpha-Fold 2  
にてリン酸化サイト  
をミミックした部分  
配列を解析してみた。

ORF3

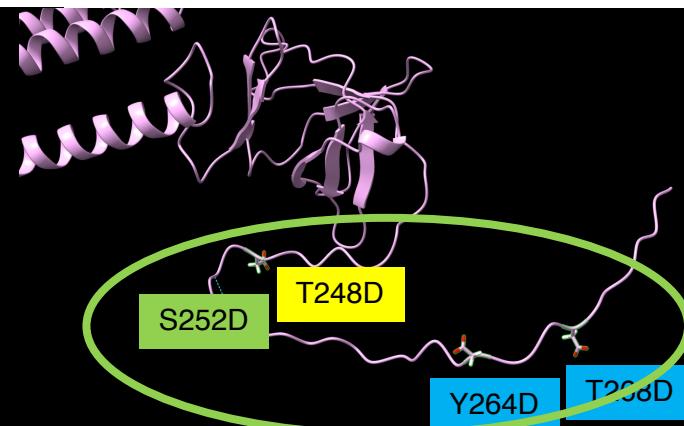


ORF3 T248D,  
S252D



βシート構造の位置が  
大きく変わる

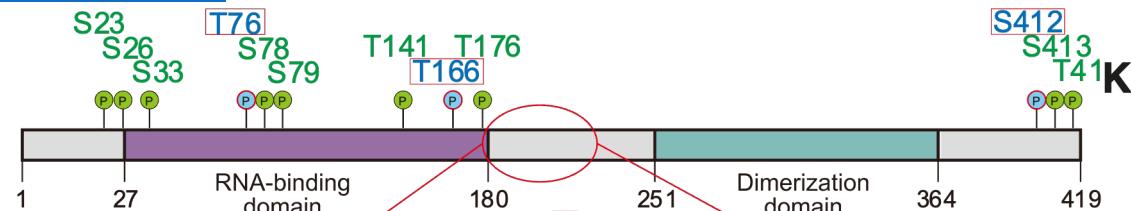
ORF3 T248D, S252D, Y264D,  
T268D



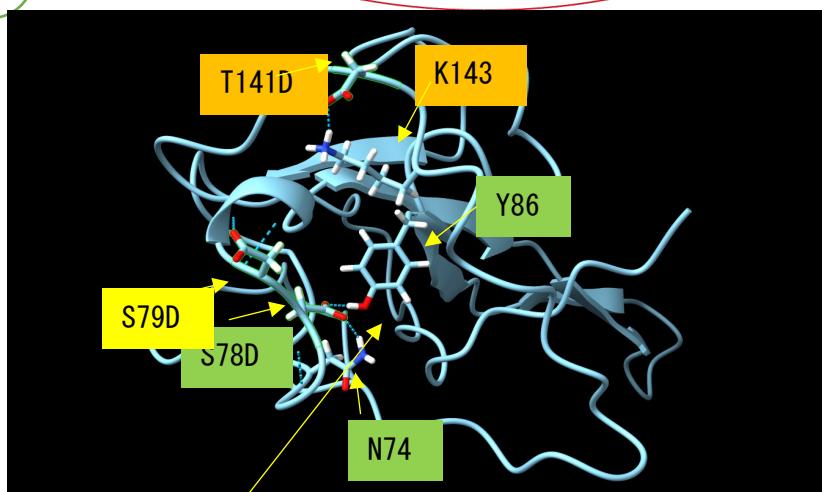
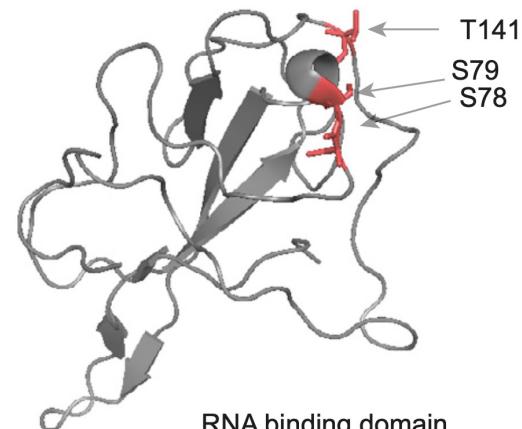
Cytoplasmic domainのC末端  
がfoldしなくなる

# Phosphorylated sites on SARS-CoV-2 proteins

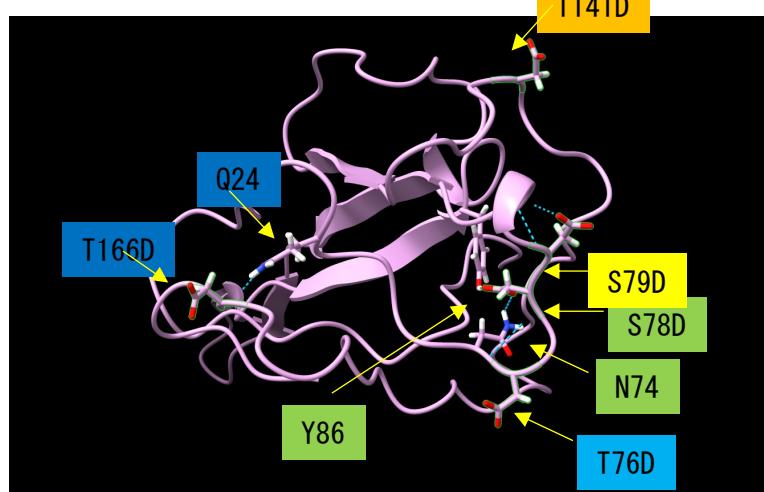
P0DT9 (N) (ORF 9)



- (P) オリジナル結果のみ
- (P) 両結果共通
- (P) jPOSTのみ



S78DがY86と水素結合するようになる

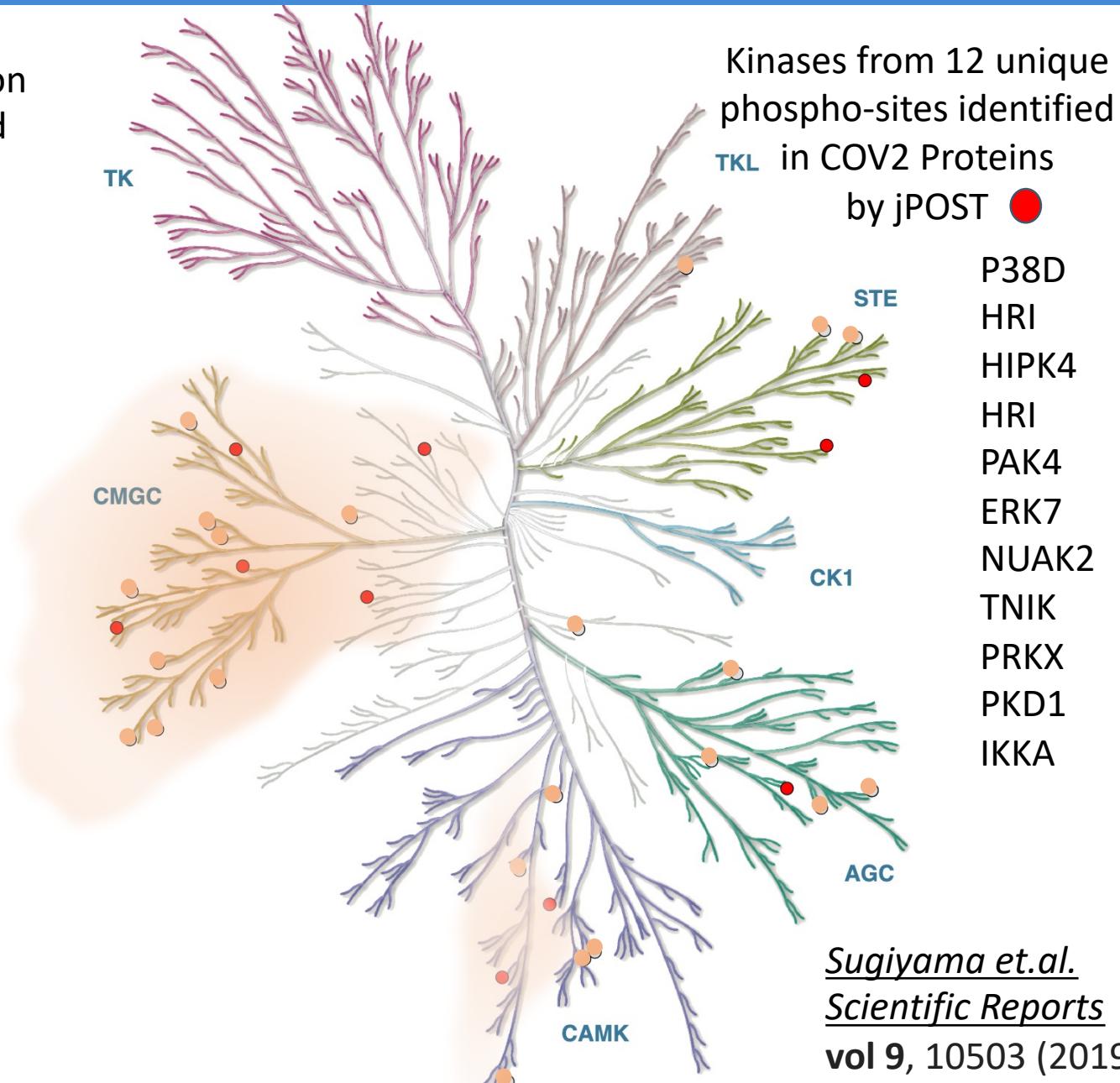


S78DがY86と水素結合するようになる

# Prediction of activated Kinases in SARS-COV2 infected Cells

Kinases from 28 common  
Phospho-sites identified  
in COV2 proteins

KHS1	CYCB1
LATS1	PKCH
MARK3	STK33
GPRK7	CDK9
MOK	CYCLINK
MOK	PKCH
MST1	ICK
ACTR2	HIPK3
CDK9	CDK9
CYCT1	CYCT1
CDK3	ERK5
CYCE1	ACTR2
TLK2	CK2A2
NIM1	MAPKAPK3
PKCZ	MAPKAPK2
MOK	CDK6
CDC2	CYCLIND1



# <https://jpostdb.org>

→ ⌂ 🗃 https://jpostdb.org

jPOST  
Repository / Database

Japan Proteome Standard  
Repository/Database

Recent posts

other

jPOST member's co-authored  
paper about USI has been  
published.

⌚ 2021-06-30 by jpost

The Universal Spectrum Identifier (USI) is an essential mechanism for the wide use of proteomics data provided by the ProteomeXchange (PX) repositories. It has been discussed for time in the HUPO Proteomics Standards Initiative, in which jPOST member Prof. Kawano has contributed greatly. The USI facilitates access to the huge amount of spectral data registered in the PX repositories, and is expected to make proteomics data more findable, accessible, interoperable, and reusable. We expect that the USI leads to the use of

この様な再解析によって、より正確なリン酸化サイトからキナーゼ候補を絞り込み、コロナ感染症に有効であるキナーゼ阻害剤などが創出できる可能性があります。

再解析は様々な生物学的応用が可能。jPOSTが全面的なサポートであなたのデータを再解析します!

ProteomeXchange resources are analyzed by the jPOST re-analysis workflow.

AQ Contact 🔍

ntaining re-analysis  
a for proteome data

ion of tools we have  
r commonly used  
try-based proteomics.

T resources.

# Journal of Proteome Data and Methods (JPDM) 創刊 (2019.9.30)

<https://www.jhupo.org/jpdm/>



Japanese Proteomics Society  
日本プロテオーム学会

## Journal of Proteome Data and Methods

[Submit paper](#)

[Instruction to authors](#)

[Guide to reviewers](#)

[Editorial board](#)

[FAQ](#)

[Ethics policies](#)

### About JPDM



Proteomics is a rapidly growing research area that produces large amounts of data, which has led to complex challenges around data management. Proteomics data and datasets need to become more interoperable, discoverable and trusted, and therefore better used, re-used and more valuable. To address these challenges and facilitate better proteome data management, the field needs to develop formal structures and procedures. To this end, the Japanese Proteomics Society (JPrOS) is proposing to launch a new journal – **the Journal of Proteome Data and Methods**.

### News

2021.11.12

Updated Editorial board.

2020.12.15

Updated Instructions to Authors.

2019.12.25

The first Data Descriptor article has been published.

2019.9.30

Editorial article has been published.

2019.9.30

JPDM website was formally opened.

### Article list

J-STAGE : Journal of Proteome Data and Methods

# キュレーションの深化と強化 Journal of Proteome Data and Methods (JPDM) 創刊 (2019.9.30)

JPDM  
Journal of Proteome Data and Methods

About JPDM

News

2018.11.6  
Web site open.

Proteomics is a rapidly growing research area that produces large amounts of data, which has led to complex challenges around data management. Proteomics data and datasets need to become more interoperable, discoverable and trusted, and therefore better used, re-used and more valuable. To address these challenges and facilitate better proteome data management, the field needs to develop formal structures and procedures. To this end, the Japanese Proteomics Society (JPros) is proposing to launch a new journal – the Journal of Proteome Data and Methods.

See our publishing plan in PDF

ウェブサイト  
<https://www.jhupo.org/jpdm/>

JPDM  
Journal of Proteome Data and Methods

Submission

Step 1: Type, Title, & Abstract  
Step 2: File Upload  
Step 3: Attributes  
Step 4: Authors & Institutions  
Step 5: Reviewers & Editors  
Step 6: Details & Comments  
Step 7: Review & Submit

Step 1: Type, Title, & Abstract

Select your manuscript type from the list. Enter your manuscript title and abstract into the appropriate boxes below. If you need to insert a special character, click the "Special Characters" button. When you are finished, click "Save & Continue." [Read More...](#)

\* = Required Fields

Type:

CHOICE	TYPE
<input type="radio"/>	Data Descriptors
<input type="radio"/>	Protocols
<input type="radio"/>	Data Processing Notes
<input type="radio"/>	Reviews

投稿システム (ScholarOne)  
<https://mc.manuscriptcentral.com/jpdm>

JPDM  
Journal of Proteome Data and Methods

Instructions to Authors

AIMS & SCOPE

The Journal of Proteome Data and Methods is dedicated to publishing standardized accounts of original proteomics data and datasets, as well as the protocols used to derive and utilize them. It is international.

Guide to Reviewers

About the journal  
Conflict of interest  
Timing  
Confidentiality  
Submitting your review  
About the journal

Journal & Ethics Policies

Author Responsibilities  
Submission  
Duplicate submission  
Originality  
Preprints  
Scoring  
Authorship  
Image integrity  
Reproducing copyrighted material  
Availability of data and materials  
Authoritarian experimentation  
Specimen collection  
Clinical trial registration  
Reporting guidelines

Frequently Asked Questions (FAQs)

Data Submission

Open Access: What is Open Access?

How much does it cost to publish articles in the journal?

There are many costs associated with publishing scholarly journals, such as those of managing peer review, copy editing, typesetting,

Instructions to Authors

Guide to Reviewers

Ethics Policies

FAQ

License to Publish

Manuscript Number	Journal Name (the "Journal")
Article Title (the "Title")	
Authors (the "Author(s)") (Please list all authors on a new sheet if necessary)	

The Japanese Proteomics Society (the "Society") will consider publishing the Article in the Journal pursuant to the terms below.

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- 3) Sublicense others to do all or any of (1) and (2).

License to Publish form

- 各種ドキュメントの整備
- ウェブサイト構築
- 投稿システム構築
- JST J-stage システムから提供開始

# MANUSCRIPT TYPES

The journal publishes four article types: Data Descriptor, Protocol, Data Processing Note, and Review.

**Data Descriptor** is detailed descriptions of a dataset's metadata, as posted in jPOST or another recognized repository. The descriptions include the culture conditions, the procedures for the preparation of samples and their modification, the settings of each experiment device, and the relationships between experiments and data files. This information is in addition to details of biological samples and liquid chromatograph - mass spectrometer information, which must already be in the metadata for the original submission to the repository.

**Protocol** is detailed, step-by-step descriptions of the experimental procedures used to generate proteome data, which the authors have tested and standardized. Proteome experiments use a broad range of methods and devices for sample preparation, data collection and data analysis, and the journal is keen to facilitate the wide sharing of these techniques and tips.

**Data Processing Note** is detailed descriptions of the computational procedures used to analyze proteome data, including software and web tools. Once proteome data have been produced, various procedures – such as quality checks, peak pickings, peptide/protein identification and quantification, and detection of modifications – are used to derive scientific knowledge. By describing the algorithms and procedures used to analyze proteome data, the journal aims to improve the re-use of these data.

**Review** is an article presenting novel or unique overviews of recent and important developments in proteomics. Review must present clear and original insights into the questions of interest, using appropriate and fully presented evidence; long, general summaries are not published. Review is approximately 5000 words and can investigate several aspects of importance in a subject area. Review is by invitation only, but the journal welcomes proposals from authors. If the proposal meets the criteria of the *Journal of Proteome Data and Methods*, the Editor-in-Chief will invite the proponent to be the author of the Review.

# JPDM: 科研費によるサポート開始 (2021年より5年間)

JP  
Journal of Pro

掌振事第20号

令和3(2021)年度科学研究費助成事業(科学研究費補助金)(研究成果公開促進費)

## 「国際情報発信強化」交付決定通知書

日本プロテオーム学会

会長 小寺 義男 様

さきに交付申請がありました令和3(2021)年度科学研究費助成事業(科学研究費補助金)(研究成果公開促進費)「国際情報発信強化」につきましては、独立行政法人日本学術振興会科学研究費助成事業(科学研究費補助金)取扱要領(平成15年独立行政法人日本学術振興会規程第17号。以下「取扱要領」という。)第11条第2項の規定により、下記のとおり交付することに決定しましたので、取扱要領第11条第4項の規定により通知します。

令和3年6月21日

独立行政法人日本学術振興会

理事長 里見 進

(公印省略)

すでにjPOSTにデータを登録して作成した基本となる論文中の、方法論とメタデータを詳細に記載して、新たな論文として投稿いただくものですので、同じプロテオームデータから追加の論文が出ることになります。  
サプリメンタルデータとしての詳細なメタデータの登録をJPDMのサポートメンバーがお手伝いいたします。

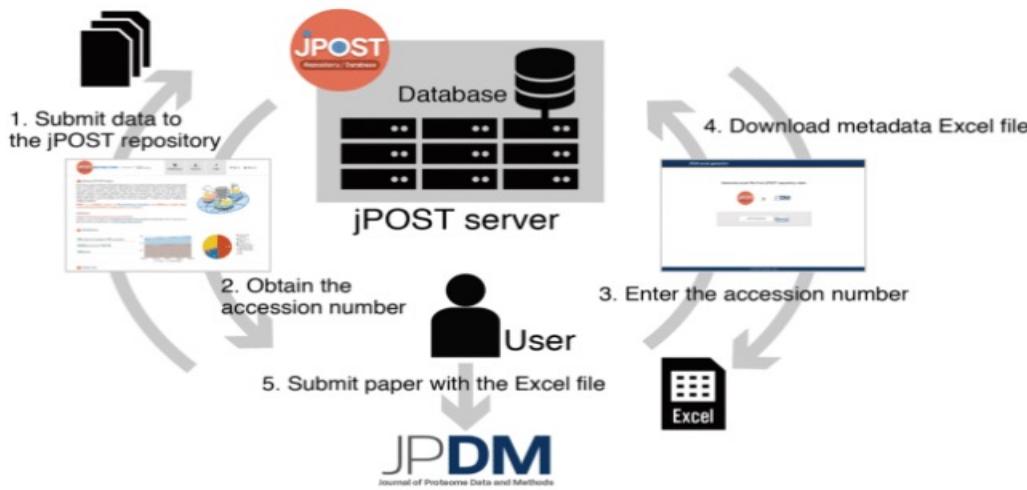
**どうぞ、気楽に投稿してください！**

# Journal of Proteome Data and Methods (JPDM)

## JPDM (Journal of Proteome Data and Methods) 用データのエクスポート

リポジトリで入力されたメタデータから、JPDMでの論文投稿に必要な情報を自動作成する機能を追加 (<https://repository.jpostdb.org/jpdm-excel/>)。

JPDM (Journal of Proteome Data and Methods) はjPOSTのメタデータ完全版の収録を一つの目的として2019年に創刊されたプロテオームのデータジャーナルであり、JPDMへの論文投稿とメタデータの質向上に貢献する。



jPOSTrepo: an international standard data repository for proteomes  
S. Okuda et al., Nucleic Acids Res., 45:D1107-D1111 (2017).

The jPOST environment: an integrated proteomics data repository and database  
Y. Moriya et al., Nucleic Acids Res., 47:D1218-D1224 (2019).

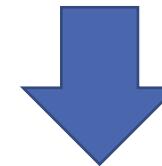
2019 annual report of the jPOST repository  
Y. Watanabe, S. Okuda, J. Proteome Data and Methods, 2:1 (2020).

# 使ってください jPOST

提案：データサイエンス研究者とデータベース研究者の融合



“使う”人はいつも外部ユーザー



つくる人とつかう人が相互に役に立ち、画期的な実験結果を創出できるプロジェクトをめざしています！



バイオサイエンス  
データベースセンター



面白いアイディア持ってるデータサイエンティストの皆さん、  
jPOSTを使いたいと思っておられるウェットサイエンティスト  
の皆様、何でもお問い合わせください。

jpostdb@gmail.com