AJACSオンライン 10（20220120）

jPOSTを使って
プロテオーム解析をする

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本日のテーマ

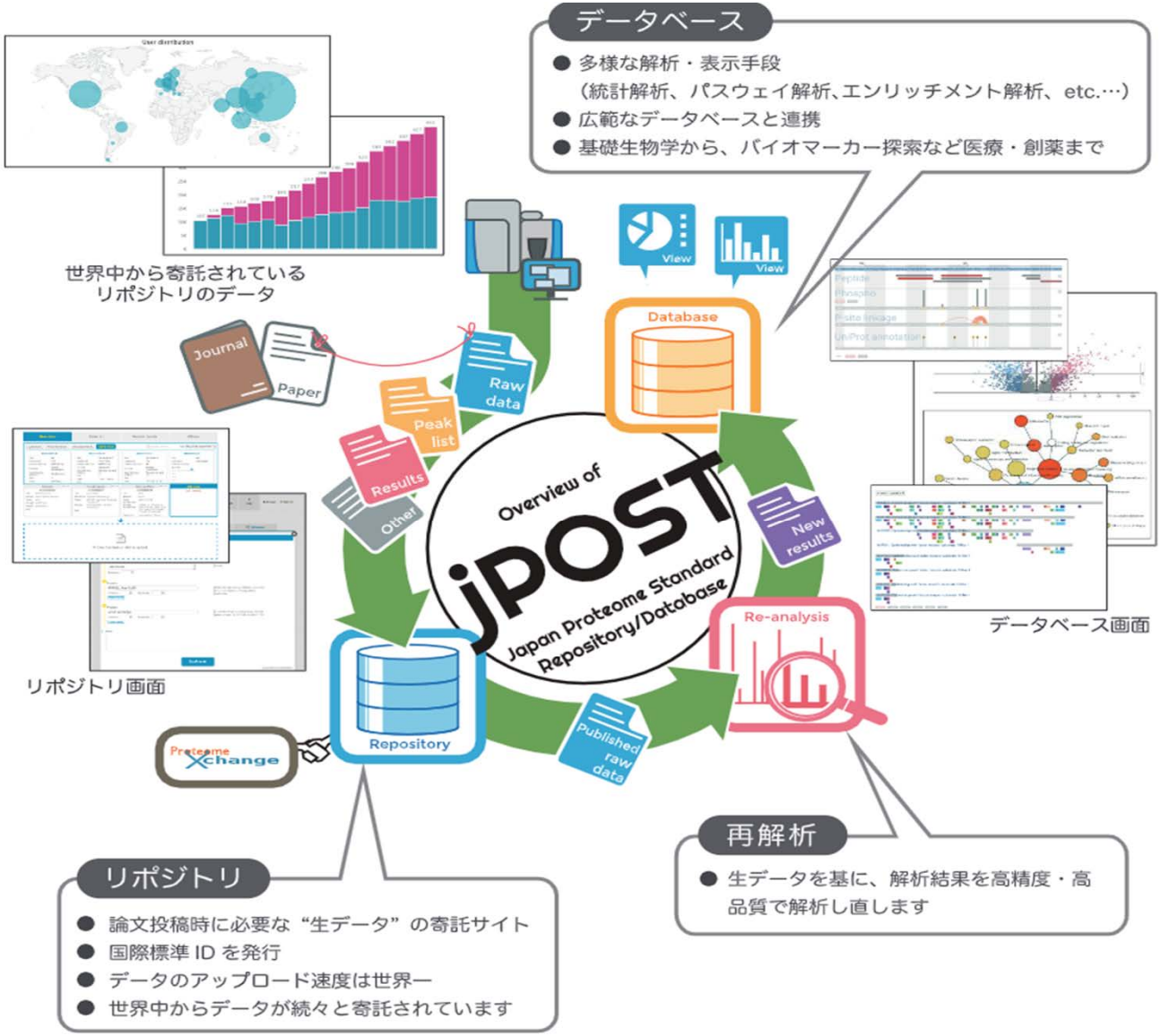
JPOSTを使ってプロテオーム解析をする

- JPOSTとは？
- 格納されるプロテオームデータとは？
- レポジトリーの説明と登録のこつ
- 登録データの再解析について
- 再解析後の高品質なプロテオームデータの蓄積・可視化と応用
- コロナDBの構築・再解析による新たな情報の創出と応用の可能性(リン酸化プロテオームを標的にして)
- JPDM誌の創刊と紹介

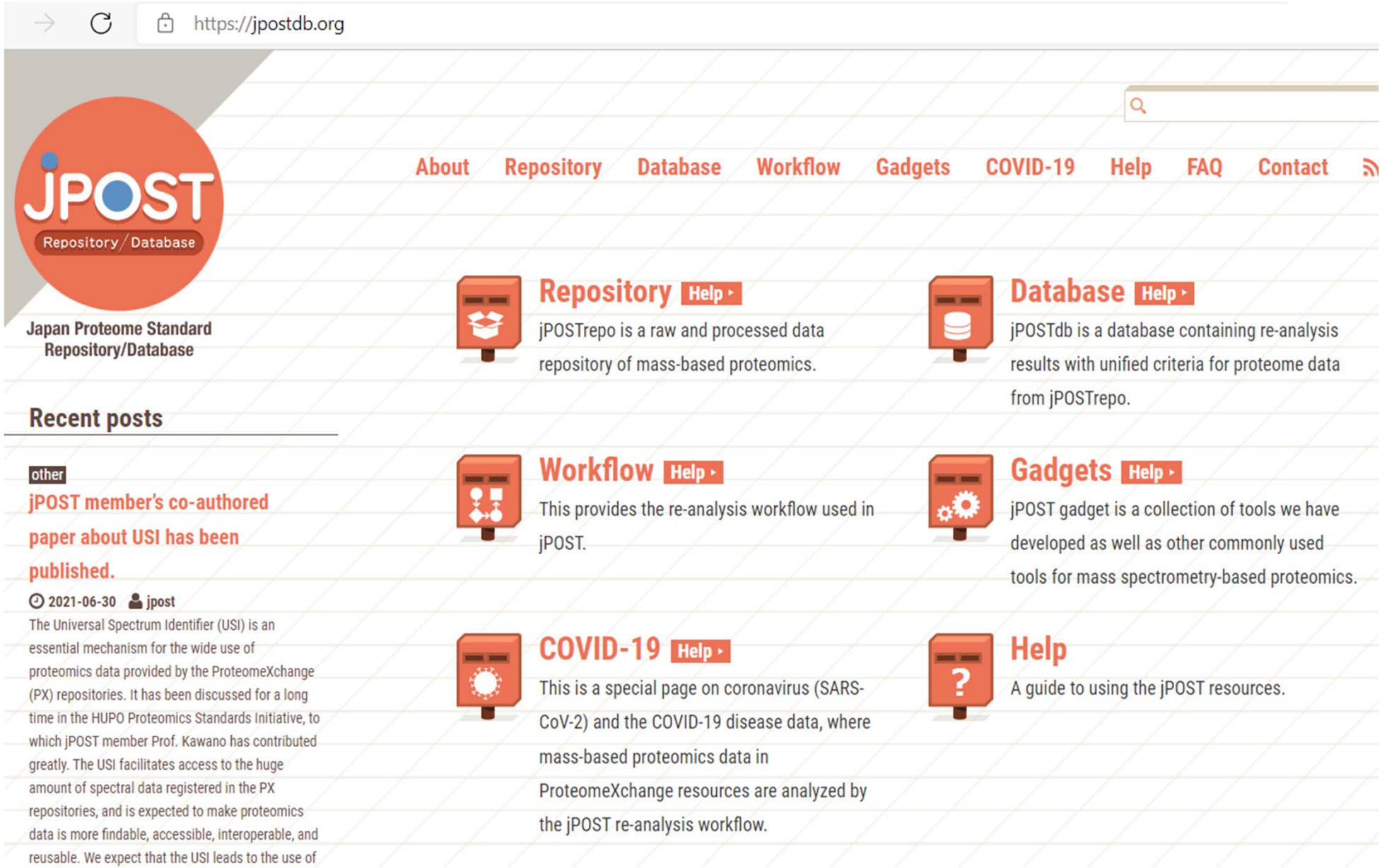
jPOST とは？
(Japan Proteome Standard Repository/Database)

https://jpostdb.org

国内外に散在している種々の質量分析に基づくプロテオームデータを統合し、各種のデータベースと連携しながら統一された信頼基準で結果を再解釈し、画期的かつ有用な新たな発見をもたらすことを目標に、2015年よりJSTの統合化推進プログラムのサポートのもと、構築を進めている、



https://jpostdb.org

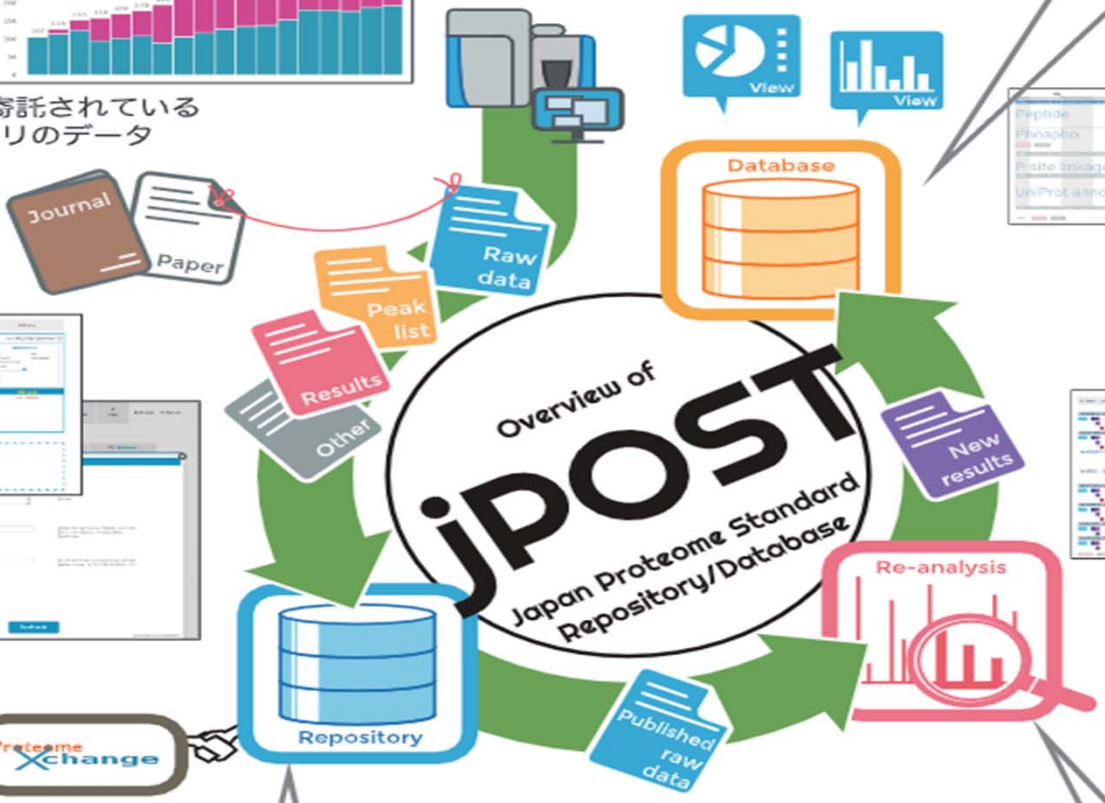


jPOST とは？
(Japan Proteome Standard Repository/Database

世界中から寄託されている
リポジトリのデータ

リポジトリ画面

データベース画面



データベース

- 多様な解析・表示手段
  （統計解析、パスウェイ解析、エンリッチメント解析、etc.…）
- 広範なデータベースと連携
- 基礎生物学から、バイオマーカー探索など医療・創薬まで

リポジトリ

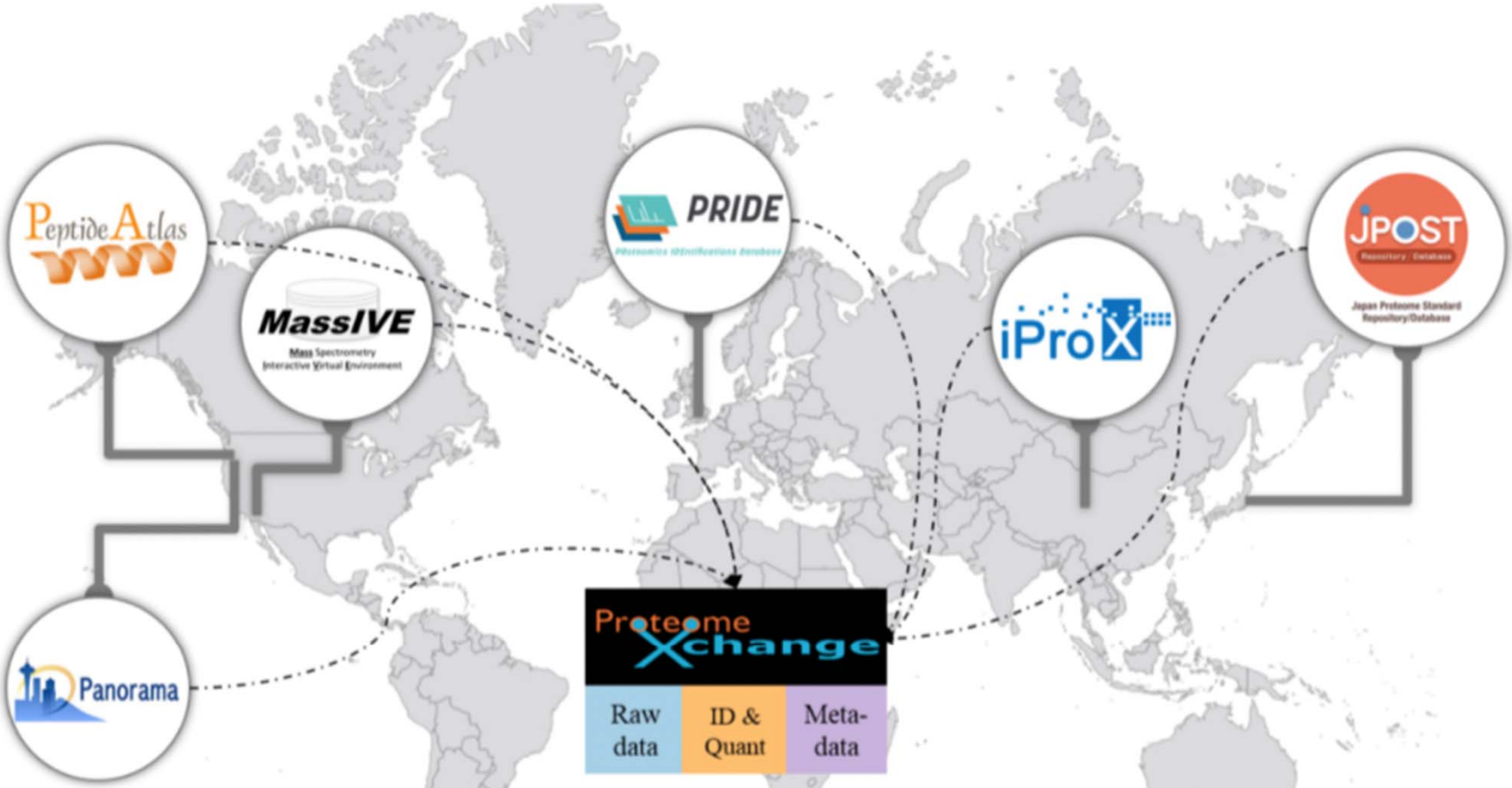
- 論文投稿時に必要な“生データ”の寄託サイト
- 国際標準 ID を発行
- データのアップロード速度は世界一
- 世界中からデータが続々と寄託されています

再解析

- 生データを基に、解析結果を高精度・高品質で解析し直します

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

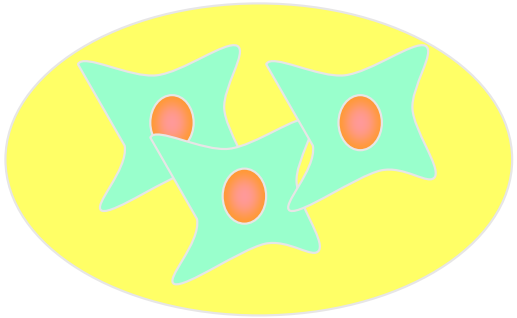
質量分析（Mass Spectrometry/MS）で
プロテオームを測定する。

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



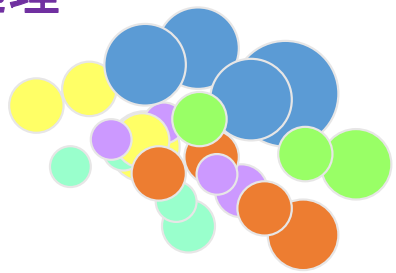
Trypsin: Lysine(K)またはArginine(R)の
C末端側のペプチド結合を加水分解
する酵素

生体試料 (培養細胞、組織、体液、菌など)

Trypsin

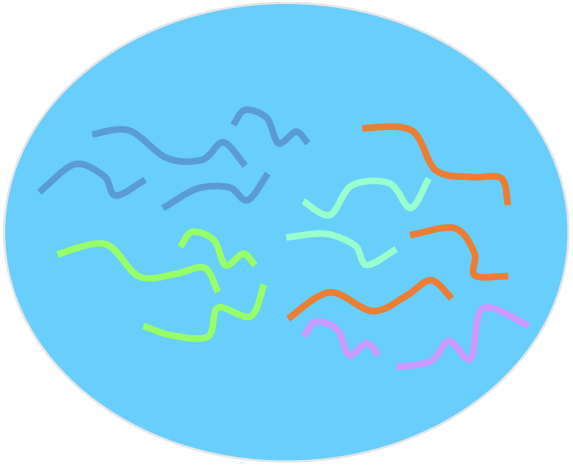
抽出

前処理



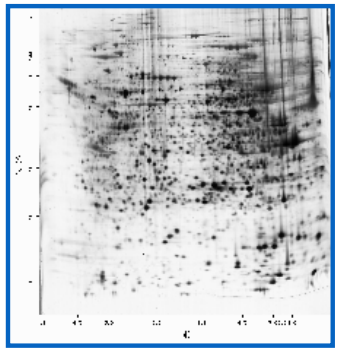
Protein

消化



Peptide mixture

2次元電気泳動



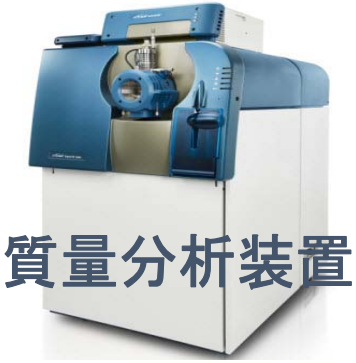
Proteome Analysis Workflow

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）

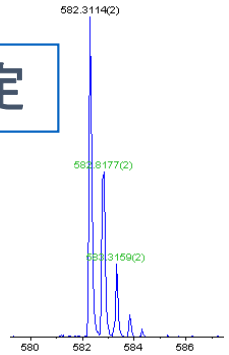
Peptide mixture

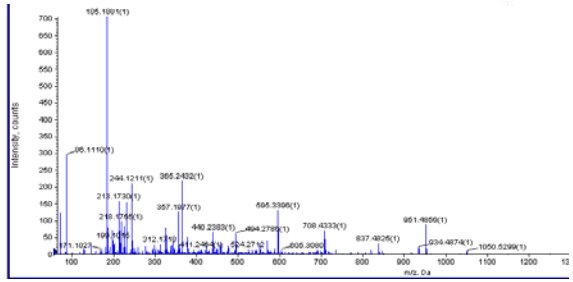
Nano LC
(ペプチド分離)



質量分析装置

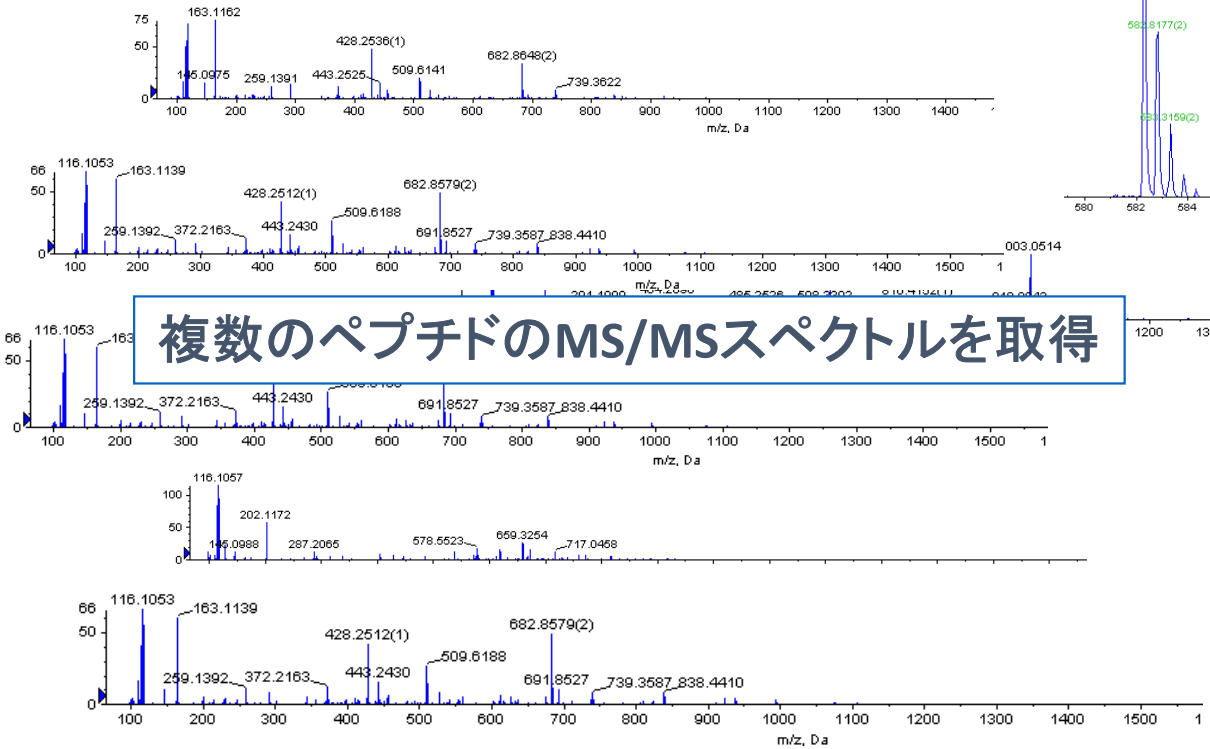
MS測定





MS/MS測定

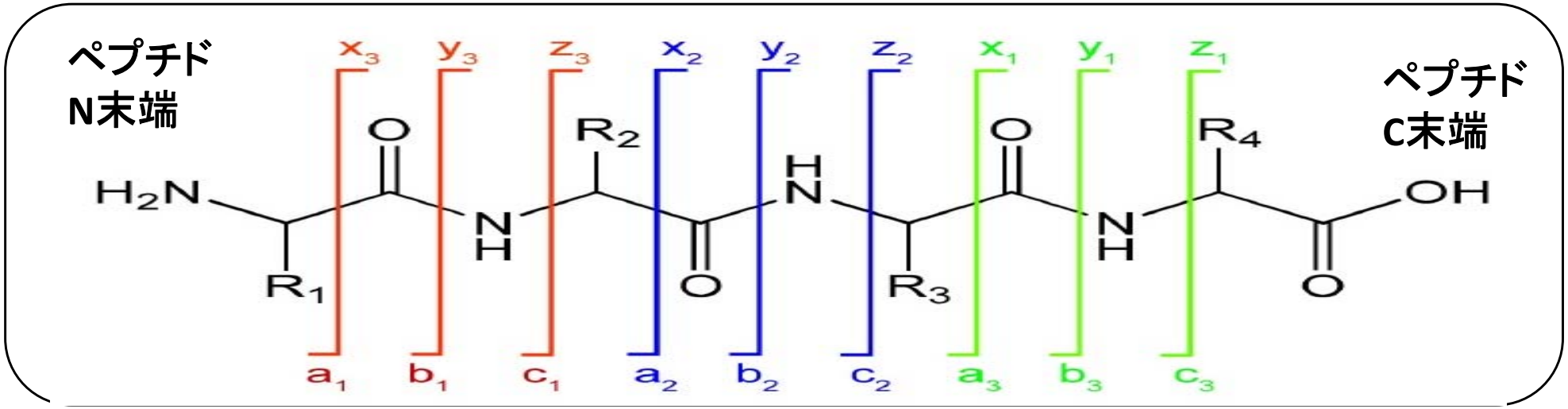
複数のペプチドのMS/MSスペクトルを取得



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



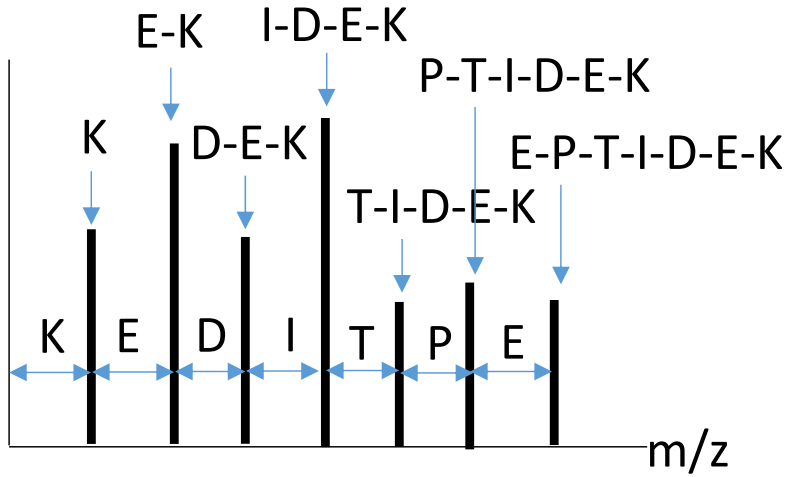
ペプチド

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

Collision

-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-

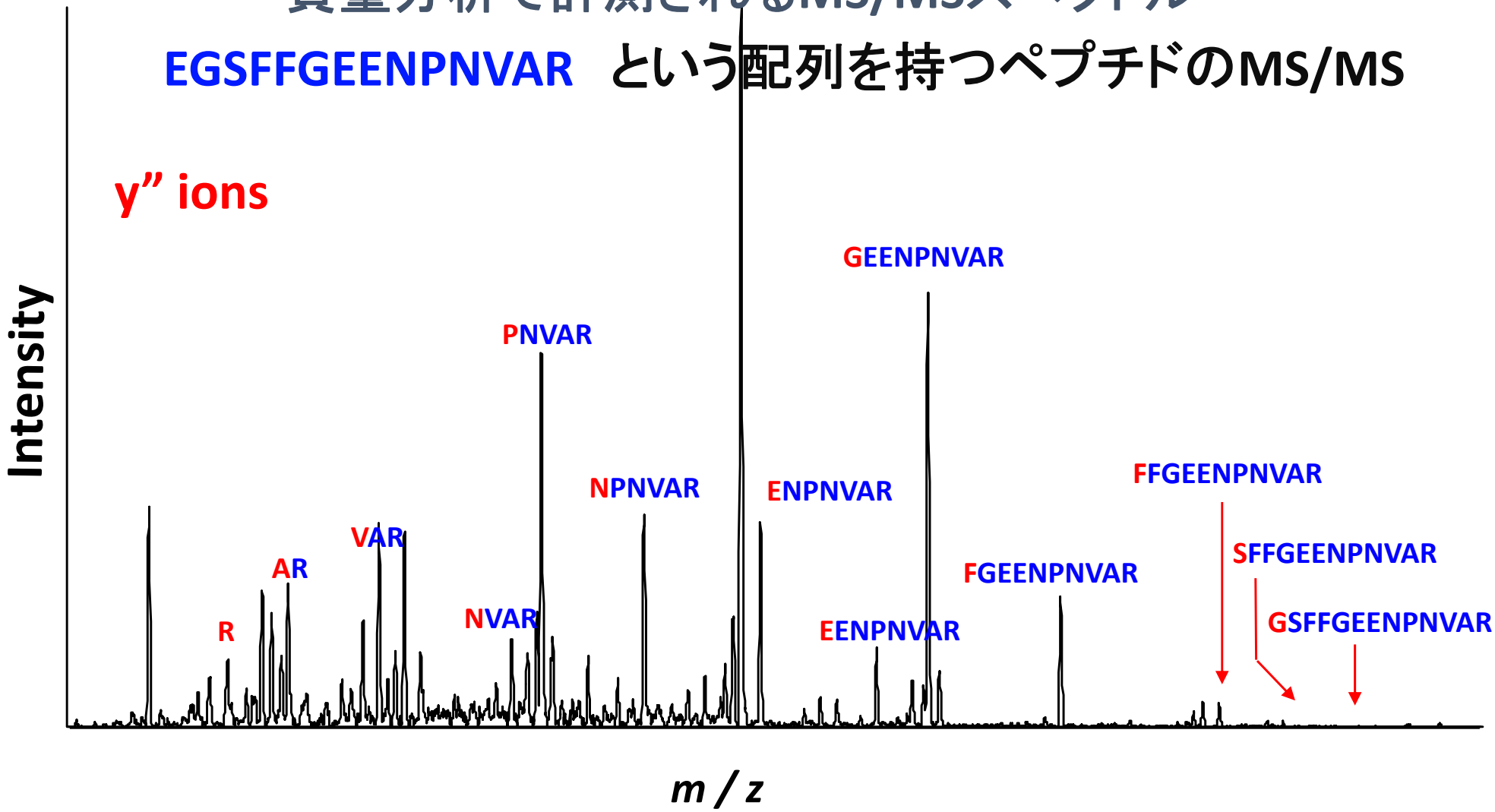
MS/MS スペクトル



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

質量分析で同定されるヒト細胞タンパク質の数と解析時間の変遷

Changes in the number and analysis time of human cell proteins identified by mass spectrometry

Year (instru-ment)	Total spectra	Identified peptides	Identified proteins	Total analysis time	参考文献
2007 (QSTAR Pulser i)	80,088	12,769	902	～1 week 100 ug	Kobayashi et al. MCP 2009
2011 (QSTAR Elite)	286,025	68,790	3,582	～3 days 50 ug	Kobayashi et al. MCP 2013
2018 (OrbiTrap Fusion TT6600)	100,000 ～ 1,000,000	50,000 ～ 120,000	3,000 ～ 9,600	1～19 hrs 200 ng ～5 ug	In-house Data 2018

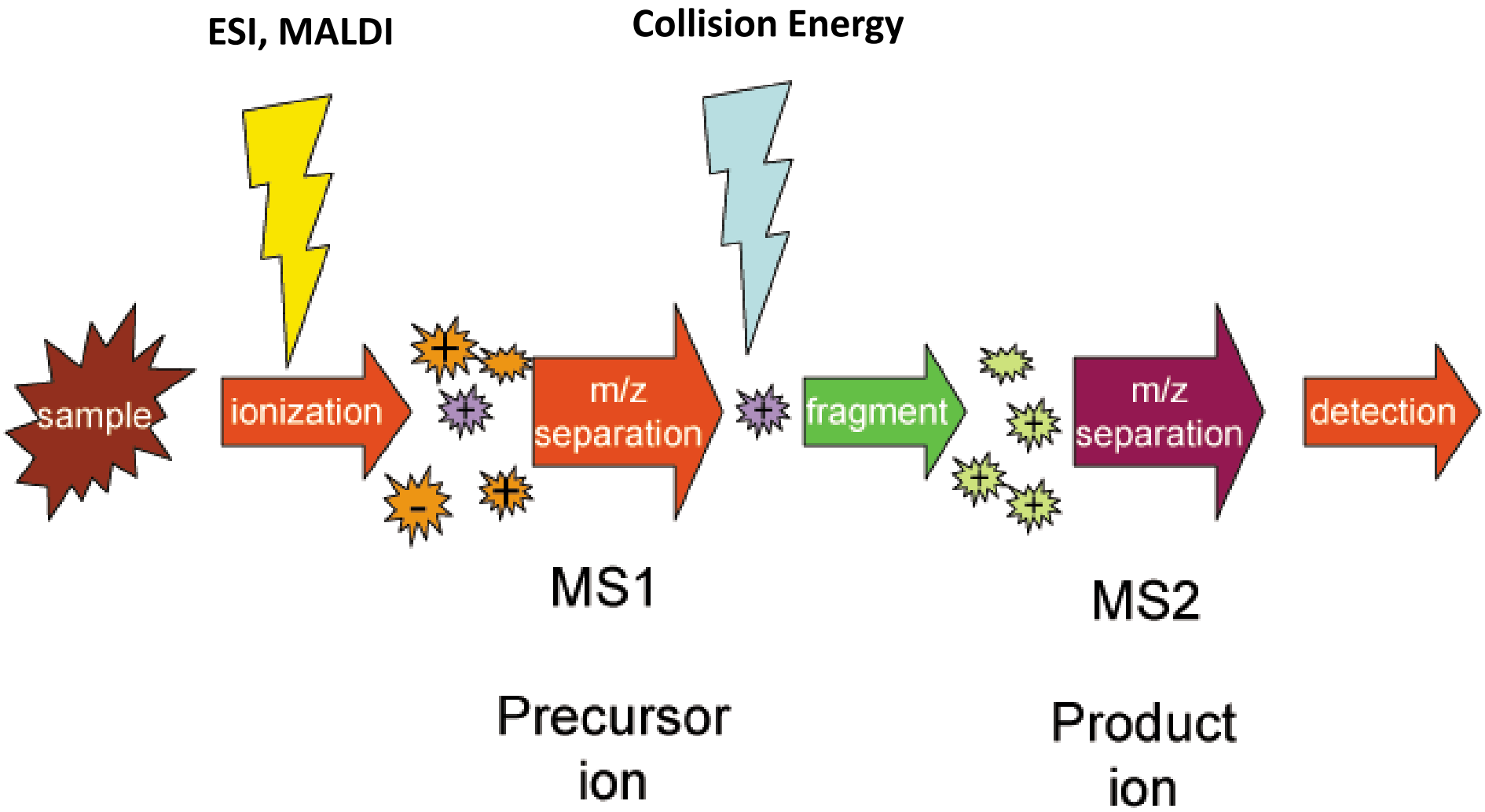
質量分析装置の高感度化・高精度化・迅速化が進み、短時間で同定されるタンパク質の数が飛躍的に増加!!! Mass spectrometers are becoming more sensitive, more accurate and faster, protein numbers identified has increased dramatically.

膨大なデータが次々と生み出されるため、情報処理のスピード化がカギとなる。

Generated enormous amounts of data need to be processed by high speed bioinformatics

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

質量分析装置でサンプル（ペプチド）がどのようにして検出されているのか？？

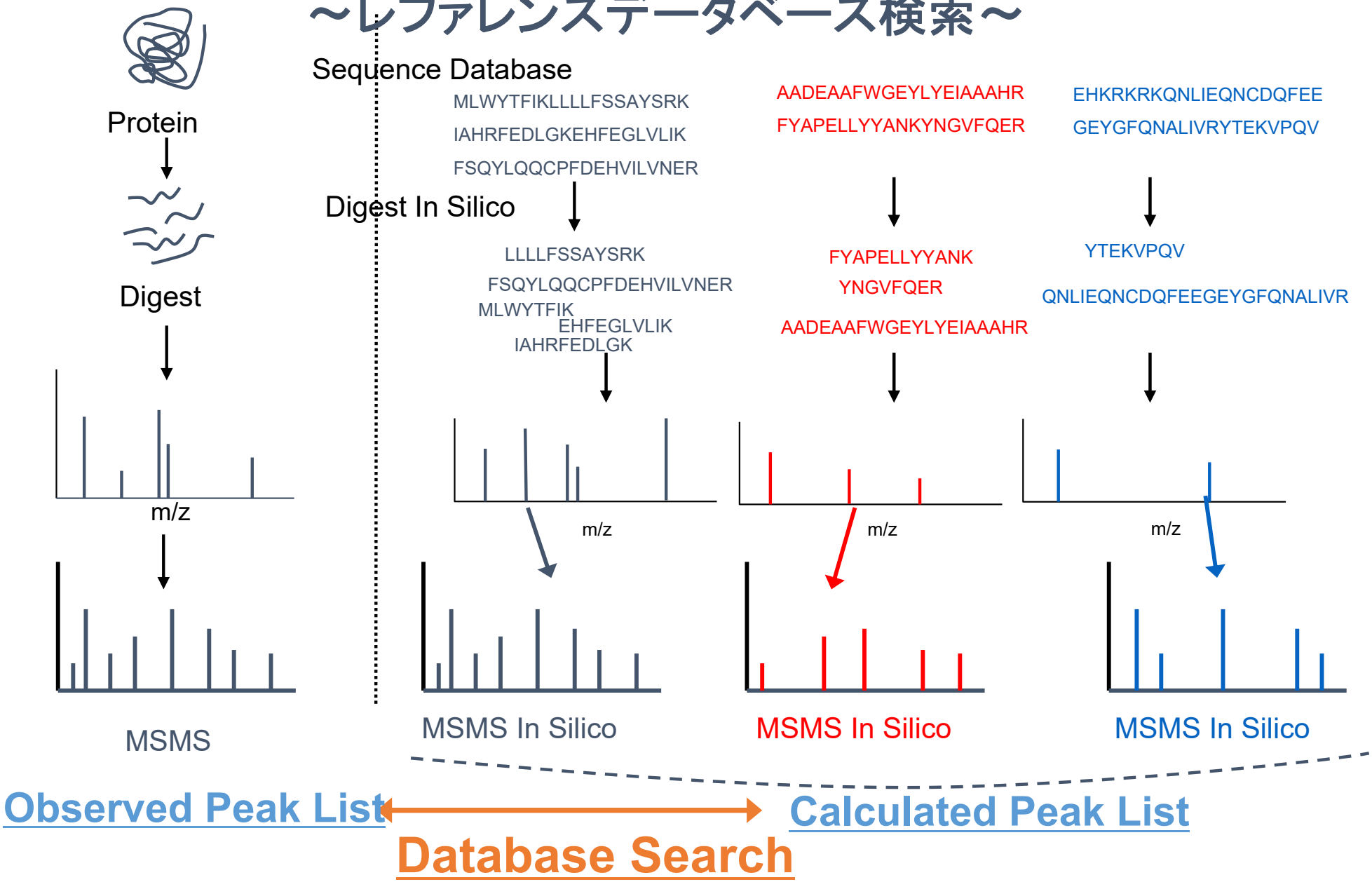


ESI: Electron spray ionization
MALDI: Matrix-assisted laser desorption/ionization

wikipediaより改変

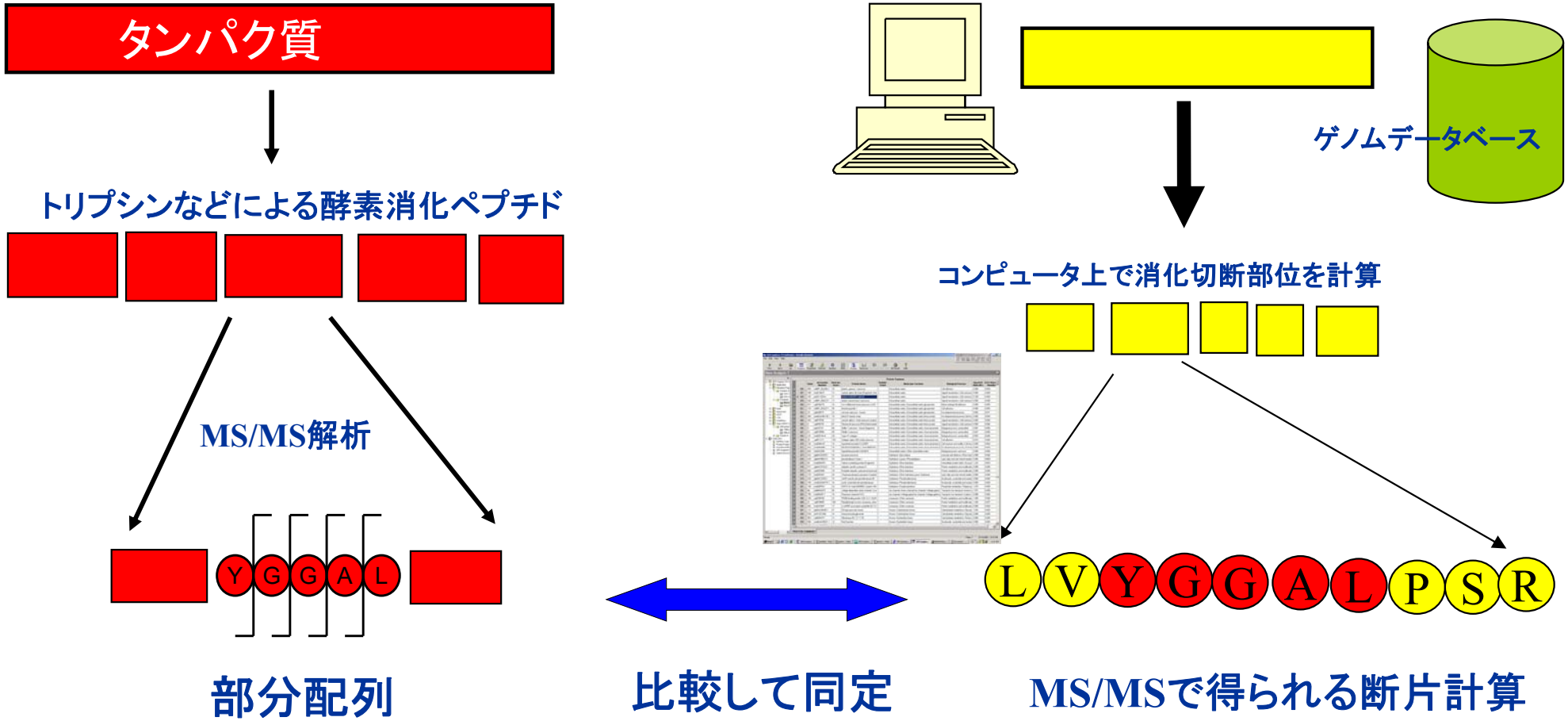
Proteome Analysis Workflow

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～



Proteome Analysis Workflow

Sequence Tag法
MS/MSによるタンパク質同定の標準法



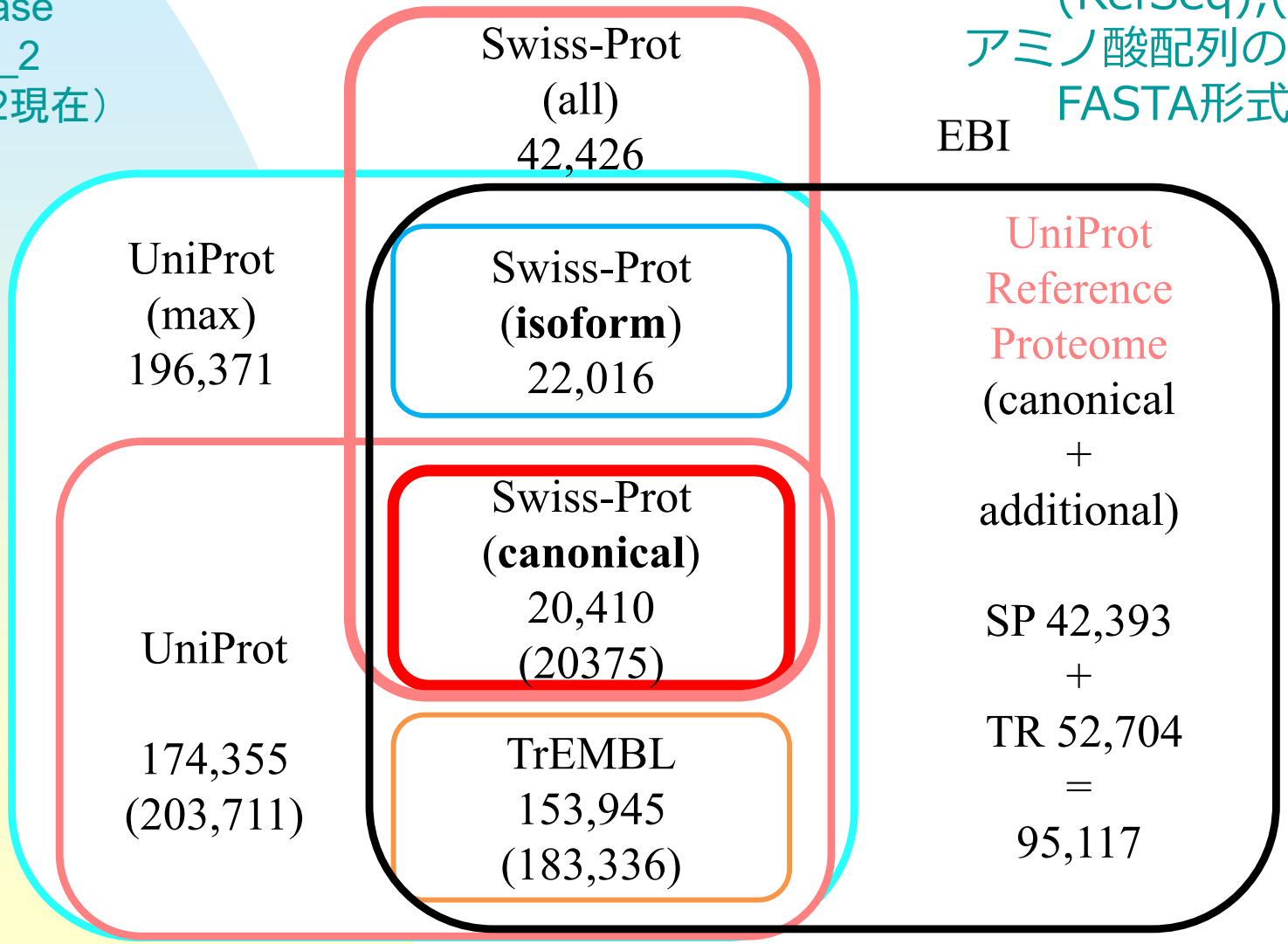
親となるペプチドの質量と分解したアミノ酸部分配列の情報
（シーケンスタグとよばれる）を組合わせてデータベース検索する

Reference Protein Database
Sequence collection

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

ヒトの場合

Release
2018_2
(2022現在)



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膨大なデータが次々と生み出されるため、情報処理のスピード化がカギとなる。

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と溜まっていく！→
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

学術論文雑誌の投稿規定

Scientific Data

関連するデータセットは投稿前に適切な公開リポジトリに必ず登録してください。掲載受理された場合には、制限をつけずに、これらのデータセットの一般公開を必ず行ってください

PLoS

PLOS journals require authors to make all data underlying the findings described in their manuscript fully available without restriction, with rare exception.

Molecular & Cellular Proteomics

We require that all raw mass spectrometric output files in the original instrument vendor file format be deposited in a publicly accessible repository at the time of submission.

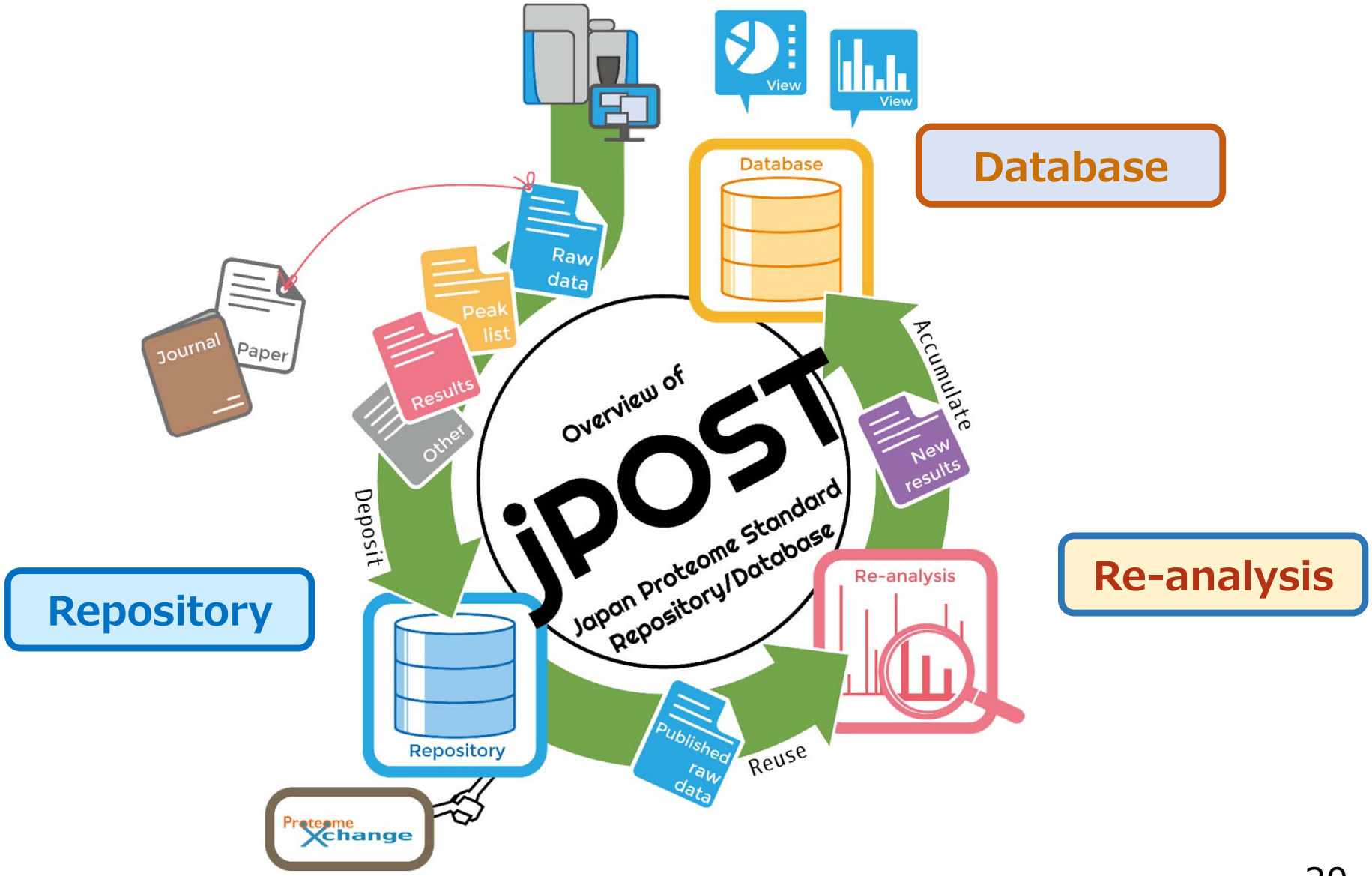
Journal of Proteome Research

As of January 1, 2018, the Journal of Proteome Research will require SUBMISSION OF RAW DATA to a public repository such as a ProteomeXchange (PRIDE or MASSIVE), or CHORUS, or an equivalent repository when the paper is submitted.

Etc. **現在、ほとんどのJournalがこれに追随している。**

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 repository

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

https://jpostdb.org

https://jpostdb.org

Japan Proteome Standard Repository/Database

About Repository Database Workflow Gadgets COVID-19 Help FAQ Contact

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

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 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

jPOST REPOSITORY A member of ProteomeXchange

Repository | Submit | Help | Sign in | 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

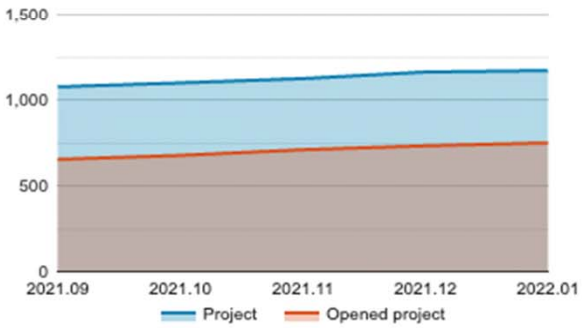
Please cite the following article when using jPOSTrepo:
Okuda, S. et al. jPOSTrepo: an international standard data repository for proteomes. Nucl. Acids Res. 45 (D1): D1107-D1111 (2017). doi: 10.1093/nar/gkw1080 [pubmed]

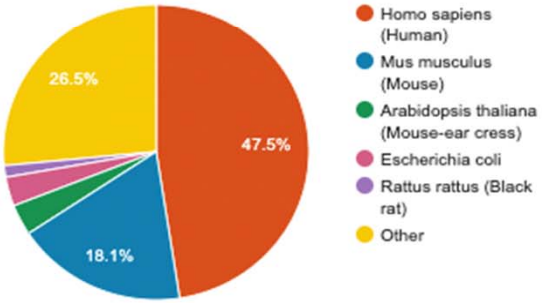
Statistics

1170 projects are registered. **749** are opened.

87193 files amount to **40.0 TB**.

187 species.





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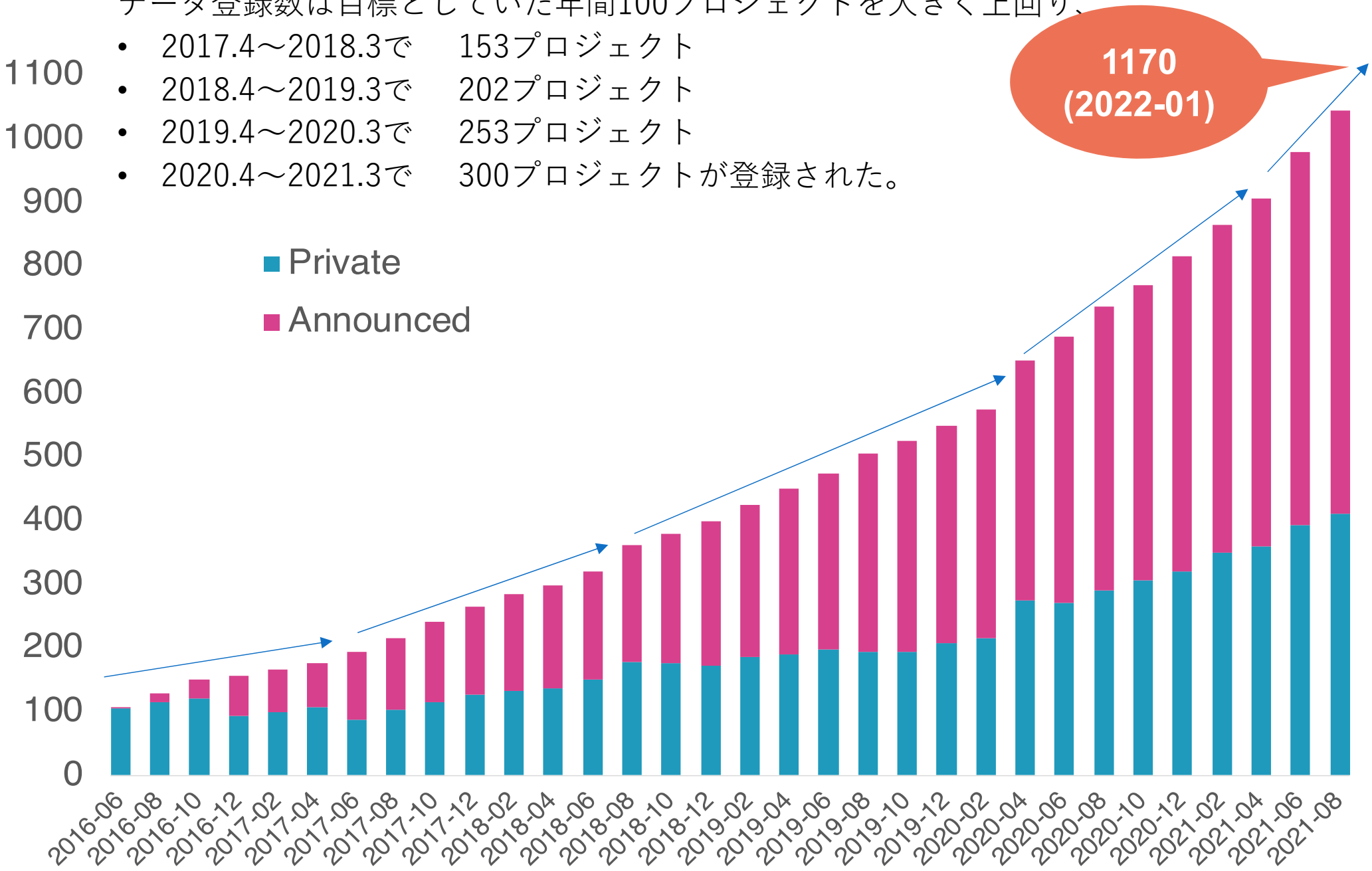
特徴

MSによって得られた生データ(Ras data, Peak list) 、解析データ(process data)の格納
オントロジーにより整理されたメタデータの入力、
メタデータとデータファイルの柔軟な対応
PXD IDの発行、高速アップロードシステム、ウェブブラウザのみで完結

jPOST repository – Current status

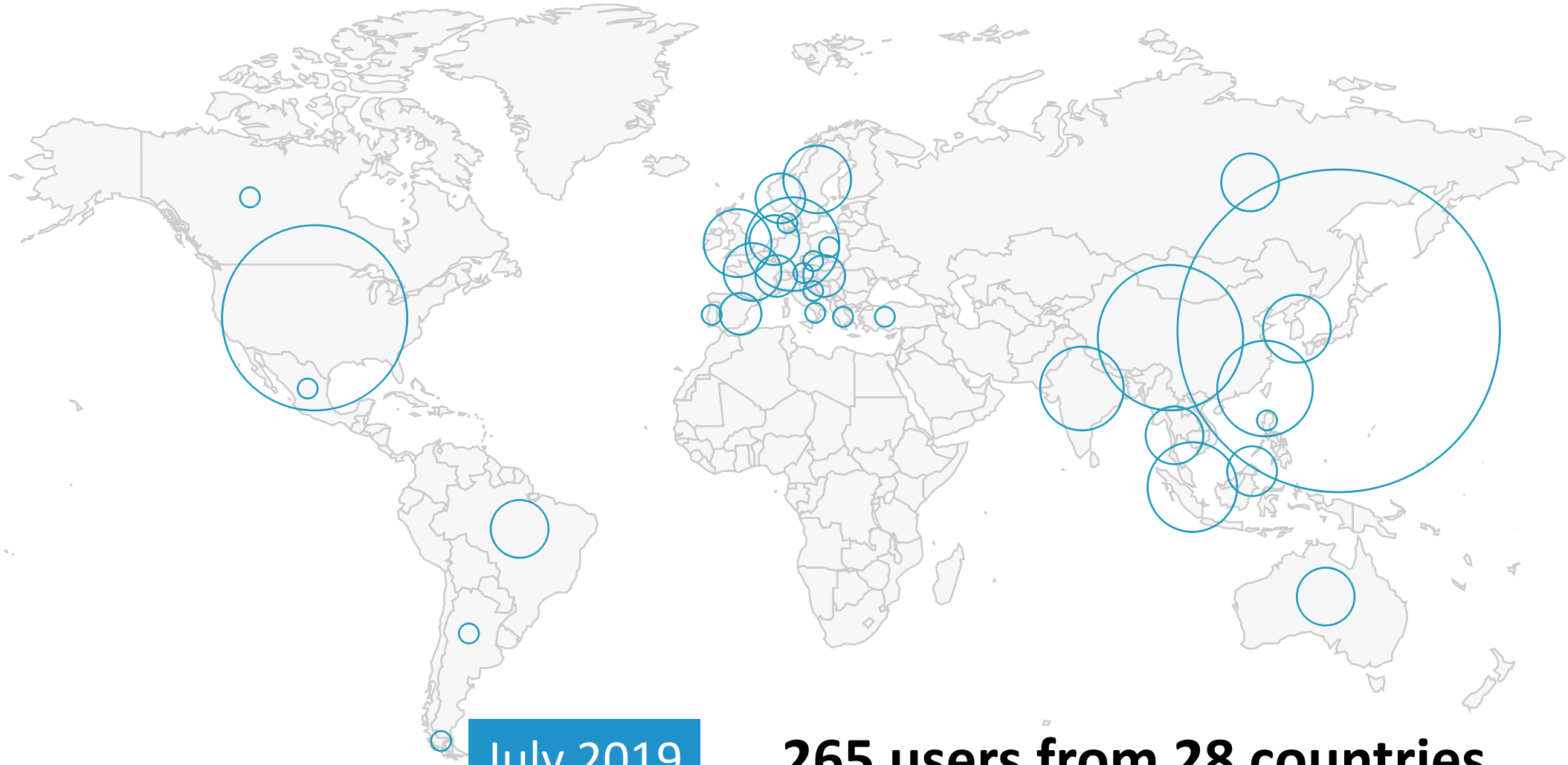
データ登録数は目標としていた年間100プロジェクトを大きく上回り、

- 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。



jPOST User Distribution

User distribution



July 2019	**265 users from 28 countries**
July 2020	**391 users from 37 countries**
Sep 2021	**543 users from 37 countries**

Statistics

Nov 2020

798 projects are registered. **479** are opened.

65623 files amount to **26.3 TB**.

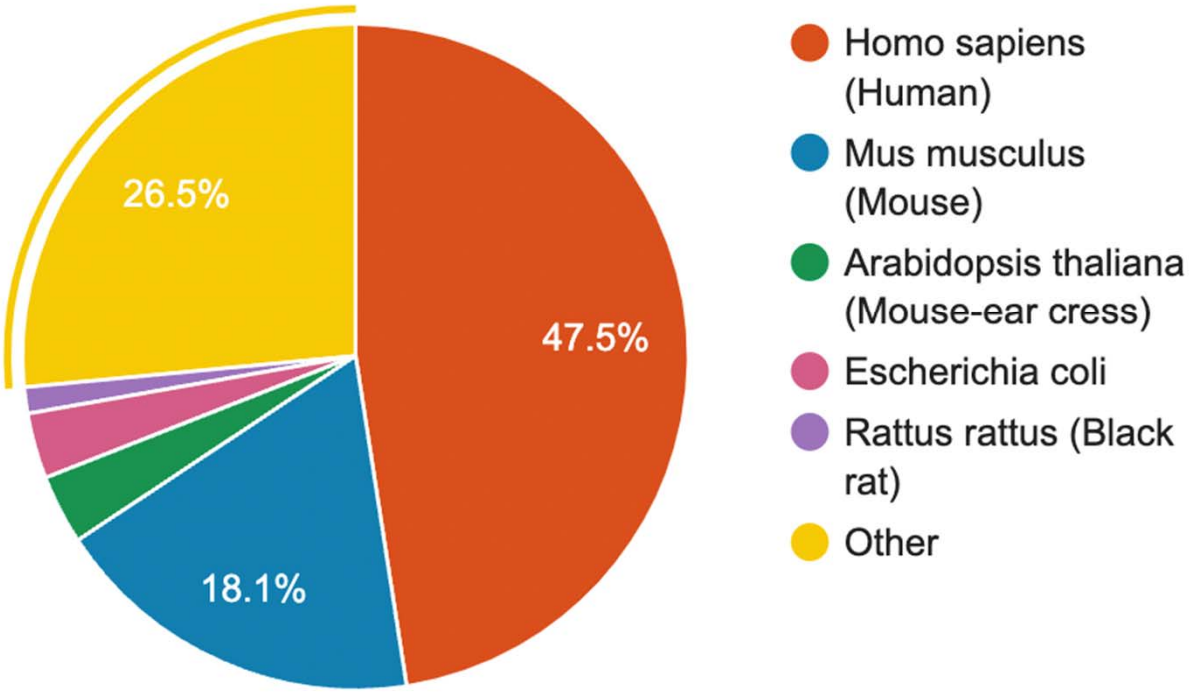
126 species.

Sep 2021

1170 projects are registered. **749** are opened.

87193 files amount to **40.0 TB**.

187 species.



jPOST repository
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

jPOST REPOSITORY A member of ProteomeXchange

Repository | Submit | Help | Sign in | 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 [pubmed]

Statistics

1170 projects are registered. **749** are opened.

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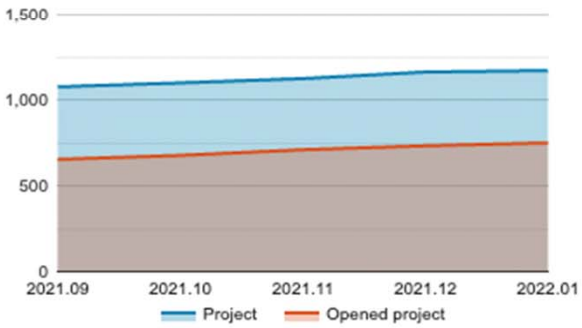

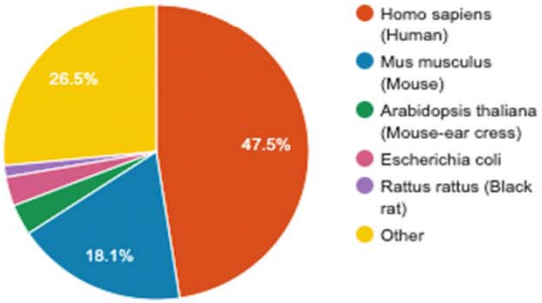

jPOST repository
https://repository.jpostdb.org

Data

Free word

phospho

Project type

All Ma

Data list

Free word | Ontology keyword

colon cancer phospho

Project type

All | Mass spectrometry | Gel electrophoresis | Antibody

Search | Reset

Search result

Search result colon cancer phospho

1 - 9 / 9 1

jPOST ID	jPOST ID	PXID	Project title	Description	Complete / Partial	Publication	Principal investigator	Announcement date	
JPST001055	JPST000973	PXD021750	Mike' s S89A Project on the intestinal effects	S89A mouse intestinal change analysis by proteomic …	Partial	Pre-publication	Michael Kahn City of Hope	2021-09-30	Detail page Quick view
	JPST000718	PXD016898	GBM cell line secretome analysis	Glioblastoma (GBM) is the most common and aggressi …	Partial	32628487	Sumio Ohtsuki Kumamoto University	2020-09-19	Detail page Quick view
JPST001237	JPST000538	PXD012251	Phosphoproteomics of endoscopic biopsy	Phosphoproteomics were obtained from endoscopic bi …	Partial	Pre-publication	Takeshi Tomonaga National Institute of Biomedical Innovation, Health, and Nutrition	2019-12-02	Detail page Quick view
JPST001437 JPST001256	JPST000396	PXD009032	Phosphoproteomics of Matrigel-embedded samples	Phosphoproteomics data of Matrigel-embedded HCT116 …	Partial	Pre-publication	Takashi Tomonaga National Institute of Biomedical Innovation, Health, and Nutrition	2019-02-24	Detail page Quick view
JPST001186			pY IP of Colorectal cancer	Phosphotyrosine status were			Takeshi Tomonaga National Institute of		Detail page

jPOST repository
https://repository.jpostdb.org

NIH National Library of Medicine
National Center for Biotechnology Information

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PubMed.gov

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User Guide

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> Sci Rep. 2021 Dec 20;11(1):24254. doi: 10.1038/s41598-021-03260-5.

MYCL promotes iPSC-like colony formation via MYC Box 0 and 2 domains

Chiaki Akifuji [1], Mio Iwasaki [1], Yuka Kawahara [1], Chiho Sakurai [1], Yu-Shen Cheng [1], Takahiko Imai [1], Masato Nakagawa [2]

Affiliations – collapse

Affiliations

1 Department of Life Science Frontiers, Center for iPS Cell Research and Application (CiRA), Kyoto University, Kyoto, 606-8507, Japan.

2 Department of Life Science Frontiers, Center for iPS Cell Research and Application (CiRA), Kyoto University, Kyoto, 606-8507, Japan. nakagawa@cira.kyoto-u.ac.jp.

PMID: 34930932 PMCID: PMC8688507 DOI: 10.1038/s41598-021-03260-5

Free PMC article

Abstract

Human induced pluripotent stem cells (hiPSCs) can differentiate into cells of the three germ layers and are promising cell sources for regenerative medicine therapies. However, current protocols generate hiPSCs with low efficiency, and the generated iPSCs have variable differentiation capacity among different clones. Our previous study reported that MYC proteins (c-MYC and MYCL) are essential for reprogramming and germline transmission but that MYCL can generate hiPSC colonies

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nature publishing group

PMC FREE Full text

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PAGE NAVIGATION

< Title & authors

Abstract

Conflict of interest statement

Figures

jPOST repository
https://repository.jpostdb.org

Search result phospho

1 - 20 / 191 1 2 3 ... 10 GB)

jPOST ID	PXID	Project title	Description	Complete / Partial	Publication	Principal investigator	Announcement date	
JPST001055	PXD023475	Peptidome analysis of the hypothalamus in a single mouse.	A 2-mg frozen section of hypothalamus from a singl ...	Partial	Pre-publication	Yoshio Kodera Center for Disease Proteomics, Kitasato University School of Science	2022-01-08	Detail page Quick view

JPST001055 summary

Species	Mus musculus (Mouse) [10090]
Tissue	brain [BTO:0000142]
Fixed modification	none
Variable modification	Oxidation (M) [UNIMOD:35#M], Acetyl (K) [UNIMOD:1#K], Acetyl (N-term) [UNIMOD:1#N-term], Amidated (C-term) [UNIMOD:2#C-term], Deamidated (N) [UNIMOD:7#N], Deamidated (Q) [UNIMOD:7#Q], Dehydrated (D) [UNIMOD:23#D], Dehydrated (S) [UNIMOD:23#S], Dehydrated (T) [UNIMOD:23#T], Dehydrated (Y) [UNIMOD:23#Y], Dehydrated (N, C-term), Dehydrated (Q, C-term), Sodium (D), Sodium (E), Sodium (C-term), Phospho (S) [UNIMOD:21#S], Phospho (T) [UNIMOD:21#T], Phospho (Y) [UNIMOD:21#Y], Gln->pyro-Glu (Q) [UNIMOD:28#Q], Methyl (K), Methyl (R)
Taxonomy	Mus musculus (Mouse) [10090]
Instrument	Q Exactive [MS:1001911]
Instrument mode	DDA-high res.
Purpose	spectrum identification result details [MS:1001405]
Quantification platform	Precursor ion label free
File format	other
Software	PEAKS

1

Differences of

jPOST repository
https://repository.jpostdb.org

Files

Download all (1.09 GB)

File Name	Experimental presets (Sample / Fractionation / Enzyme/Mod. / MS mode)	File Size	Detail
Ankgw123_001_Hy_AWK85_1_0o012ug_6ug_T50_2.raw Raw	S Mouse Hypothalamus F none E Endogenous peptides in mouse hypothalamus M Peptide identification and non-label quantification	497.7 MB	Detail
Ankgw123_002_Hy_AWK85_2_0o012ug_6ug_T50_2.raw Raw	S Mouse Hypothalamus F none E Endogenous peptides in mouse hypothalamus M Peptide identification and non-label quantification	448.2 MB	Detail
Ankgw123_003_Hy_AWK85_3_0o023ug_6ug_T50_2.raw Raw	S Mouse Hypothalamus F none E Endogenous peptides in mouse hypothalamus M Peptide identification and non-label quantification	461.8 MB	Detail
DB search psm.csv Result PEAKS		834.9 kB	Detail
protein-peptides.csv Result PEAKS		353.3 kB	Detail
proteins.csv Result PEAKS		49.3 kB	Detail

1 - 6 / 6 1

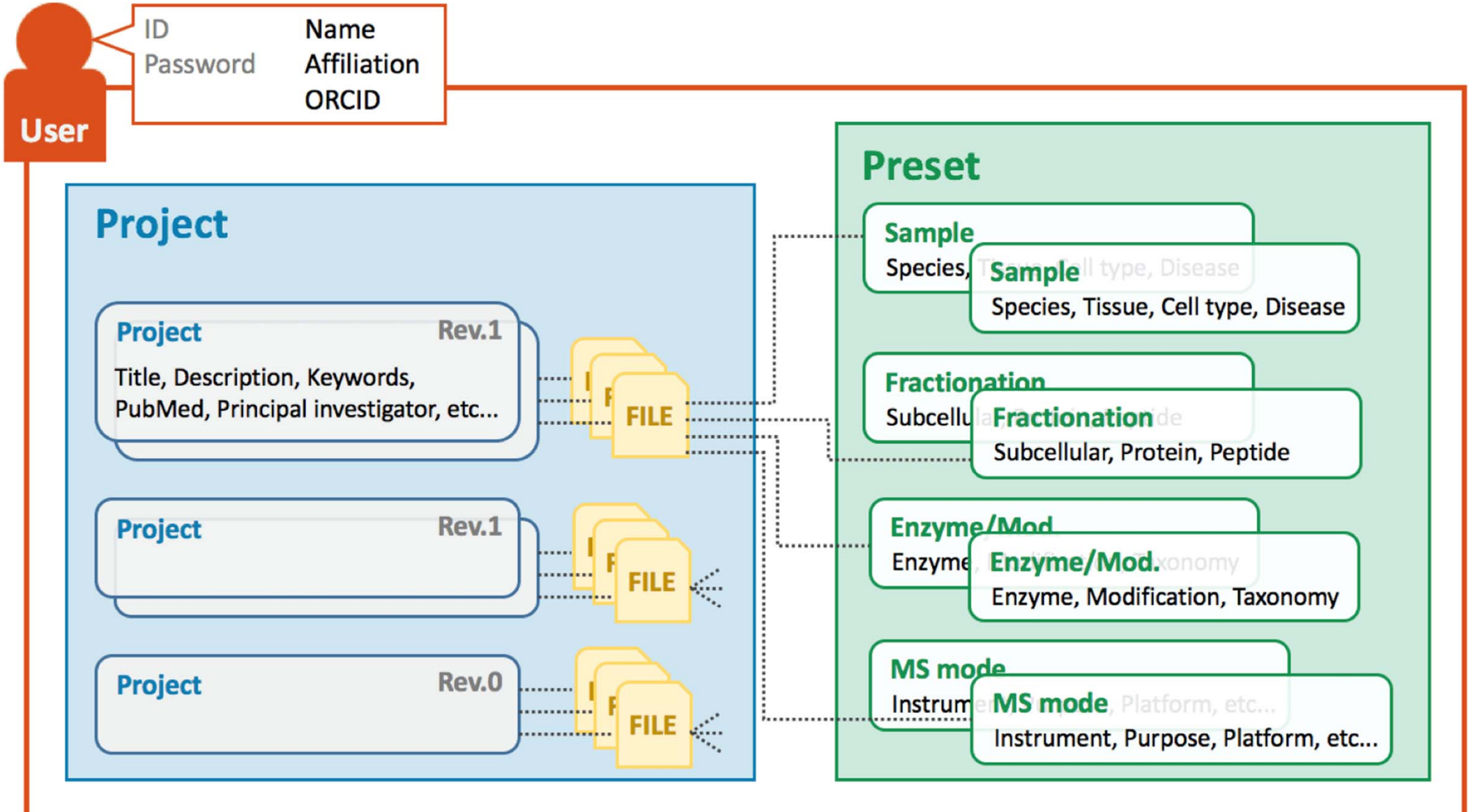
Project list

jPOST repositoryへのデータ登録する手順（Movie）

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

jPOST repositoryへのメタデータの登録

実験プロジェクトと切り離して、メタデータを保持することができ、
たとえば、予め作成した、4種類のメタデータ プリセットをファイルに紐付けることができるので、毎回毎回同じメタデータを入れる必要がない。



jPOST repositoryへのデータの登録

Complete submission

データをリポジトリに公開する際に、再利用しやすいように決まったルール(PSIの推し進めている再利用しやすい標準フォーマット)で登録する必要性がある。

- 必要十分なメタデータ
- Raw data: vender raw or mzML
- Peak list: MGF or mzML(-> mgf by PW)
- Result (process data): mzIdentML or mzTab
- raw-peak-resultファイルの関係性がきちんと紐付いていること。

Partial submission

jPOSTでは、Completeでないものは、すべてPartialとして受け付けている。(formatは問わずRawとResultの２種類のデータとメタデータがあれば登録できるが、Completeでの登録をお願いします)

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。

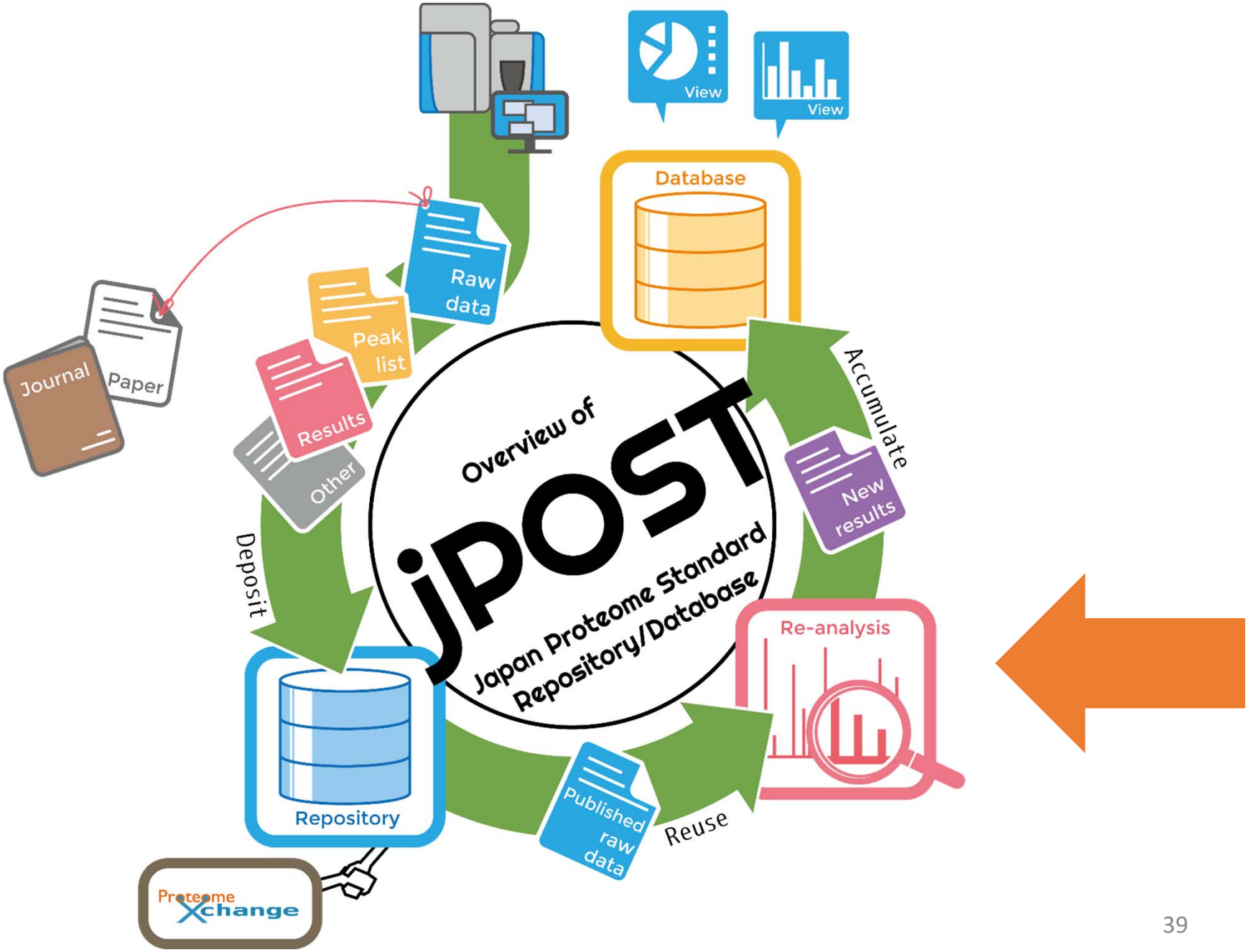
2) メタデータを正確にできるだけ詳しく入力していただく必要があります。簡易的に入力しても登録はできますが、その後の再解析やデータベースへの応用が困難になります。アンケートにて後日、その詳細をお聞きすることがあります。

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ンNO 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 [pubmed]

5) リポジトリーのデータをダウンロードする際は
ダウンロードー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

2．再解析により、データの統一化が実現される

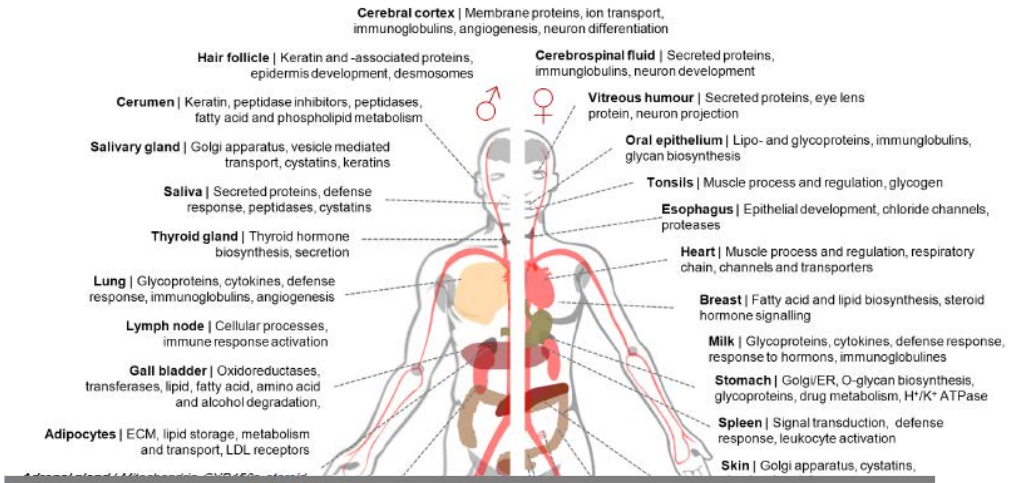
Human Proteome Project (HPP) : large scale MS data

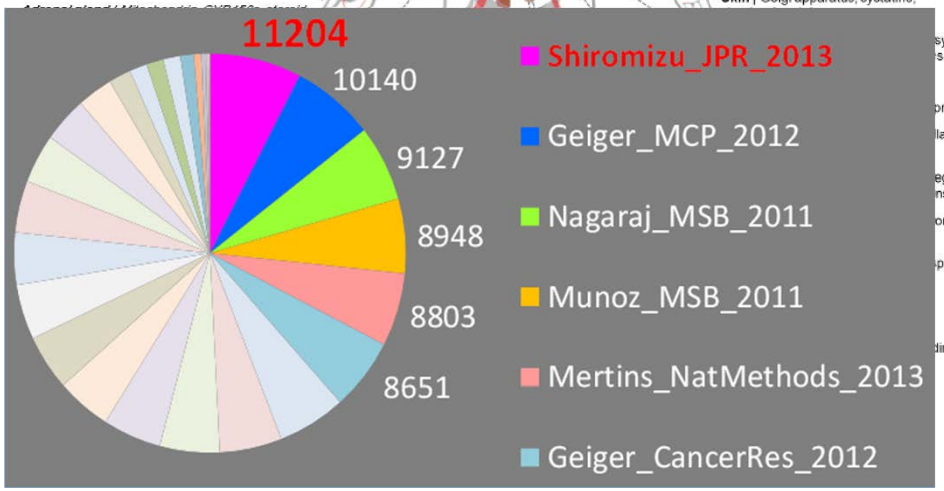
582 | NATURE | VOL 509 | 29 MAY 2014

ARTICLE

doi:10.1038/nature13319

Mass-spectrometry-based draft of the human proteome





HPP
(2010, HUPO)

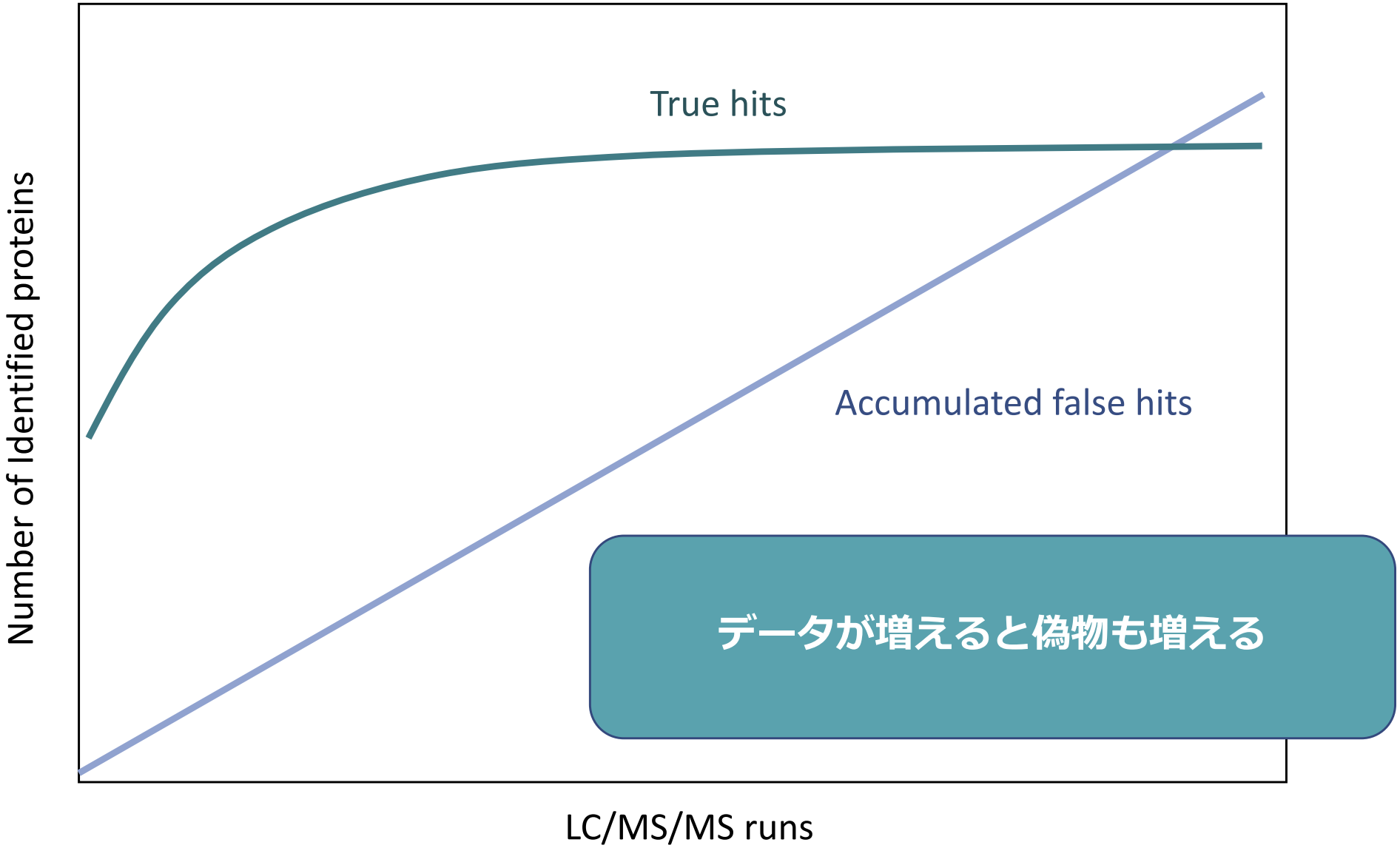
LC/MS/MS analysis: >17,000 times

Proteome data collection

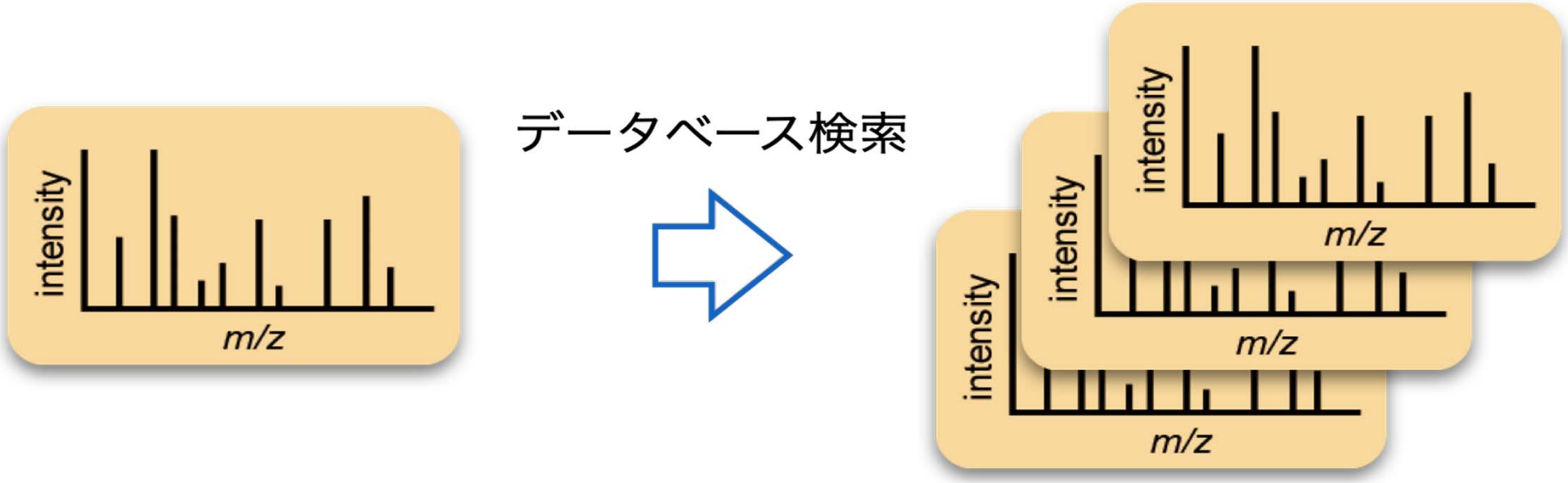
Human proteome map draft
(2014, Nature)

- **18,097 human protein identification**
- **19,376 identification of human protein isoforms**

偽ヒットのコントロール



再解析：網羅性の向上

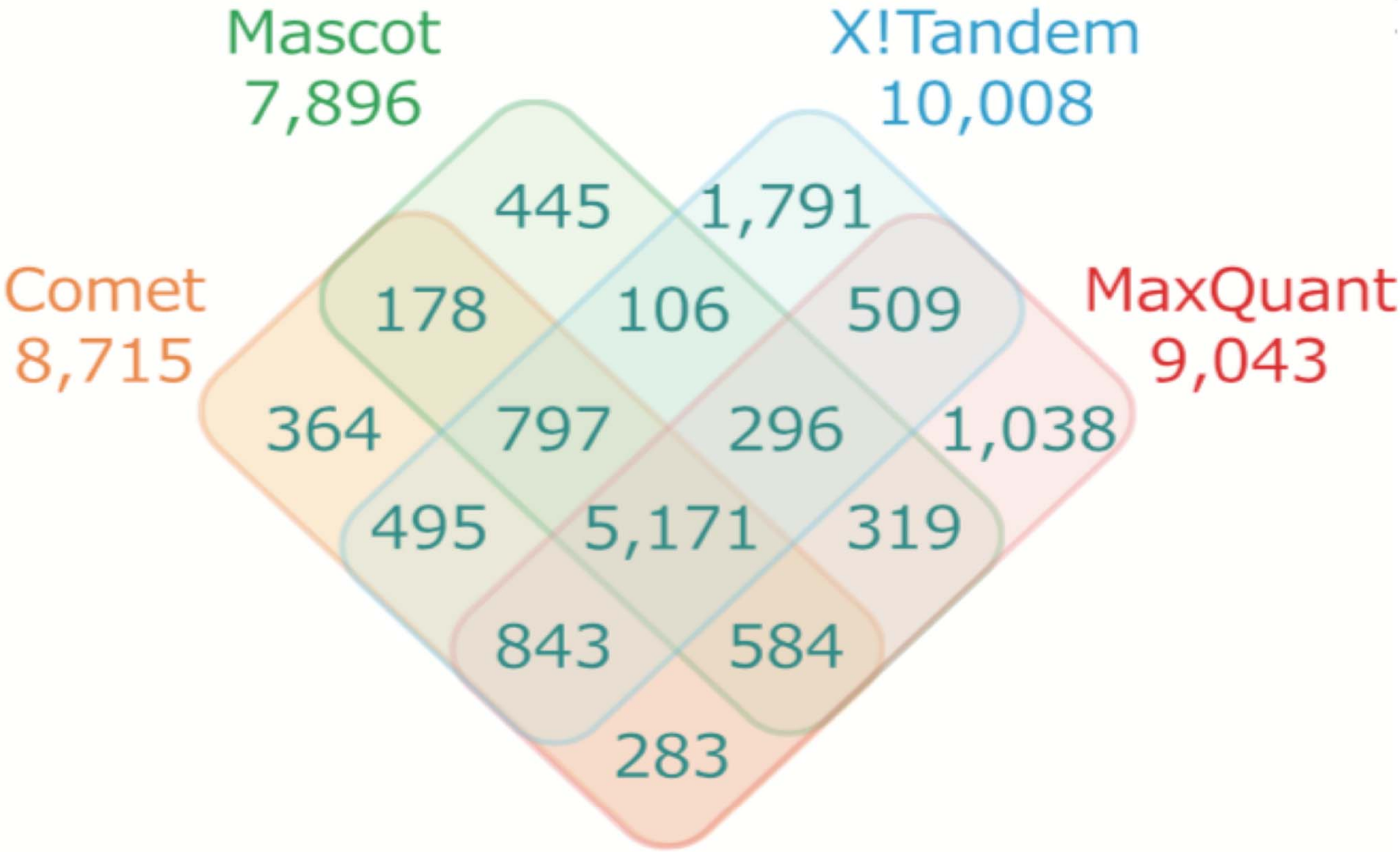


MSから出たピークリスト　　DBから作った理論ピークリスト

研究機関やプロジェクトによって、解析手法やデータフォーマット、
使用ソフトウェア・ツール、信頼基準が様々
各研究の解析結果を集めただけでは、データ間の比較が困難
偽陽性が多く混入

- Mascot, X!Tandem, MaxQuant, Comet, …

再解析：網羅性の向上



複数のソフトを使うことで網羅性を上げる

再解析：網羅性の向上

- 新規のスコアリングシステムのもとで、FDRを計算することで、信頼性を担保

プロテオミクスではデータベース検索を行う際に、実際のタンパク質配列、Targetデータベースに検索をかけるのと同時に、偽物の配列、一般的にタンパク質配列のアミノ酸を逆順にした、Decoyデータベースに検索をかけることで、実際のTarget検索での偽陽性の混入率、FDRを評価している。

b+	#	Seq	#	y+
129.1022	1	K	13	
228.1707	2	V	12	1405.7573
357.2132	3	E	11	1306.6889
444.2453	4	S	10	1177.6463
557.3293	5	L	9	1090.6143
685.3879	6	Q	8	977.5302
814.4305	7	E	7	849.4716
943.4731	8	E	6	720.4291
1056.5572	9	I	5	591.3865
1127.5943	10	A	4	478.3024
1274.6627	11	F	3	407.2653
1387.7468	12	L	2	260.1969
	13	K	1	147.1128

b-ion, y-ion が連続して検出できていれば高スコア

jPOST 新規のスコアリングシステムで、FDRを計算して信頼性を担保できるようになった。

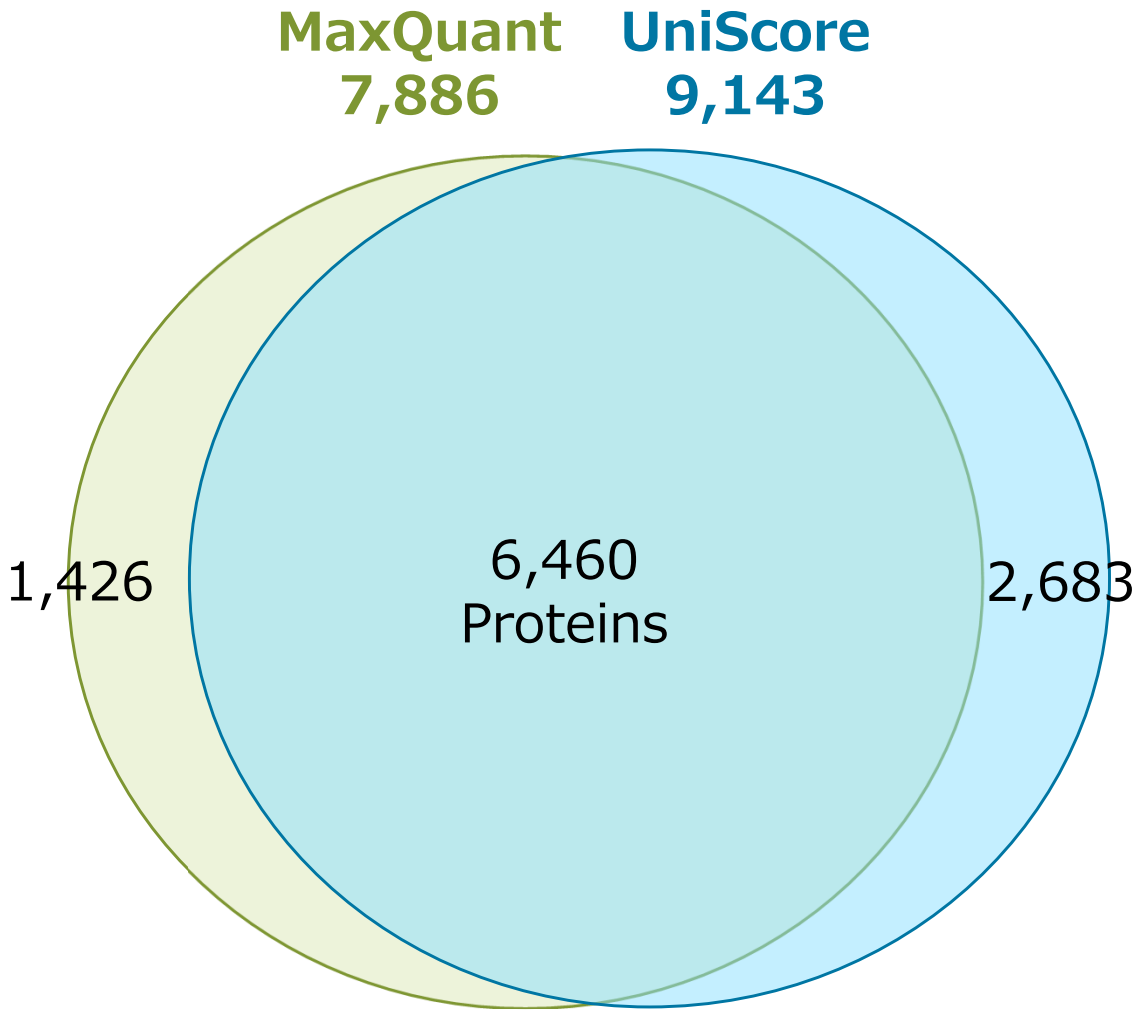
Universal index for annotated MSMS spectra

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)

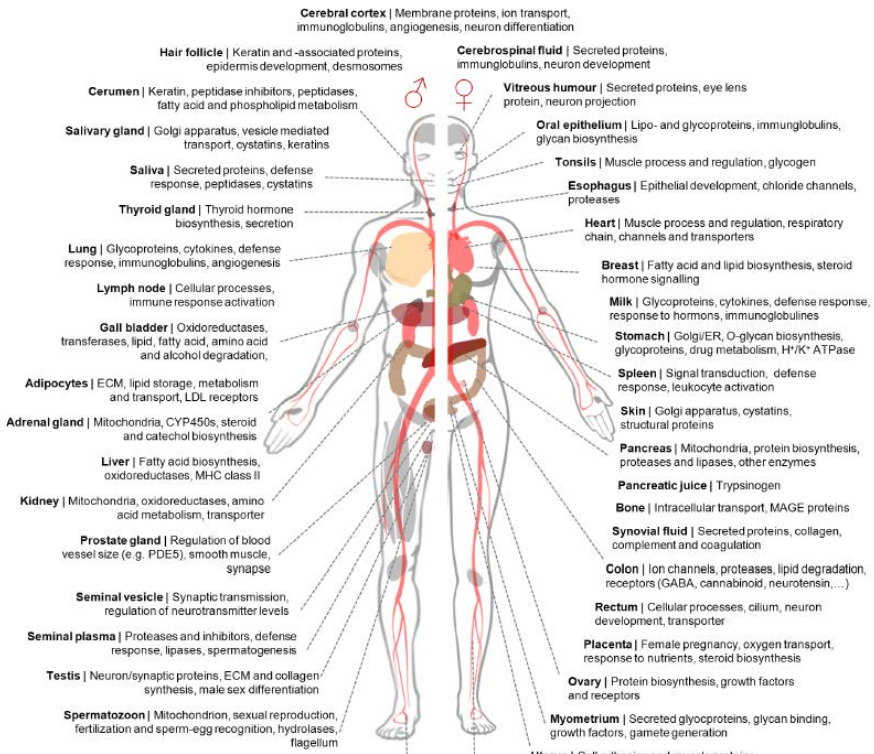
Re-analysis : Human Proteome 1st Draft

582 | NATURE | VOL 509 | 29 MAY 2014

ARTICLE

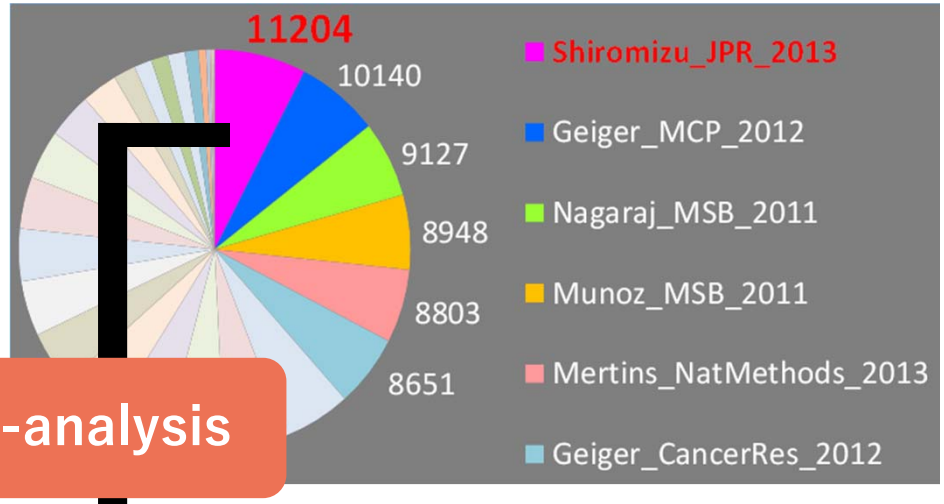
doi:10.1038/nature13319

Mass-spectrometry-based draft of the human proteome

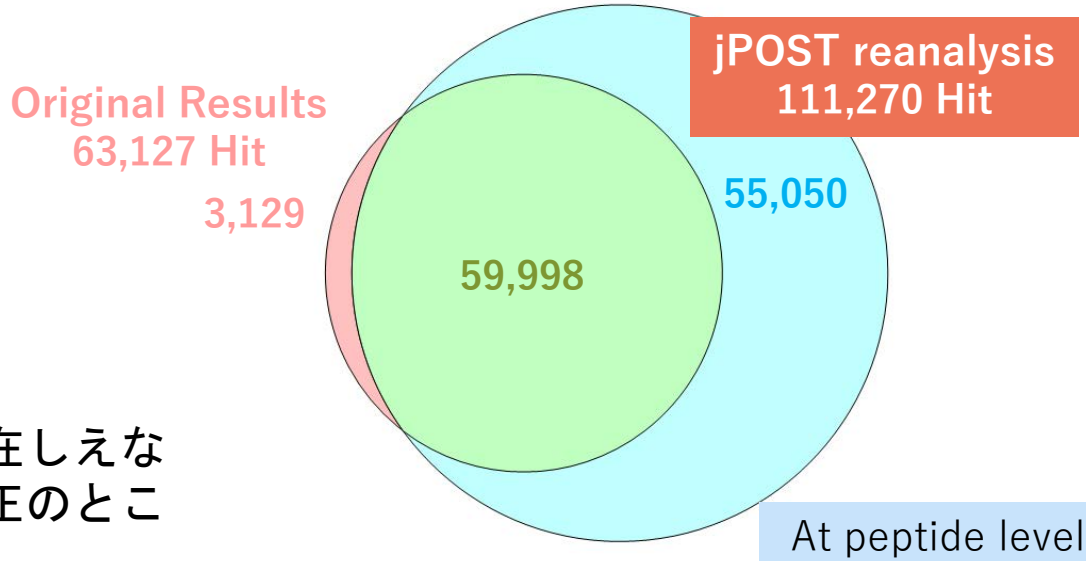


同定データには実際にその組織や細胞には存在しえないようなタンパク質が同定されており、信憑正のところで、大きな問題点があった。

10447 raw files from ProteomeXchange



Re-analysis



At peptide level (HCD)

UniScore for re-analysis of jPOSTrepo datasets

jPOST Repository / Database

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

75% 閲覧のみ

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
1									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%					
2								メタデータ作成																
3	Project ID	MS	生物種	ダウンロード生物種 Taxonomy ID	配列DBのDL日付	データ特徴	データサイズ (GB) (目安)	jPOSTメタデータ（自動）変換	interview, マニュアル作業, Sample	Fractionation, 自動後処理	メタデータチェック	配列データベース作成	プレサーチ	サーチトレランス決定	本サーチ（ピークピッキング、DBサーチ）→PSM	PSM→ペプチド同定	提出	提出ディレクトリ（SearchResult/MainSearchResult, MGF_Result/Ver）	Revision ID	RPXD	ファイル準備、JR→mzTab	submission作業（submitボタン直前まで）	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			CIDデータとHCDデータが
5	JPST000075.1	Q Exactive[MS:1001911]	Homo sapier	9606	20200318		19	2020/10/01	2020/10/01-			3/18	3/18	3/19										
6	JPST000091.1	Q Exactive[MS:1001911]	Mus musculu	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 musculu	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 musculu	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 subt	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 pn	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 sapier	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			200401提出分（in 20200331
13	JPST000121.0	Q Exactive[MS:1001911]	Homo sapier	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			SILAC 20200331提出分は
14	JPST000123.0	Q Exactive[MS:1001911]	Homo sapier	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			SILAC 20200331提出分は
15	JPST000126.0	Q Exactive[MS:1001911]	Homo sapier	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 sapier	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 sapier	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			入力metadataのFixed modifi
18	JPST000201.0	LTQ Orbitrap Velos[MS:100174	Homo sapier	9606	20200318		18	---	DK	DK	5/5	---	---	---	---	---	3/23	20200323	JPST000801.0	RPXD018475	---	2020/05/06	2020/05/27	
19	JPST000203.0	LTQ Orbitrap Velos[MS:100174	Homo sapier	9606	20200318		15	---	DK	DK	5/5	---	---	---	---	---	3/23	20200323	JPST000802.0	RPXD018476	---	2020/05/06	2020/05/27	
20	JPST000204.0	LTQ Orbitrap Velos[MS:100174	Homo sapier	9606	20200318		13	---	DK	DK	5/5	---	---	---	---	---	3/23	20200323	JPST000803.0	RPXD018477	---	2020/05/06	2020/05/27	
21	JPST000205.0	LTQ Orbitrap Velos[MS:100174	Homo sapier	9606	20200318		17	---	DK	DK	5/5	---	---	---	---	---	3/23	20200323	JPST000804.0	RPXD018478	---	2020/05/06	2020/05/27	
22	JPST000206.0	LTQ Orbitrap Velos[MS:100174	Homo sapier	9606	20200318		17	---	DK	DK	5/5	---	---	---	---	---	3/23	20200323	JPST000805.0	RPXD018479	---	2020/05/06	2020/05/27	
23	JPST000207.0	LTQ Orbitrap Velos[MS:100174	Homo sapier	9606	20200318		72	---	DK	DK	5/5	---	---	---	---	---	3/30	20200323	JPST000806.0	RPXD018480	---	2020/05/06	2020/05/27	
24	JPST000208.0	LTQ Orbitrap Velos[MS:100174	Homo sapier	9606	20200318		10	---	DK	DK	5/5	---	---	---	---	---	3/25	20200323	JPST000807.0	RPXD018481	---	2020/05/06	2020/05/27	
25	JPST000210.0	LTQ Orbitrap Velos[MS:100174	Homo sapier	9606	20200318		54	---	DK	DK	5/5	---	---	---	---	---	3/25	20200323	JPST000808.0	RPXD018482	---	2020/05/06	2020/05/27	
26	JPST000267.1	Q Exactive[MS:1001911];Triple	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				3/18	3/23	3/27										
29	JPST000379.1	Q Exactive[MS:1001911]	Homo sapier	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]	Meyerozyma guilliermondii[4929]				8	2020/10/01																
31	JPST000417.0	Q Exactive[MS:1001911]	Meyerozyma guilliermondii[4929]				8	2020/10/01																
32	JPST000067.0	QSTAR[MS:1000190]	Rattus rattus	10116	20200406	Sciex	4	---	DK	DK	5/5	4/6	4/8	4/10	4/10-4/13	4/15	4/17	20200416	JPST000809.0	RPXD018483				ファイル名にスペースが入っ
33	JPST000081.0	TripleTOF 5600[MS:1000932]	Homo sapier	9606	20200318	Sciex	10	---	DK	DK	5/5	---	---	---	---	---	3/24	20200323	JPST000810.0	RPXD018484	---	2020/05/06	2020/06/04	iPS
34	JPST000082.0	TripleTOF 5600[MS:1000932]	Homo sapier	9606	20200318	Sciex	10	---	DK	DK	5/5	---	---	---	---	---	3/24	20200323	JPST000811.0	RPXD018485	---	2020/05/06	2020/06/04	iPS
35	JPST000083.0	TripleTOF 5600[MS:1000932]	Homo sapier	9606	20200318	Sciex	10	---	DK	DK	5/5	---	---	---	---	---	3/24	20200323	JPST000812.0	RPXD018486	---	2020/05/06	2020/06/04	iPS
36	JPST000085.0	TripleTOF 5600[MS:1000932]	Homo sapier	9606	20200318	Sciex	9	---	DK	DK	5/5	---	---	---	---	---	3/24	20200323	JPST000813.0	RPXD018487	---	2020/05/06	2020/06/04	iPS
37	JPST000086.0	TripleTOF 5600[MS:1000932]	Homo sapier	9606	20200318	Sciex	9	---	DK	DK	5/5	---	---	---	---	---	3/24	20200323	JPST000814.0	RPXD018488	---	2020/05/06	2020/06/04	iPS
38	JPST000087.0	TripleTOF 5600[MS:1000932]	Homo sapier	9606	20200318	Sciex	10	---	DK	DK	5/5	---	---	---	---	---	3/24	20200323	JPST000815.0	RPXD018489	---	2020/05/06	2020/06/04	iPS
39	JPST000088.0	TripleTOF 5600[MS:1000932]	Homo sapier	9606	20200318	Sciex	9	---	DK	DK	5/5	---	---	---	---	---	3/24	20200323	JPST000816.0	RPXD018490	---	2020/05/06	2020/06/04	iPS
40	JPST000089.0	TripleTOF 5600[MS:1000932]	Homo sapier	9606	20200318	Sciex	10	---	DK	DK	5/5	---	---	---	---	---	3/24	20200323	JPST000817.0	RPXD018491	---	2020/05/06	2020/06/04	iPS
41	JPST000099.0	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/	10/2	20201002	JPST000818.0	RPXD018492	2020/10/01			
42	JPST000100.0	TripleTOF 5600[MS:1000932]	Bacillus subt	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 pn	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	QSTAR[MS:1000190]	Mus musculu	10090	20200318	TRAQ4plex	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			ファイルが一部読み取り不可
45	JPST000149.0	TripleTOF 5600[MS:1000932]	Homo sapier	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 sapier	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			200417提出分（in 20200416
47	JPST000151.0	TripleTOF 5600[MS:1000932]	Homo sapier	9606	20200318	Sciex	16	---	DK	DK	5/5	3/18	4/7	4/9	4/10-4/12	5/6	5/6	20200506	JPST000824.0	RPXD018498	2020/10/01			200417提出分（in 20200416
48	JPST000349.0	TripleTOF 5600[MS:1000932]	Mus musculu	10090	20200318	Sciex, DDA	107	---	DK	DK	5/5	3/18	4/10	4/10	4/17-4/18	4/20	4/20	20200420	JPST000825.0	RPXD018499	2020/10/01			一部のファイルはProteinPilo
49	JPST000055.1	Q Exactive[MS:1001911]	Mus musculus (Mouse)[10090]			SILAC	4	2020/10/01																
50	JPST000109.1	Q Exactive[MS:1001911]	Homo sapier	9606		TMT	29	2020/10/01	2020/10/01-															
51	JPST000159.1	Q Exactive[MS:1001911]	Rattus rattus	10116	20200406	TMT6plex	8		DK	DK	5/5	4/6	4/7	4/8	4/9-4/10	4/16	4/17	20200416	JPST000826.0	RPXD018500	2020/09/29			

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/

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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

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 pass
PXD017710	Proteome and Translatome of SARS-CoV-2 infected cells

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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 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

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

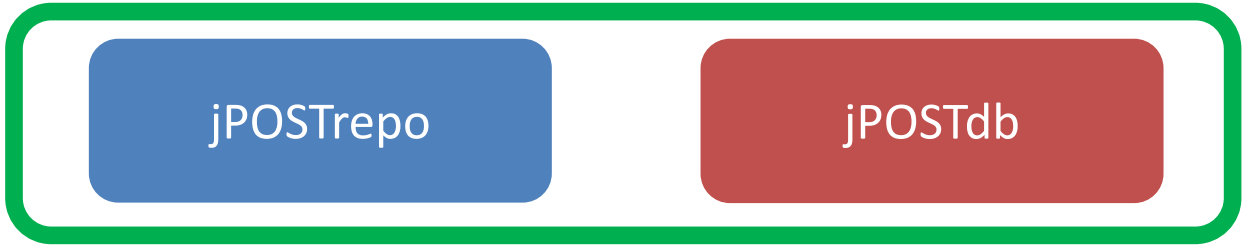
2．再解析により、データの統一化が実現される

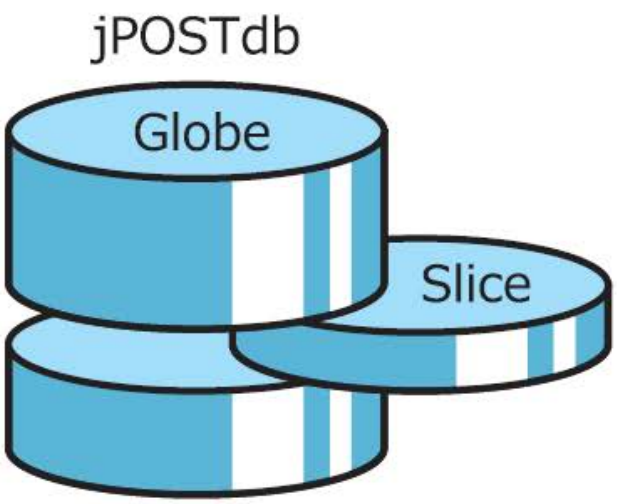
3．カスタムDBの作成ツールと可視化ツールの提供

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





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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.

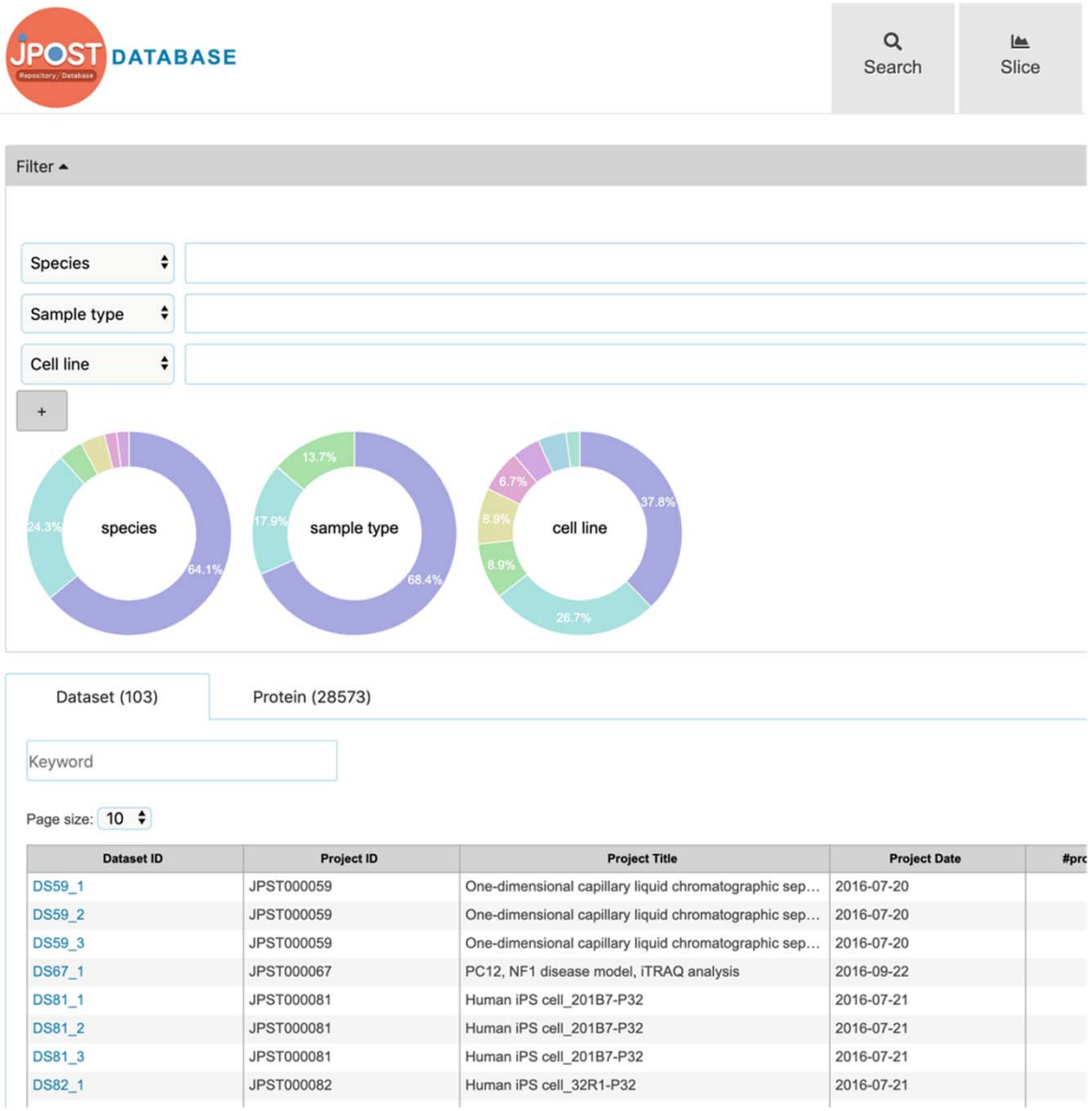
COVID-19 Help

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 Database

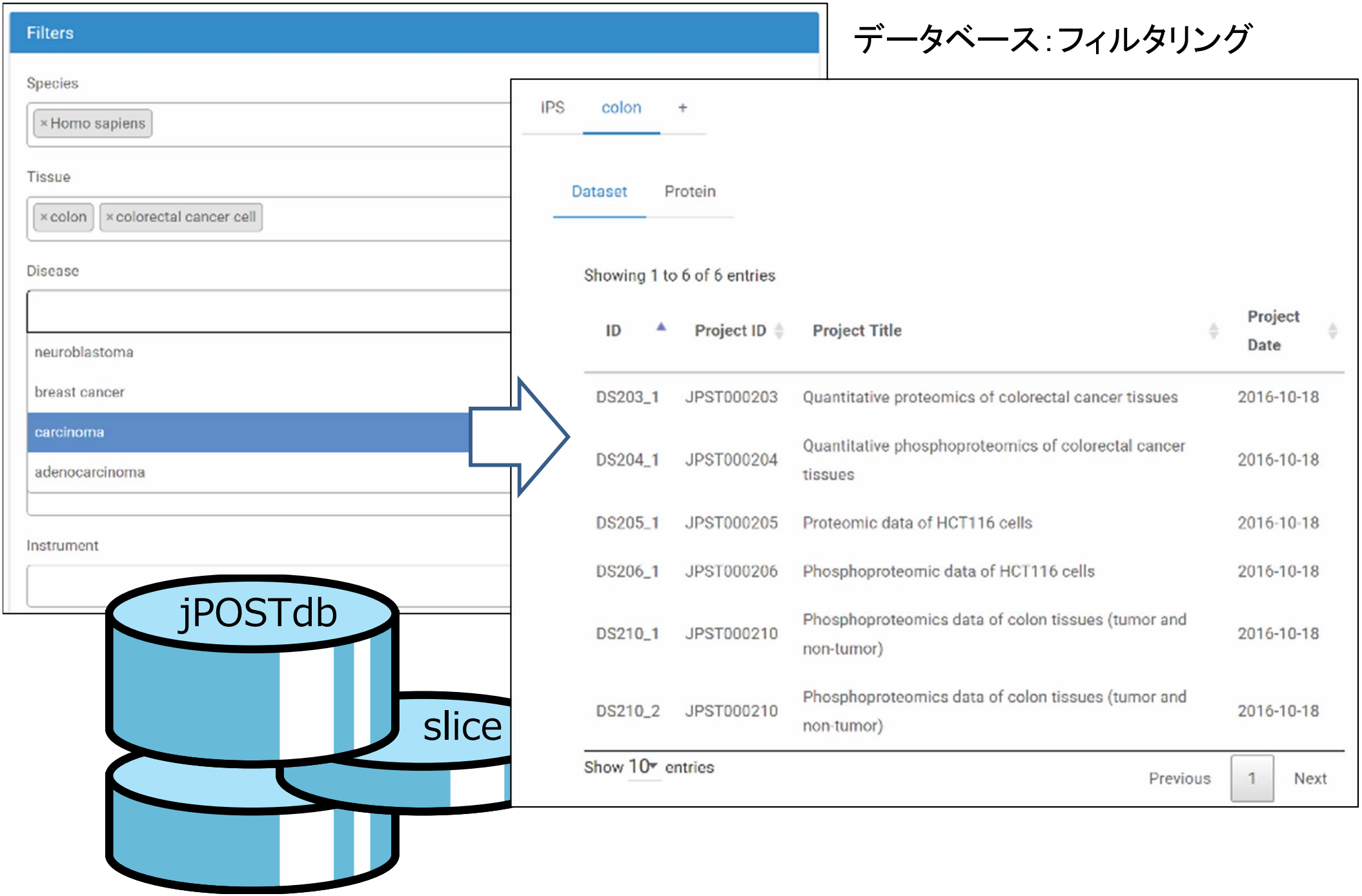


Dataset ID	Project ID	Project Title	Project Date	#prc
DS59_1	JPST000059	One-dimensional capillary liquid chromatographic sep…	2016-07-20	
DS59_2	JPST000059	One-dimensional capillary liquid chromatographic sep…	2016-07-20	
DS59_3	JPST000059	One-dimensional capillary liquid chromatographic sep…	2016-07-20	
DS67_1	JPST000067	PC12, NF1 disease model, iTRAQ analysis	2016-09-22	
DS81_1	JPST000081	Human iPS cell_201B7-P32	2016-07-21	
DS81_2	JPST000081	Human iPS cell_201B7-P32	2016-07-21	
DS81_3	JPST000081	Human iPS cell_201B7-P32	2016-07-21	
DS82_1	JPST000082	Human iPS cell_32R1-P32	2016-07-21	

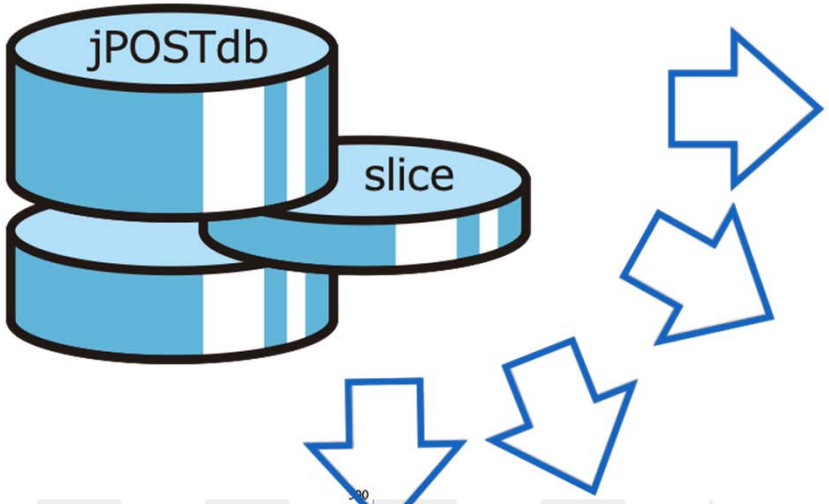
- 特徴
  - ヒト以外の生物にも対応
  - 詳細な翻訳後修飾情報
  - ユーザによるデータセットの切り出し
  - 簡易的なデータ比較
  - セマンティック・ウェブ技術の利用

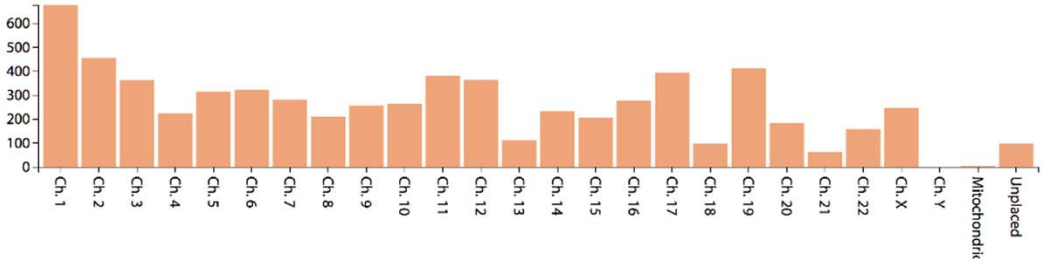
jPOST Database

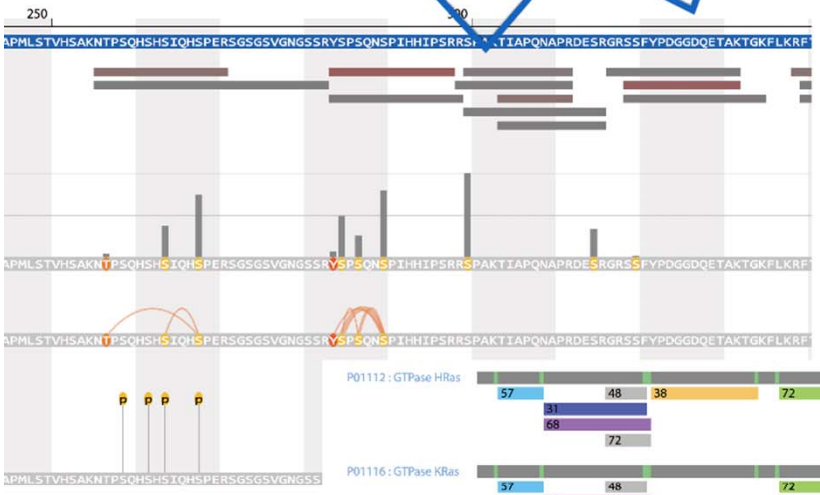
データベース：フィルタリング

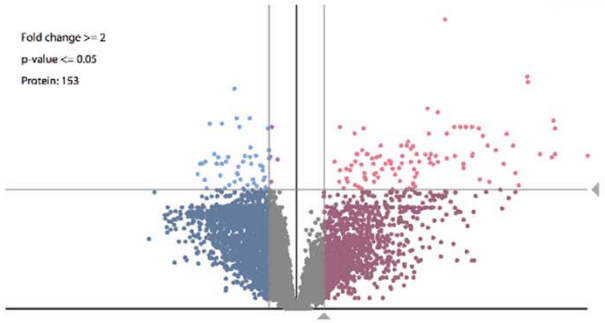


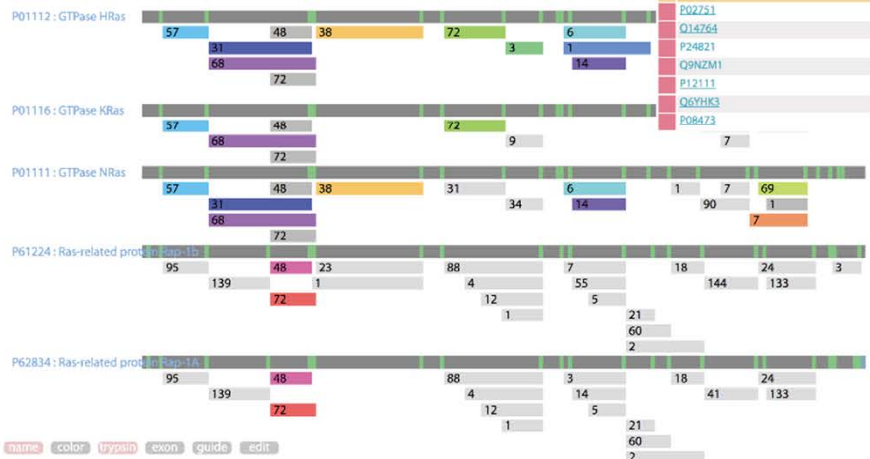
jPOST DB 様々な可視化



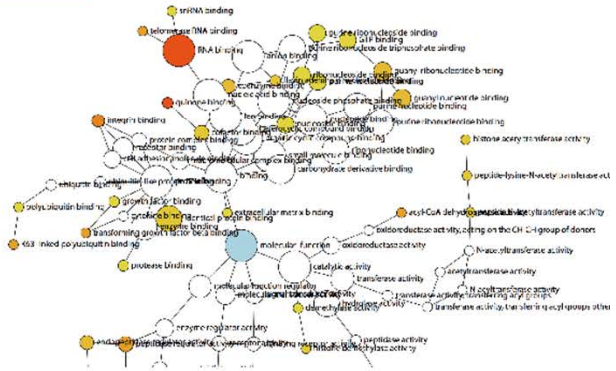






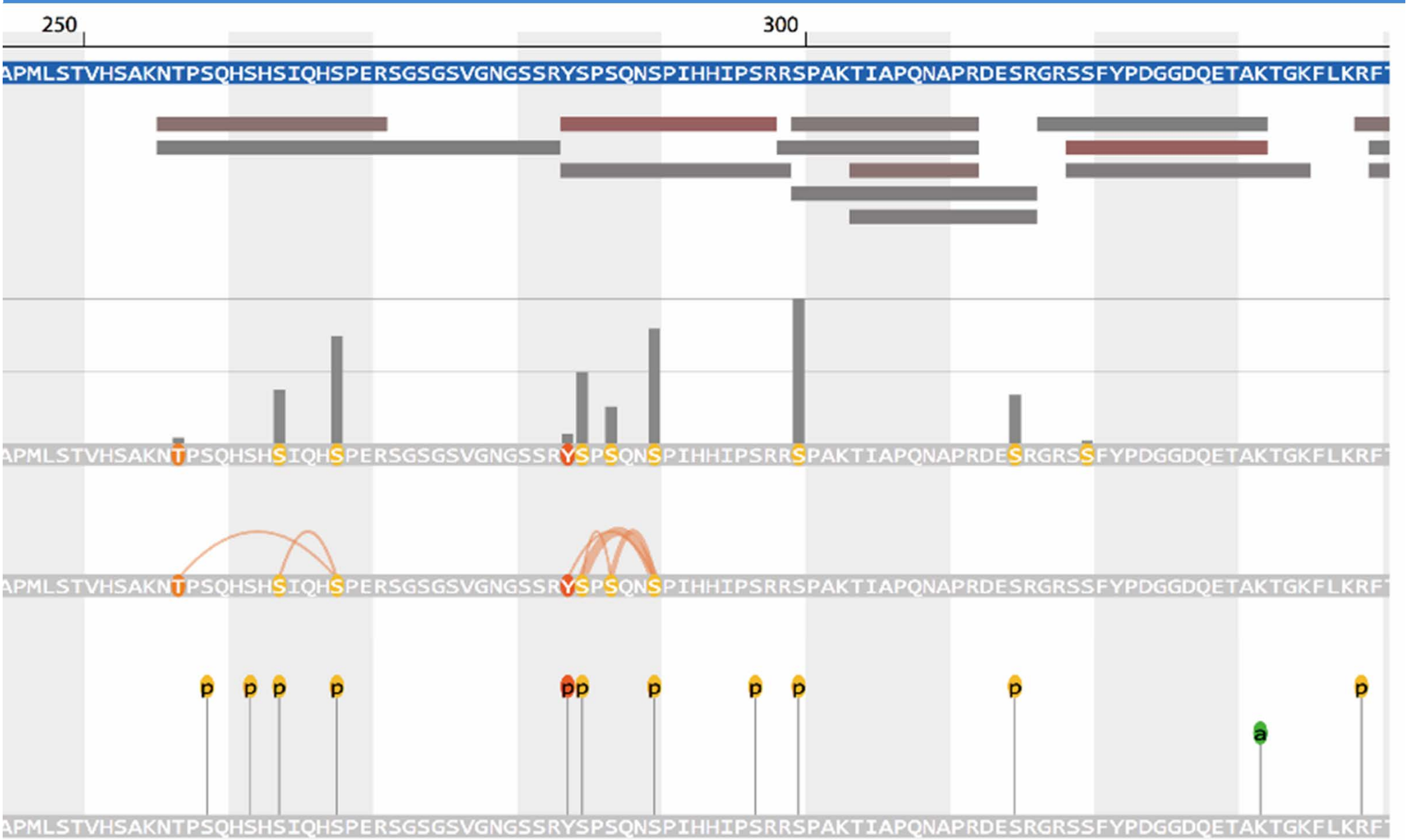


UniProt ID	log2FC	p-value
P02751	10.6	2.14e-0
Q14764	9.41	1.08e-0
P24821	9.41	2.06e-0
Q9NZM1	9.35	8.88e-0
P12111	9.29	2.23e-0
Q6YHK3	8.86	2.06e-0
P08473	8.42	3.37e-0

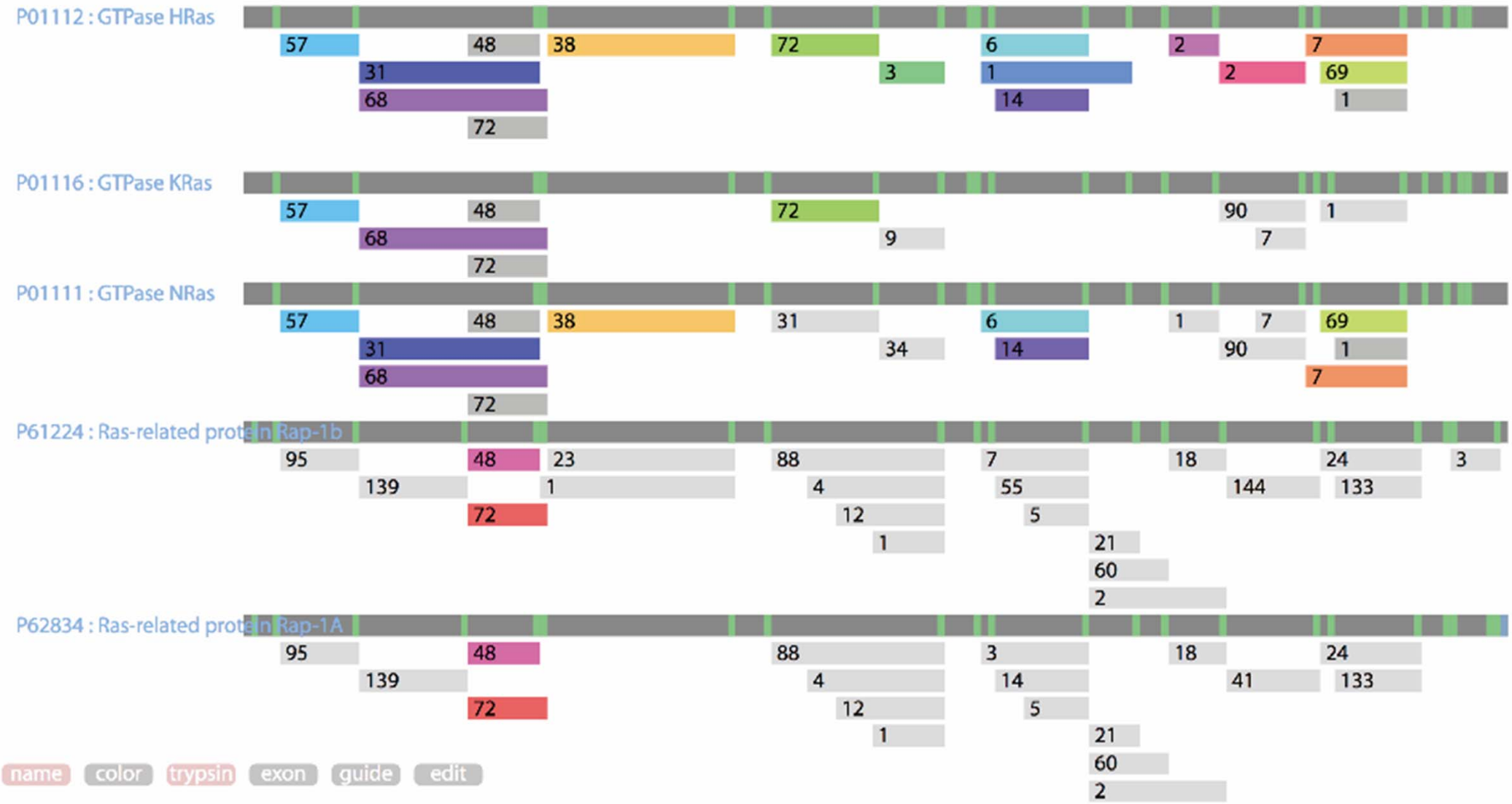


term	count	p-value
RNA binding	28	6.80e-91
quinone binding	3	3.48e-04
dipeptidyl peptidase activity	2	3.48e-04
integrin binding	4	4.75e-03
acyl-CoA dehydrogenase activity	2	5.31e-03

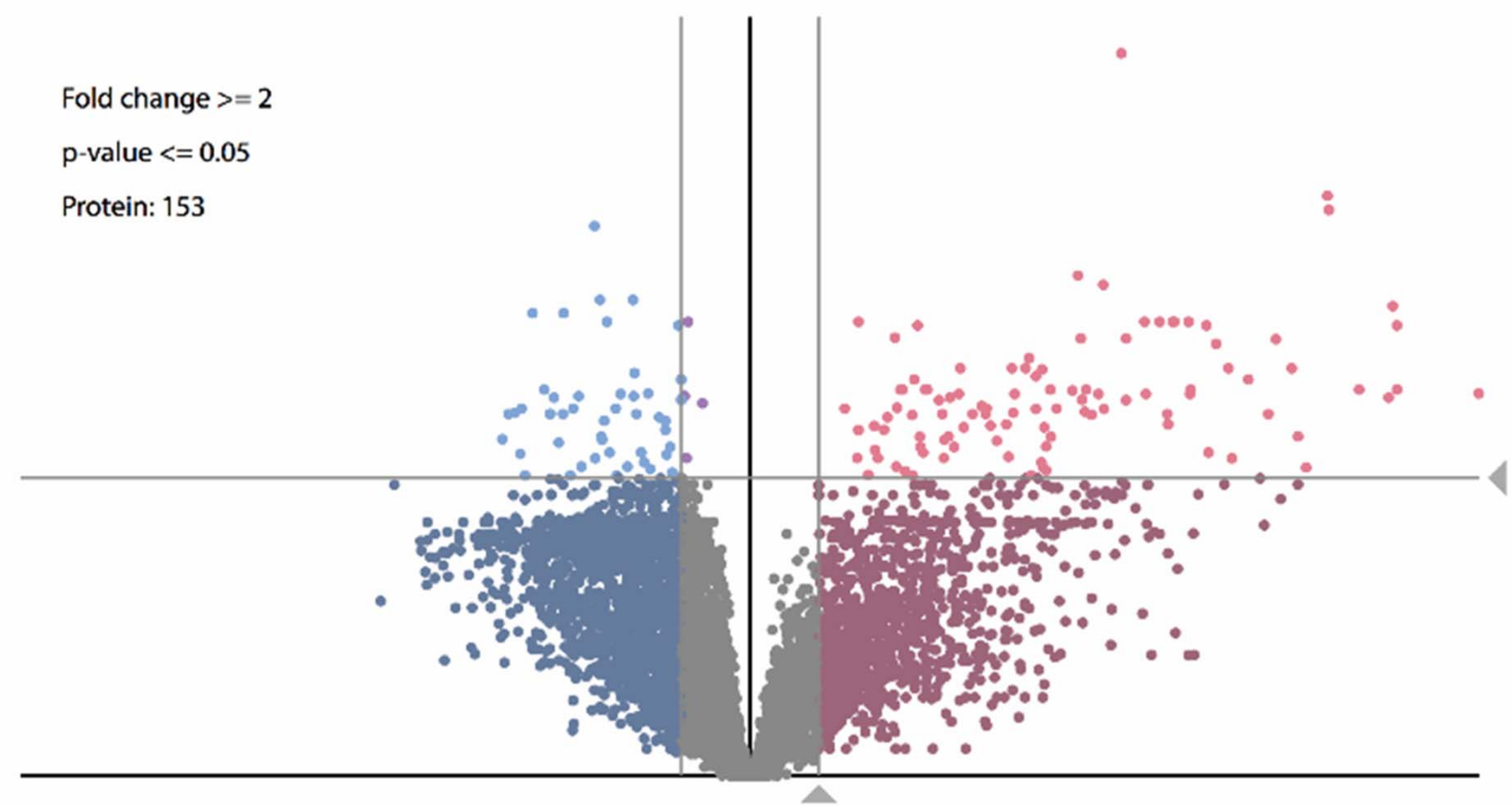
jPOST DB Protein Browser



jPOST DB Petide Sharing

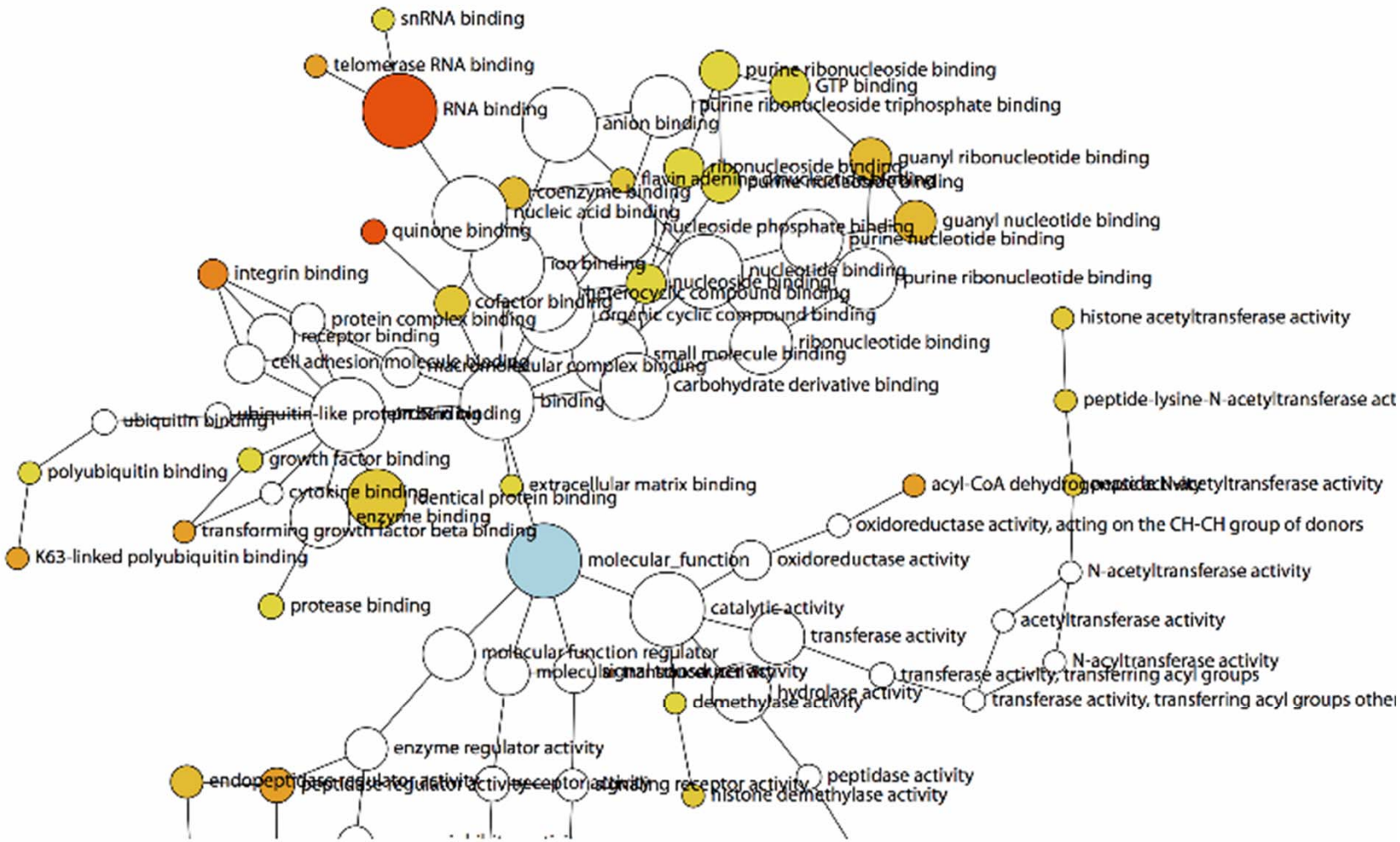


jPOST DB 発現変動解析

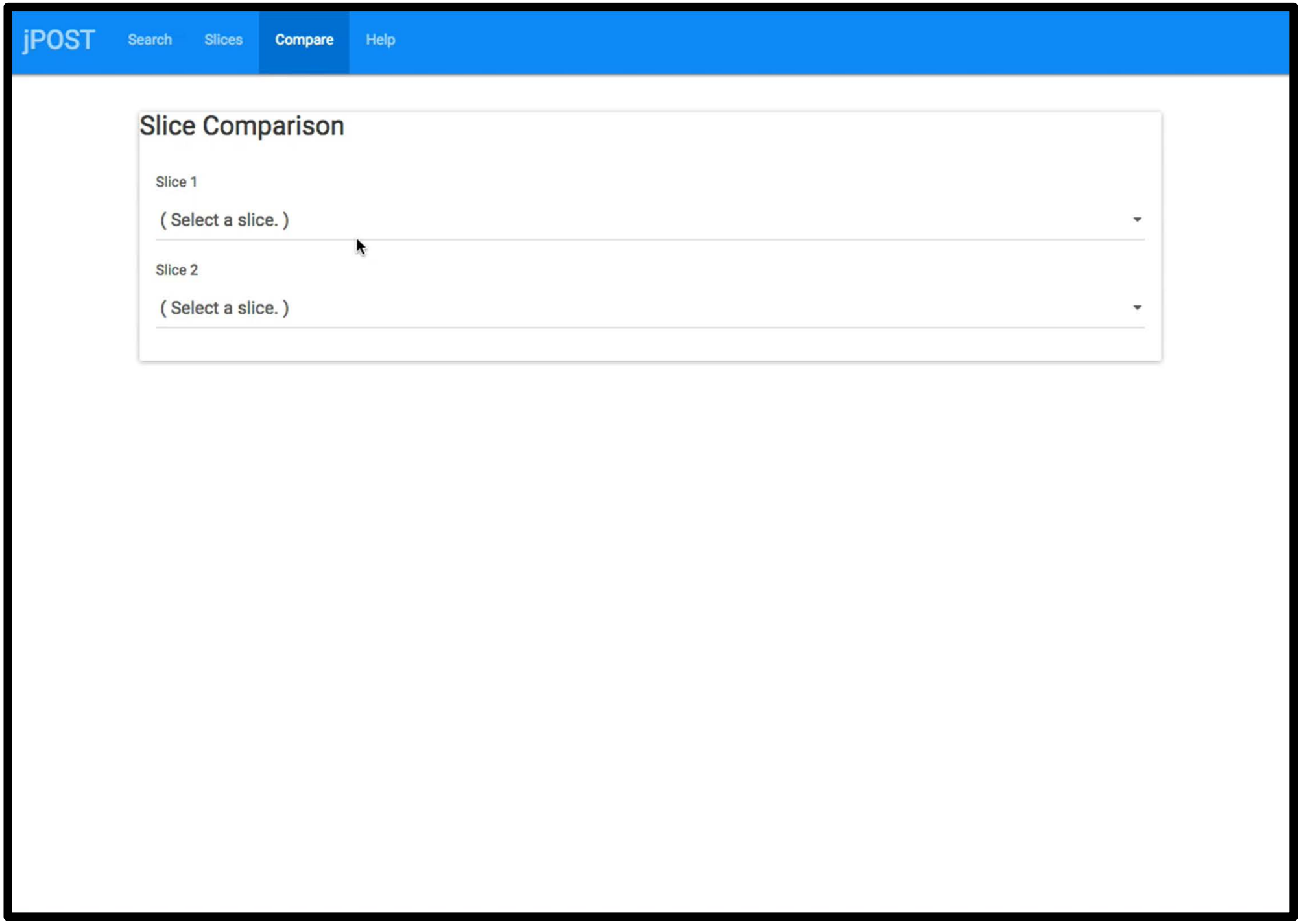


	UniProt ID	log2FC	p-value
	P02751	10.6	2.14e-02
	Q14764	9.41	1.08e-02
	P24821	9.41	2.06e-02
	Q9NZM1	9.35	8.88e-03
	P12111	9.29	2.23e-02
	Q6YHK3	8.86	2.06e-02
	P08473	8.42	3.37e-03

jPOST DB エンリッチメント解析



	term	count	p-value
	RNA binding	28	6.80e-04
	quinone binding	3	7.49e-04
	dipeptidyl-peptidase activity	2	3.48e-03
	integrin binding	4	4.75e-03
	acyl-CoA dehydrogenase activity	2	9.31e-03
	transforming growth factor beta binding	2	9.31e-03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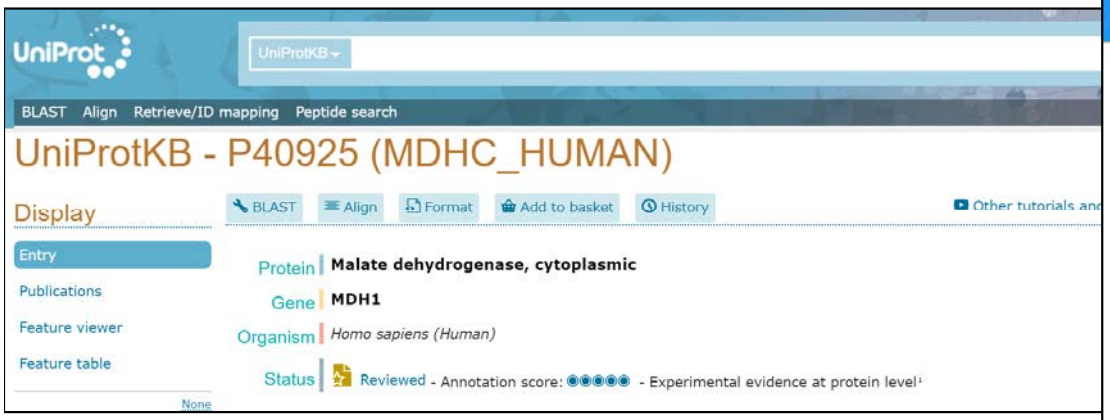
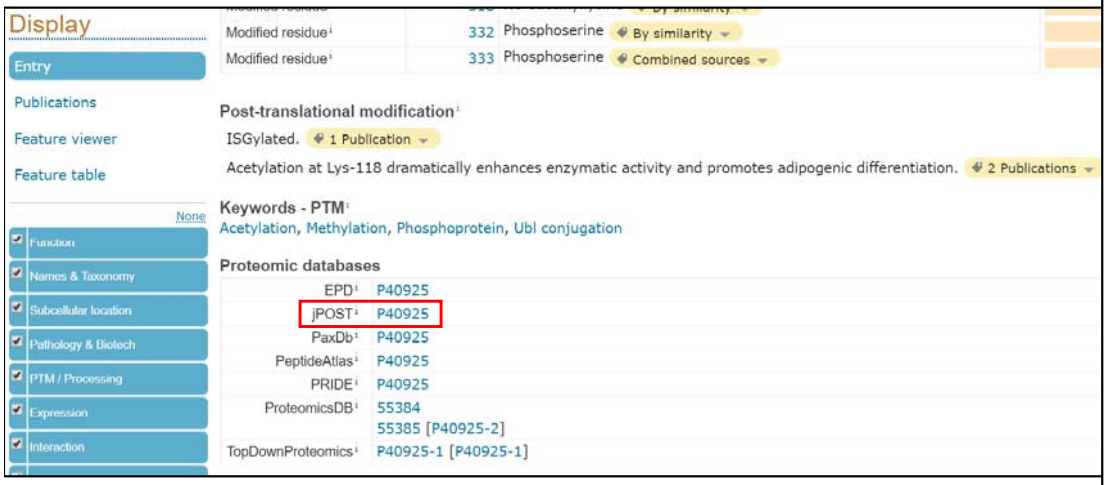
Search
Slices
Compare
Help
Slice Comparison
Slice 1
(Select a slice.)
Slice 2
(Select a slice.)

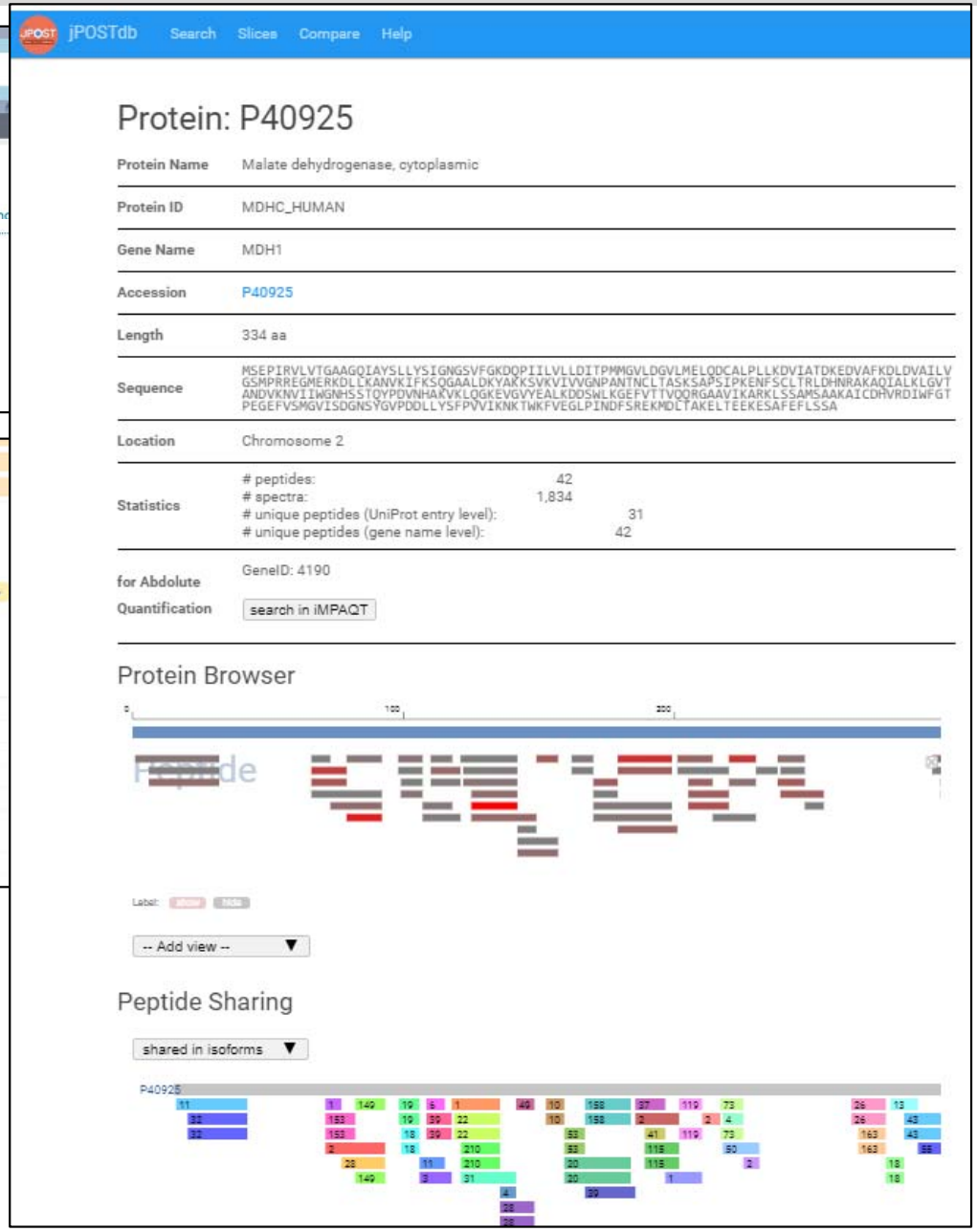
movie

UniProtとの連携：

Cross-references between UniProt and jPOST







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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

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

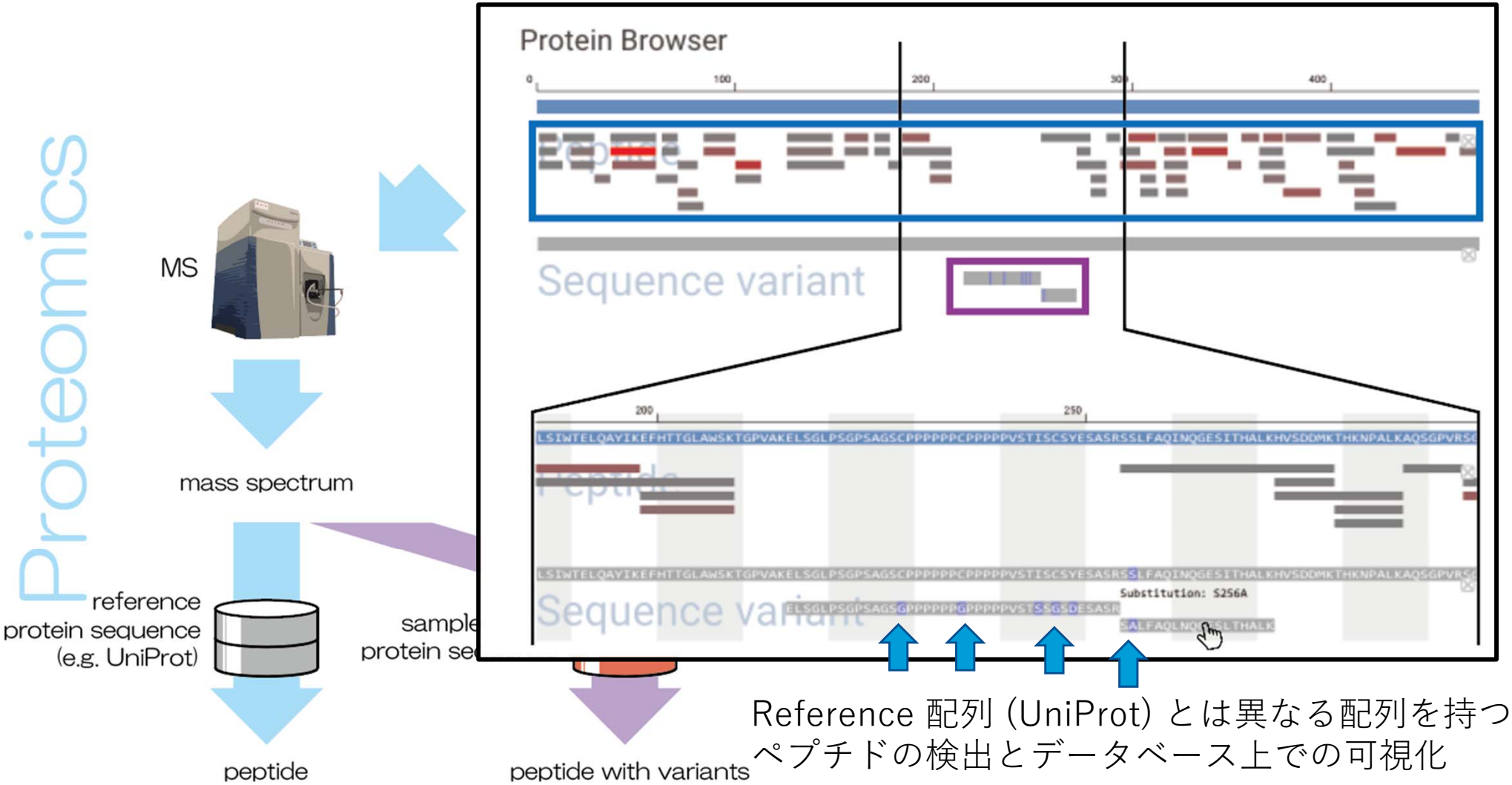
This is a special page on coronavirus (SARS-CoV-2) and the COVID-19 disease data, where mass-based proteomics data in ProteomeXchange resources are analyzed by the jPOST re-analysis workflow.

Help

A guide to using the jPOST resources.

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



Reference 配列 (UniProt) とは異なる配列を持つペプチドの検出とデータベース上での可視化

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

jPOST Repository/Database

Japan Proteome Standard Repository/Database

About Repository Database Workflow Gadgets COVID-19 Help FAQ Contact

Recent posts

other

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2021-06-30 jpost

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other

jPOST will publish the re-ana

2020-07-8 jpost

jPOST will publish the re-analyzed proteome

Current progress: 100%

COVID-19 datasets

Analysis target	
PXD019113	The Global Phosphorylation Land
PXD019645	Data, reagents, assays and merit
PXD019423	MS analysis of SARS-CoV2 protei
PXD018804	Extensive proteomic dataset of V
PXD018594	Shotgun proteomics of Vero E6 c
PXD018357	Inhibition of growth factor signali
PXD018117	A SARS-CoV-2-Human Protein-Pr
PXD018581	Proteomics of SARS-CoV and SAI
PXD018241	Characterisation of the transcript frame deletion in the spike glycop
PXD017710	Proteome and Translatome of SA

PXD018357 is an original

Dataset Summary

Title

Description

HostingRepository

AnnounceDate

AnnouncementXML

DigitalObjectIdentifier

ReviewLevel

DatasetOrigin

RepositorySupport

PrimarySubmitter

SpeciesList

ModificationList

Instrument

Dataset History

Revision	Datetime
0	2020-04-04
1	2020-05-15
2	2020-09-25

Publication List

Klann K, Bojkova D, Tasc
Cell, 80(1):164-174.e4(20

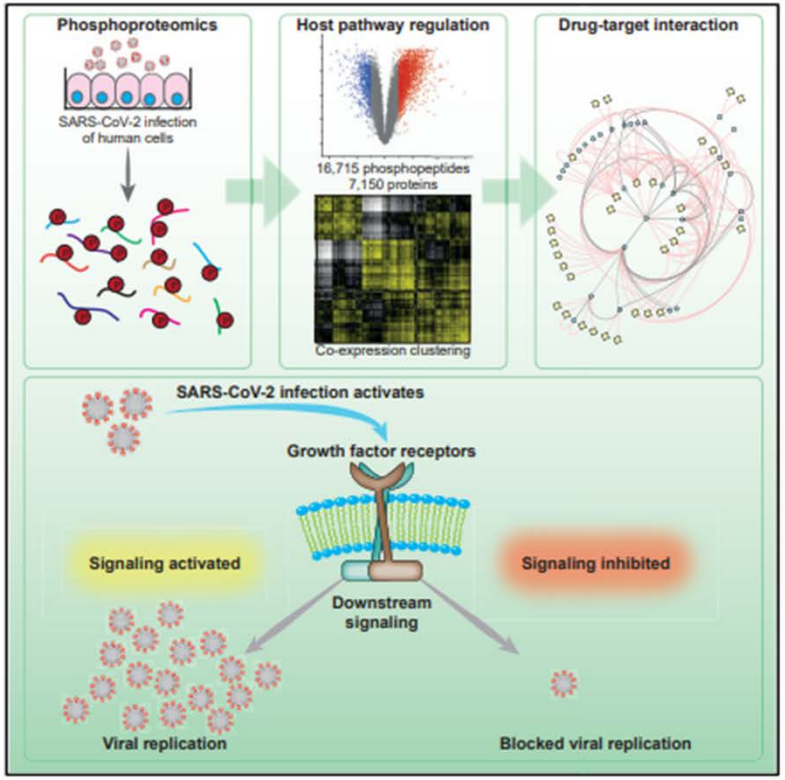
Keyword List

Resource

Molecular Cell

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

Graphical Abstract



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

Authors

Kevin Klann, Denisa Bojkova, Georg Tascher, Sandra Ciesek, Christian Münch, Jindrich Cinatl

Correspondence

ch.muench@em.uni-frankfurt.de (C.M.), cinatl@em.uni-frankfurt.de (J.C.)

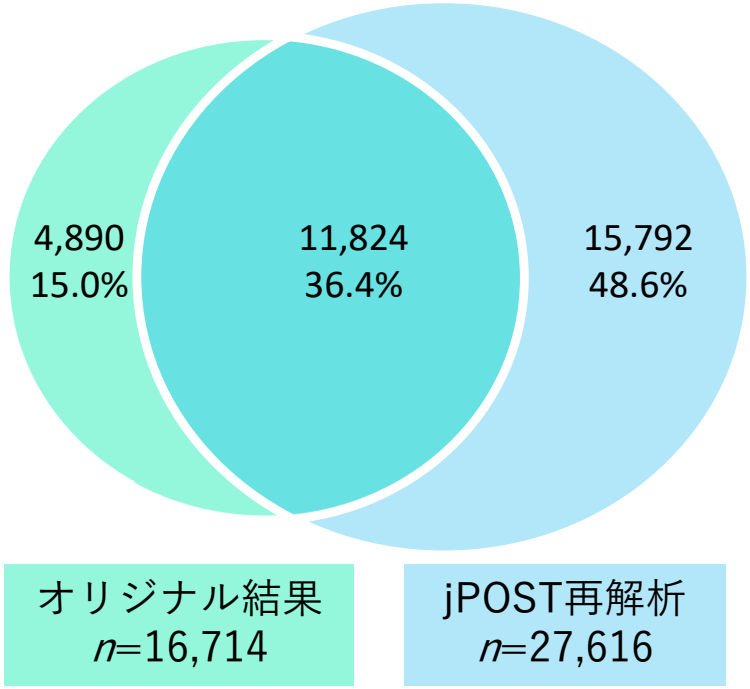
In Brief

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.

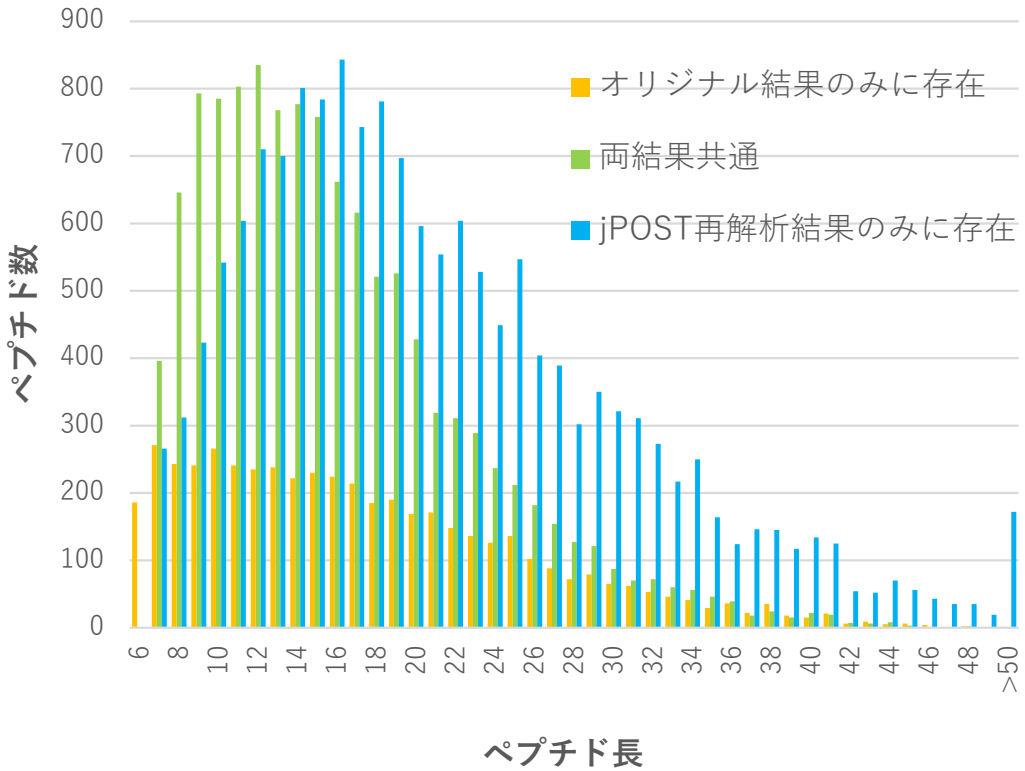
Re-analysis of COVID-19 paper

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

同定リン酸化ペプチド数の比較



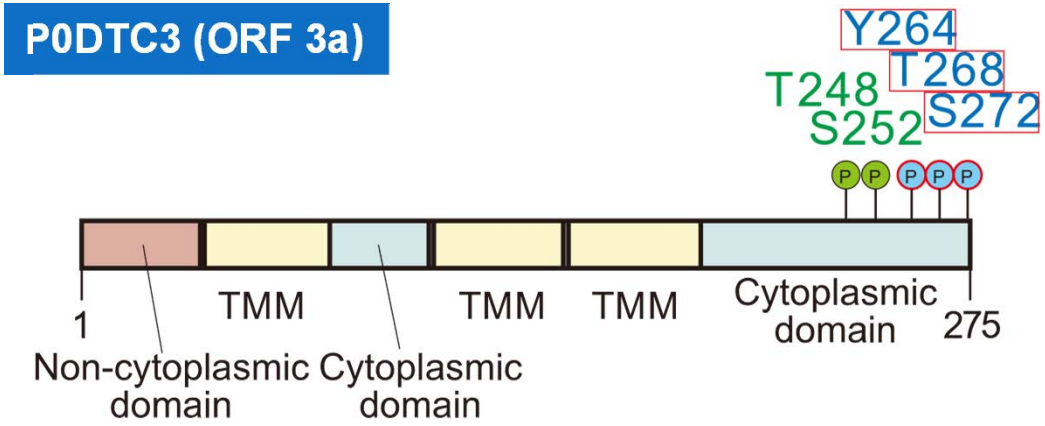
両解析結果のペプチド長ごとの比較

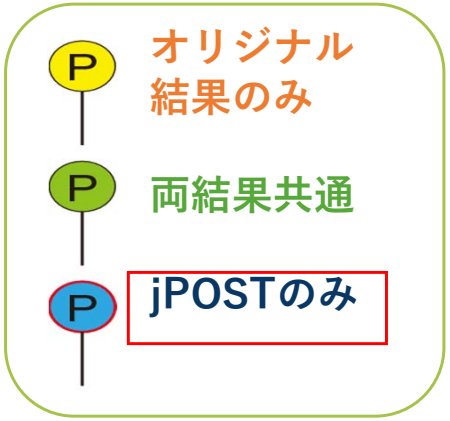


Phosphorylated sites on SARS-CoV-2 proteins

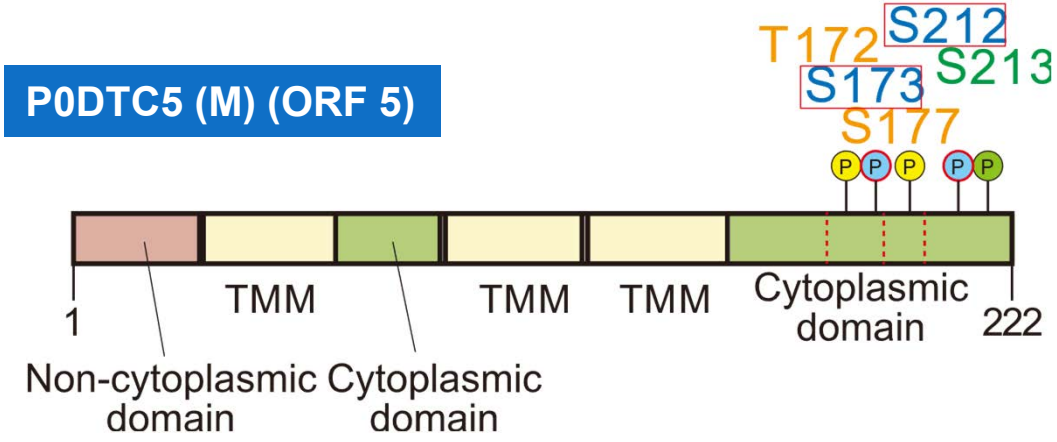
同定されたリン酸化サイトの比較

P0DTC3 (ORF 3a)





P0DTC5 (M) (ORF 5)



T172 vs S173

EITVATSR

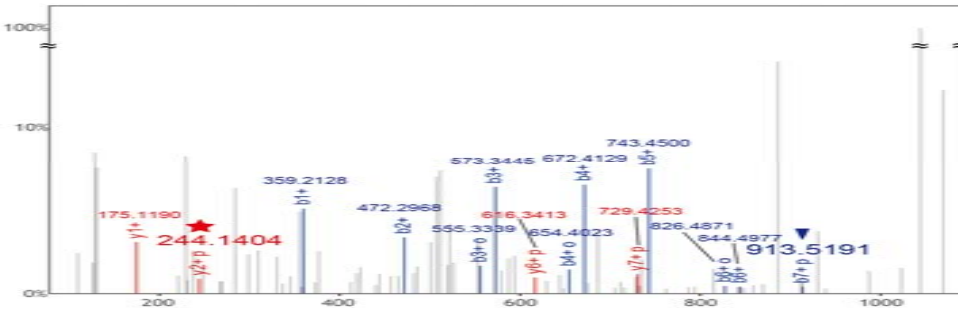
b+	#	Seq	#	y+
359.2128	1	E	8	
472.2968	2	I	7	827.4022
573.3445	3	T	6	714.3182
672.4129	4	V	5	613.2705
743.4500	5	A	4	514.2021
844.4977	6	T	3	443.1650
1011.4960	7	S	2	342.1173
	8	R	1	175.1190

[Click] to move table

Add to N-term: 229.1629

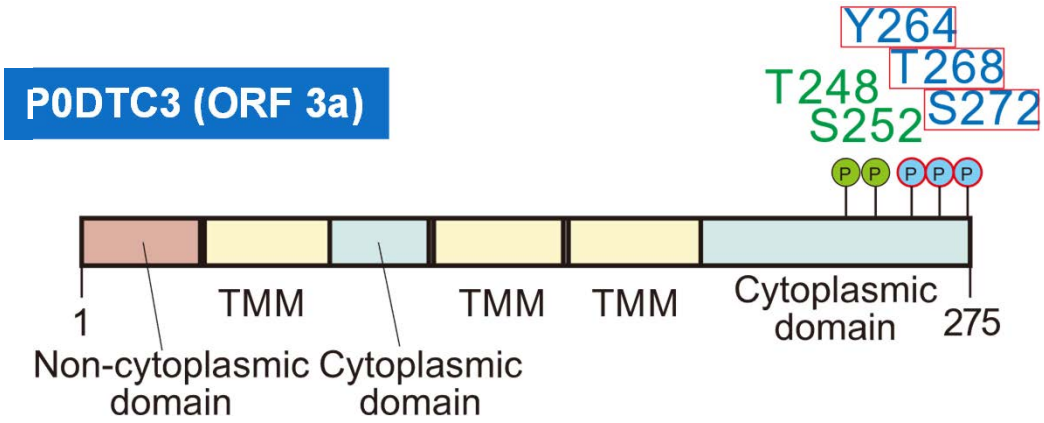
Variable Modifications:

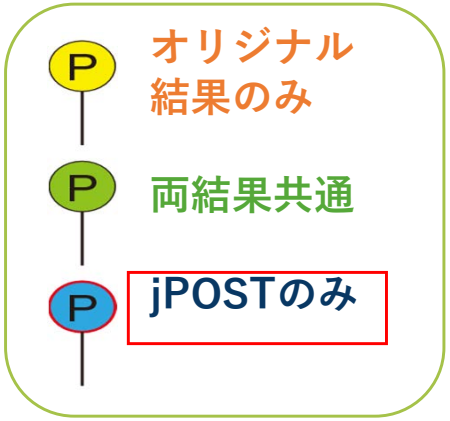
S: 79.9663 [7]



Phosphorylated sites on SARS-CoV-2 proteins

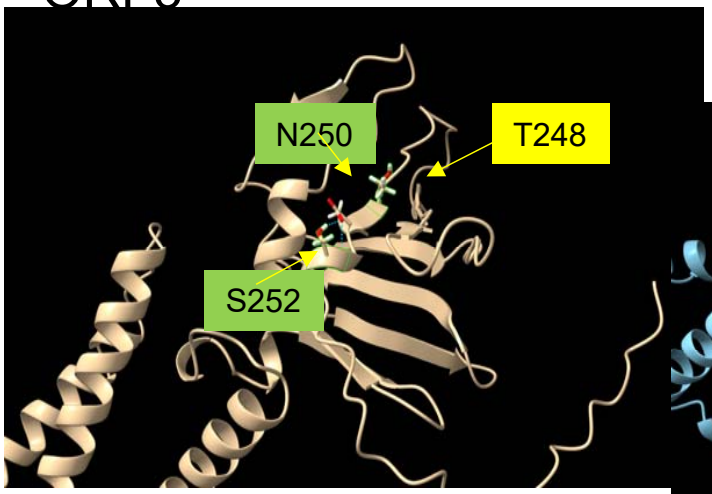
同定されたリン酸化サイトの比較



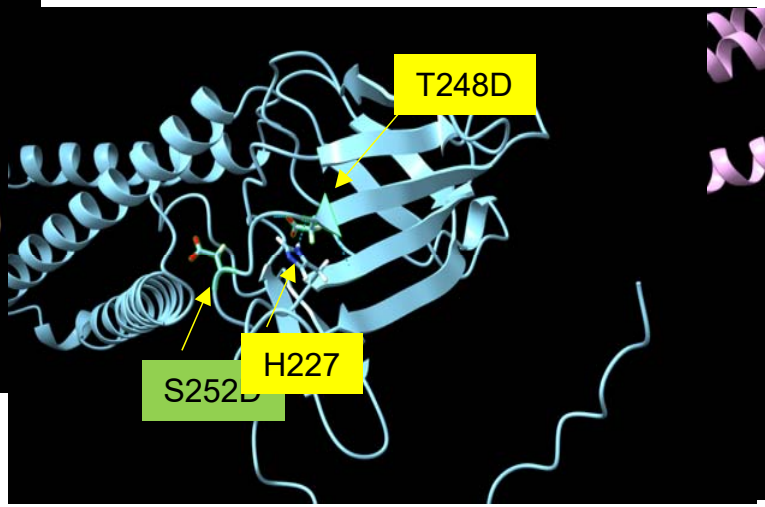


Alpha-Fold 2
にてリン酸化サイト
をDでミミックして
構造解析してみた。

ORF3

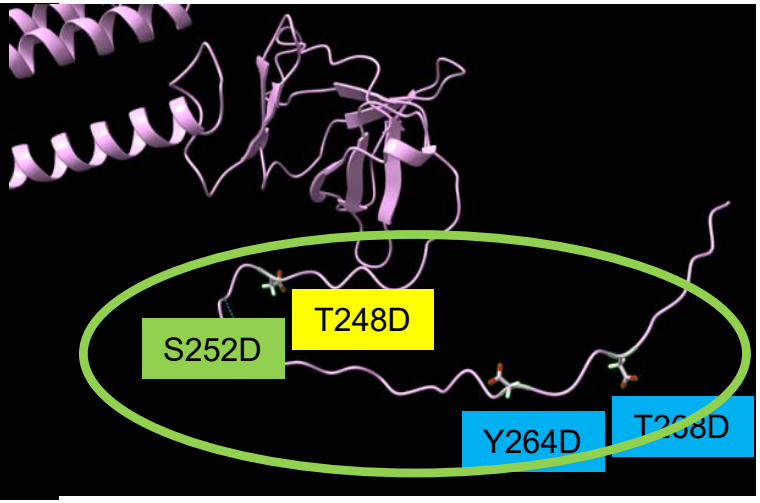


ORF3 T248D,
S252D



βシート構造の位置が
大きく変わる

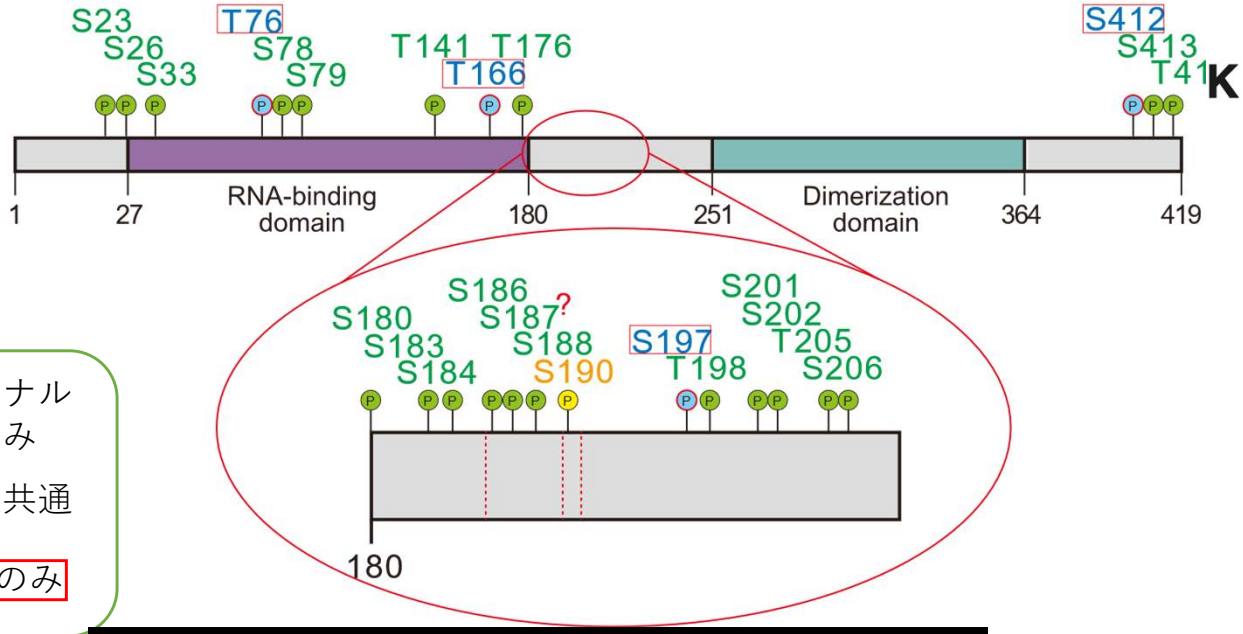
ORF3 T248D, S252D, Y264D,
T268D



Cytoplasmic domainのC末端
がfoldしなくなる

Phosphorylated sites on SARS-CoV-2 proteins

P0DTC9 (N) (ORF 9)

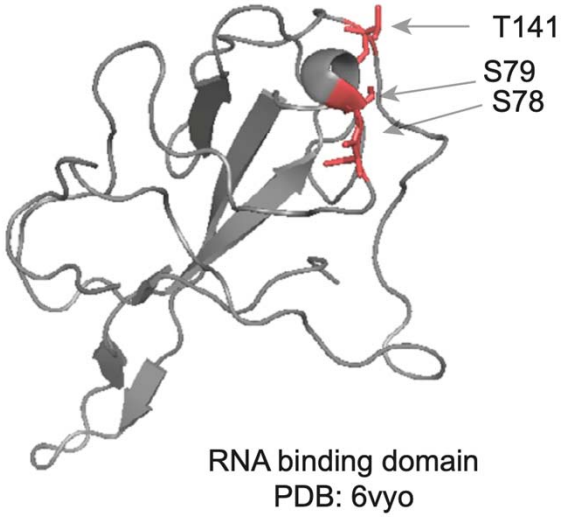


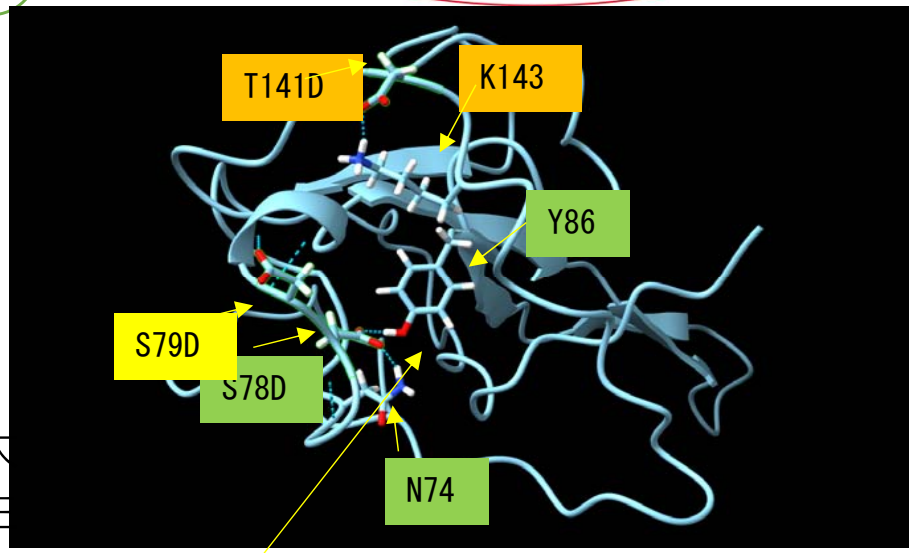
P オリジナル結果のみ

P 両結果共通

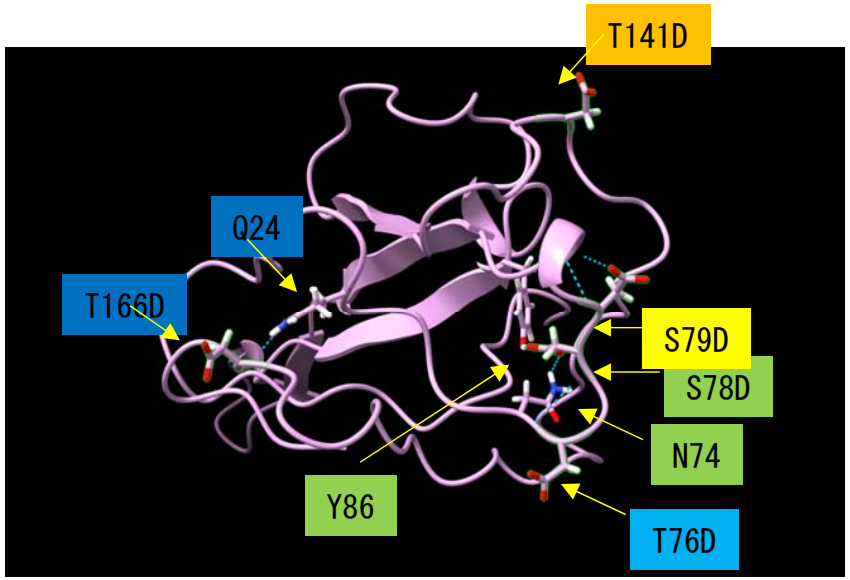
P jPOSTのみ

RNA binding site





S78DがY86と水素結合するようになる

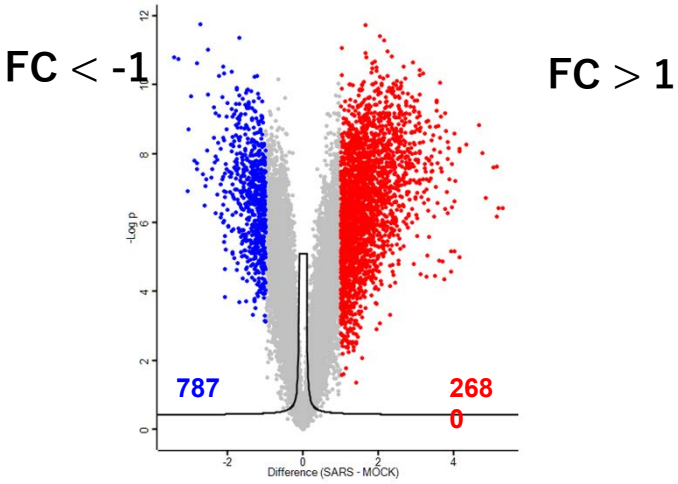


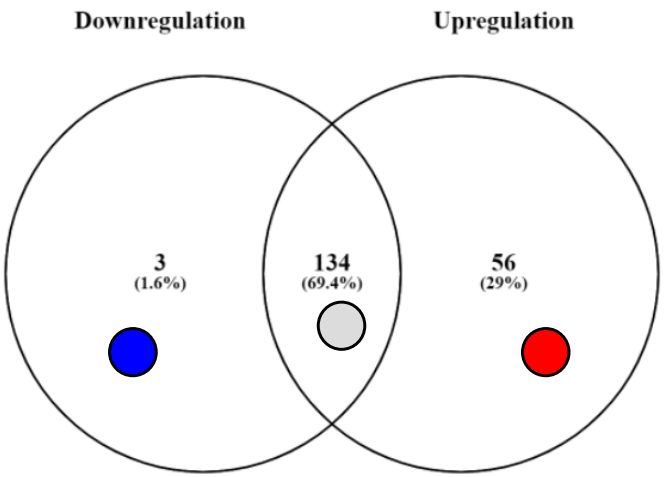
S78DがY86と水素結合するようになる

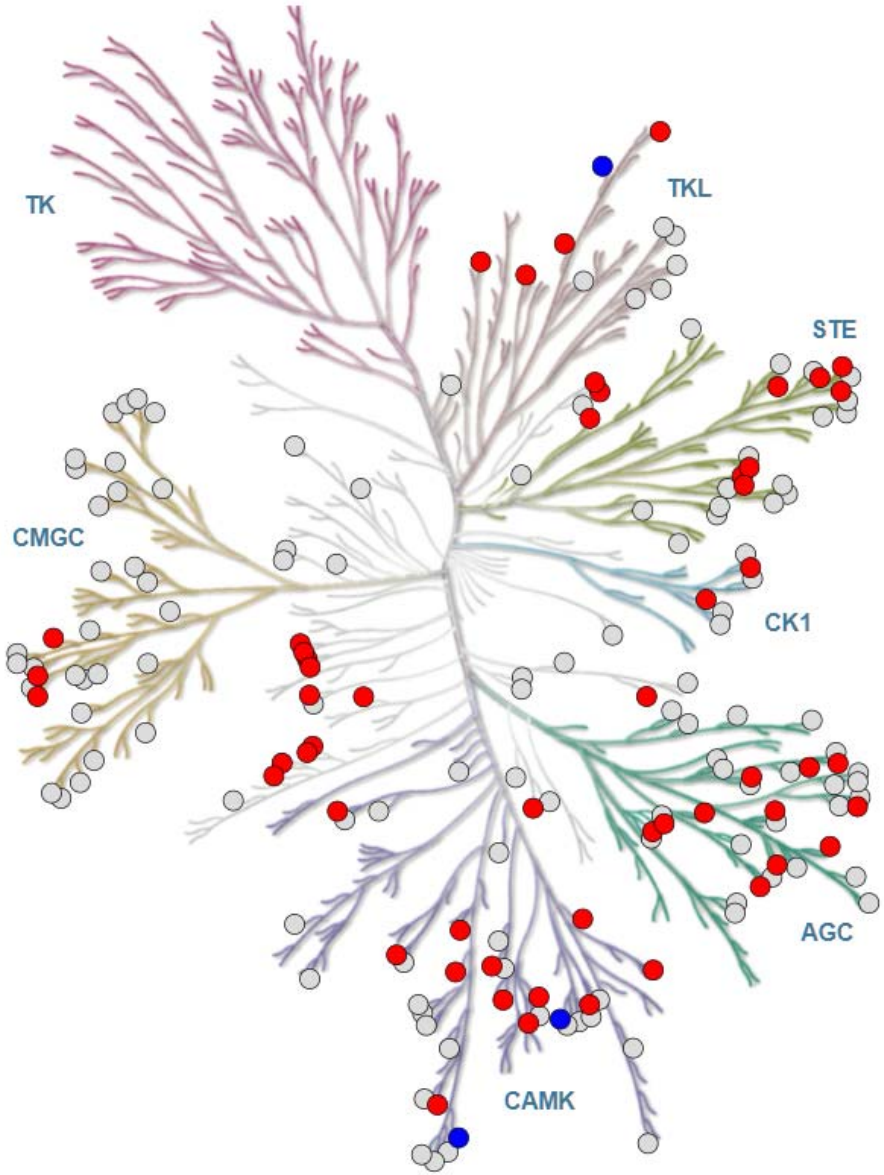
北海道医療大
北川孝雄先生
解析御協力

Prediction of activated Kinases in SARS-COV2 infected Cells

Significant: Log_2(TMT of p-sites) > |1| , FDR < 5%



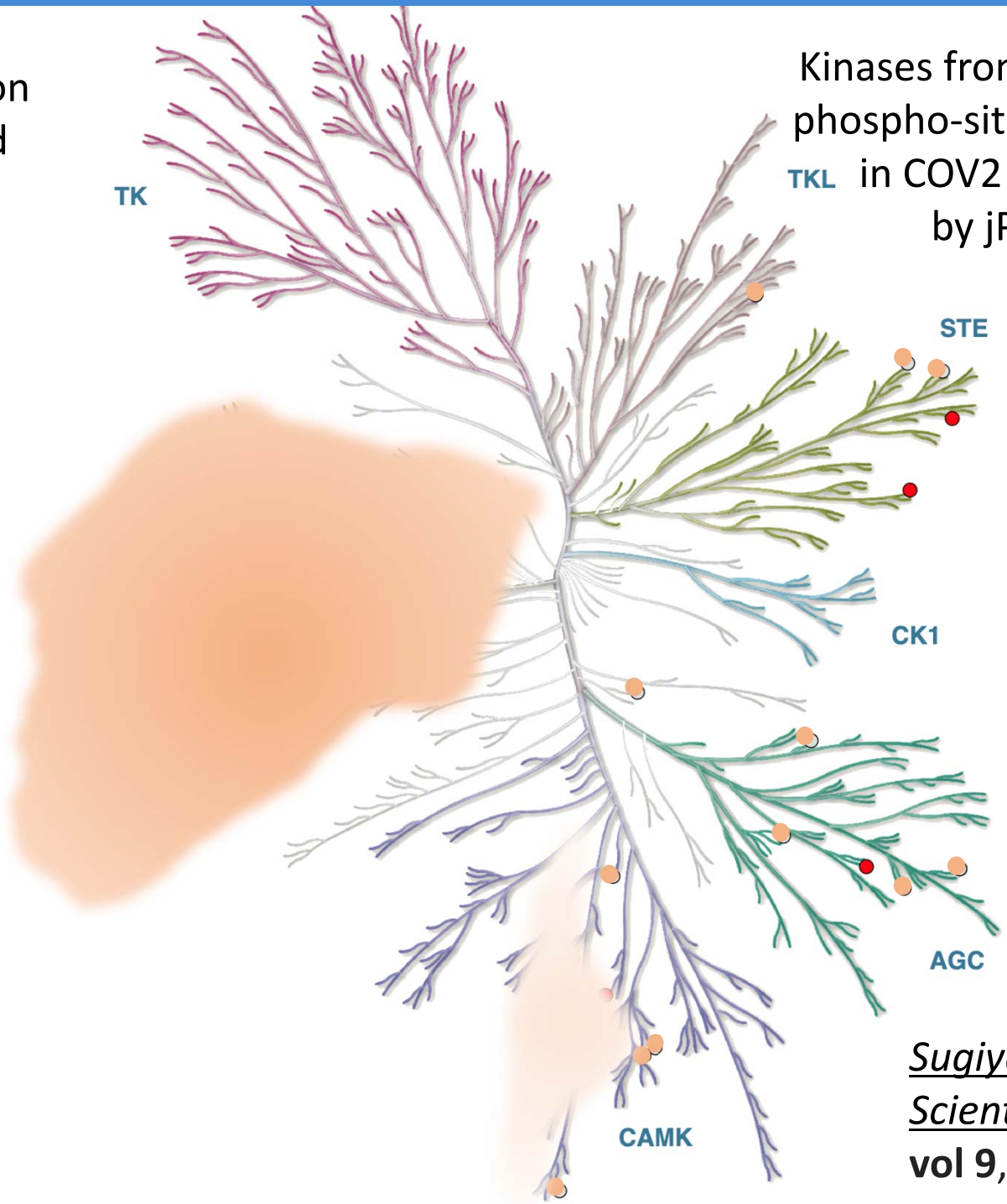




Prediction of activated Kinases in SARS-COV2 infected Cells

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

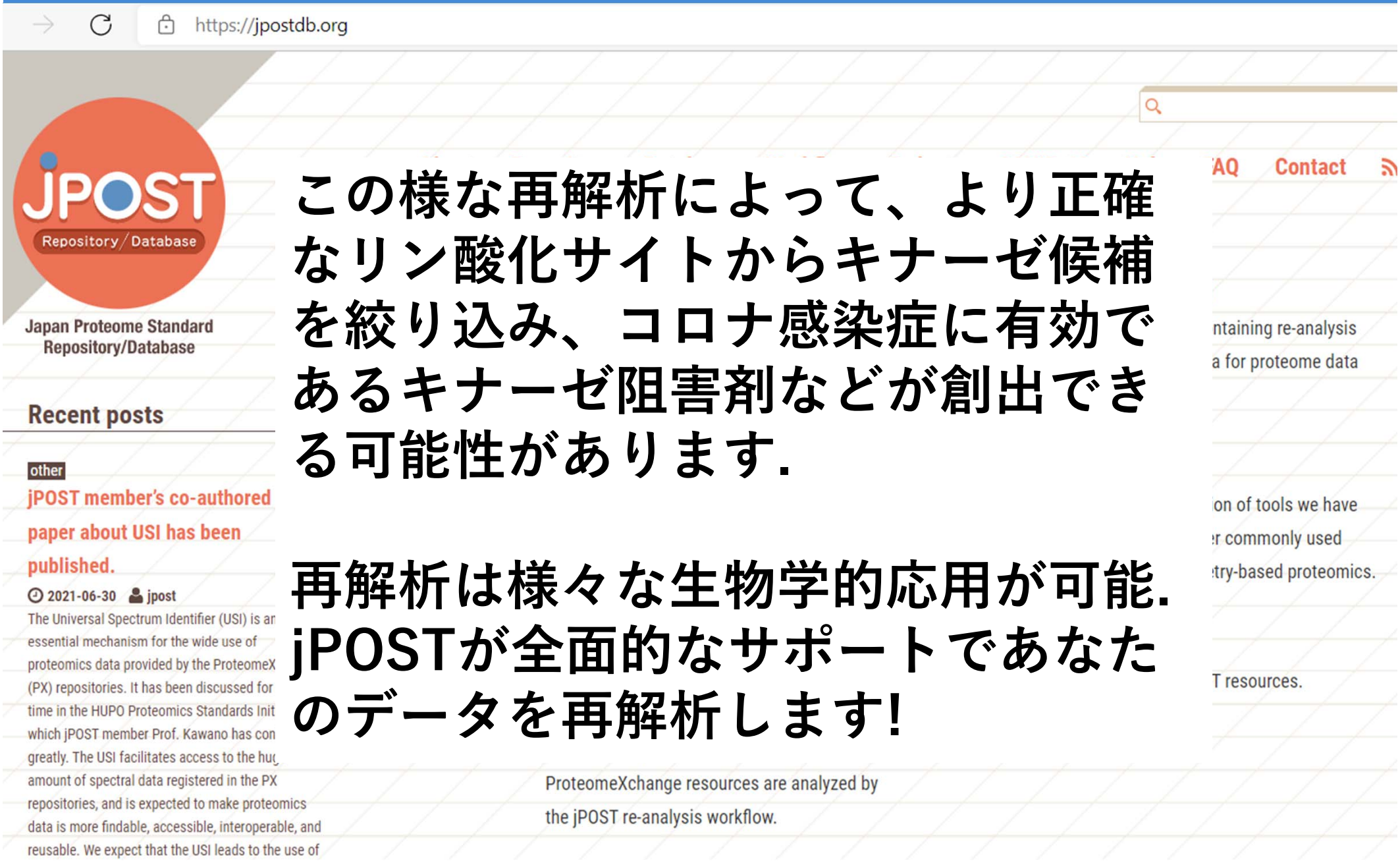


Kinases from 12 unique phospho-sites identified in COV2 Proteins by jPOST

P38D
HRI
HIPK4
HRI
PAK4
ERK7
NUAK2
TNIK
PRKX
PKD1
IKKA

Sugiyama et.al.
Scientific Reports
vol 9, 10503 (2019)

https://jpostdb.org



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!

jPOST

- ProteomeXchange Consortiumによって標準化されたメタデータの収集、プロテオームデータの公開を行っており、誰でもDLが可能である。
- リポジトリーのデータが集積されてきてメタデータの整備が必要になってきた。
- マルチプラットフォーム、オープンソース、フリーな解析ツールが利用可能になってきている。
- jPOSTでは解析結果をRDFでデータを公開しており、様々な可視化ツールを提供している。
- 生データのjPOST再解析ツールによって新たなデータの創出が可能となってきた。
- 興味のある方の参入を期待しています!

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

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

JPrOS Japanese Society of HUPO

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 reviwers | › Editorial board | › FAQ | › Ethics policies

About JPDM

JPDM
Journal of Proteome Data and Methods

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

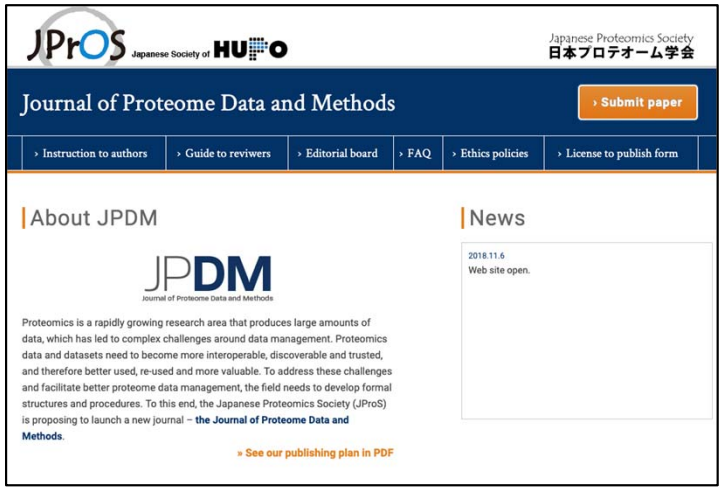
2021.11.12
Updated Editorial board.
2020.12.15
Updated Instructions to Authors.
2019.12.25
The first Data Descriptor article has been published.
2019.9.30
Editorial article has been published.
2019.9.30
JPDM website was formally opened.

Article list

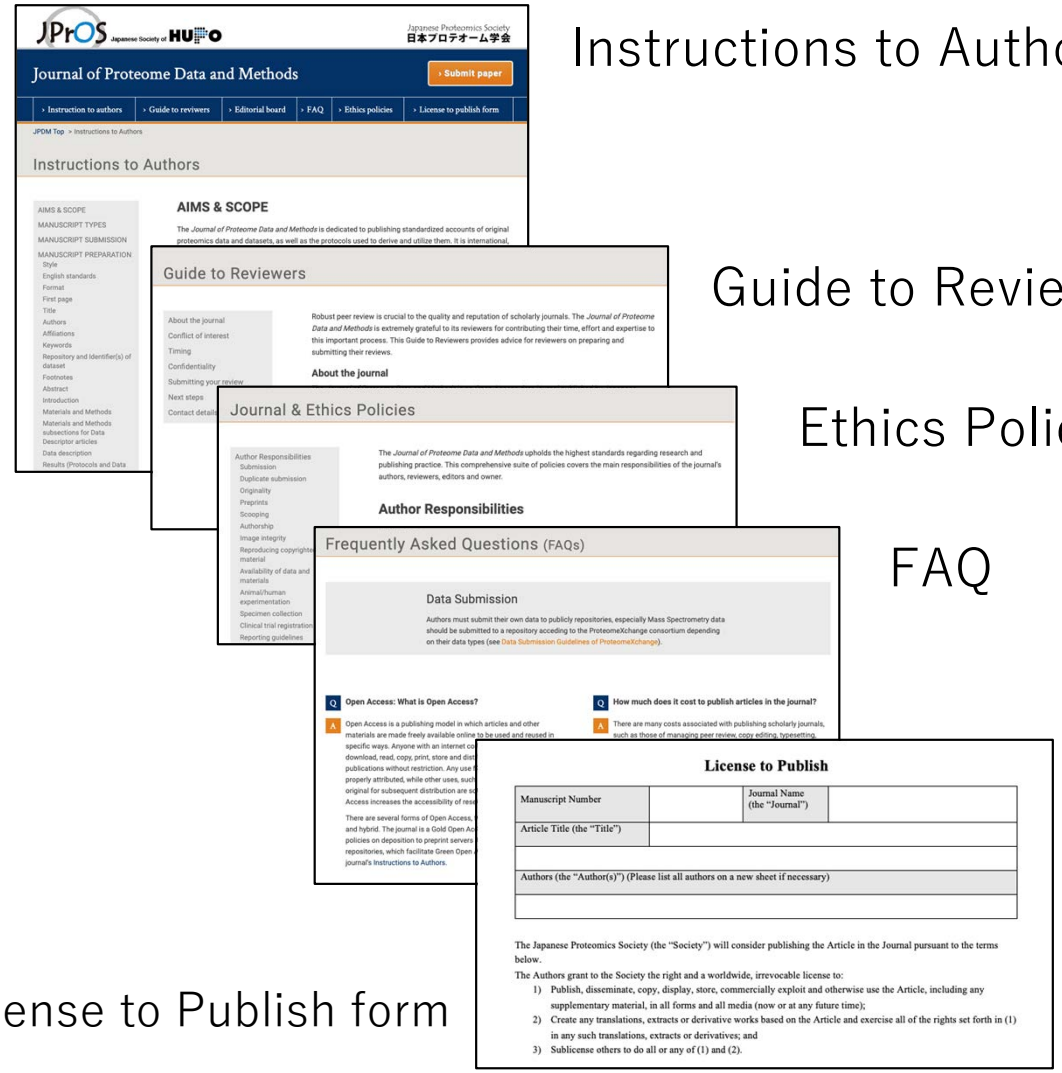
J-STAGE : Journal of Proteome Data and Methods

メタデータ完全版の収録を一つの目的として、2019年にjPOSTは日本プロテオーム学会(JPrOS)を母体とする **JPDM** (Journal of Proteome Data and Methods) というプロテオームのデータジャーナルを創刊しました。

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)



ウェブサイト
https://www.jhupo.org/jpdm/



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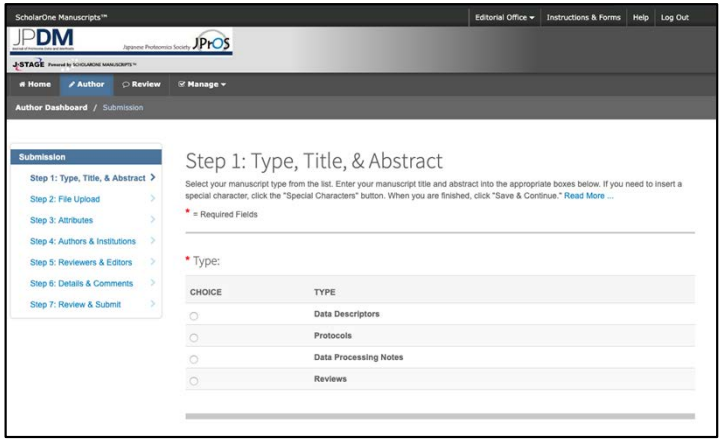

投稿システム（ScholarOne）
https://mc.manuscriptcentral.com/jpdm

- 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 s 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 s 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.

JPrOS Japanese Society of HUPO

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

Journal of Proteome Data and Methods

› Submit paper

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JPDM: 科研費によるサポート開始 (2021年より5年間)

学振事第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

さきに交付申請のありました令和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）

Journal of Pro

ch to Internet: Sharing Proteomics Data a
he Open Access Journal

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dly growing research area relating to all of bioscience fields. Advances in proteomics tec
coupled with bioinformatics had opened the way to produce large amounts of data from the e
rganism etc. under the several set of conditions. Now, these advances have given us comple
eomics data and datasets coupled with detailed metadata need to become more **Findable**, A
romote data sharing in the scientific community. To address these challenges and facil
eld needs to develop formal structures and procedures to be an applicable standard. T
(JPrOS) decided to launch a new data journal – the **Journal of Proteome Data and Metho**

ewed, fully open access and online only journal, provided via the J-stage platform. **JPDM** p
"**Protocols**", "**Data processing notes**", and "**Reviews**". The main content of the journal
tions of data, i.e., detailed metadata on the samples to be analyzed, the sample pr
he data analysis are provided, not the functional data for attempting to address hypothe
on and insight. We ask authors to fill in a **dataset summary table** to provide the basic inform
described in the JPDM article is of value to the greater scientific community. These rec
sy way and consequently more useful to others. **JPDM** tightly collaborates with Je
a (**jPOST**), one of the partner repositories in ProteomeXchange consortium (**PX**). When da
epository then post detailed metadata in **JPDM**, the journal sends a feedback to the PX rep
roteome datasets by providing detailed metadata. Since **JPDM** is a data journal that a
n still be posted to ordinary journals.

escriptors, articles in other three categories (**Protocols**, **Data processing notes**, and Rev
tocols and the computational tools that may have never left the lab, or that normally goes u

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。

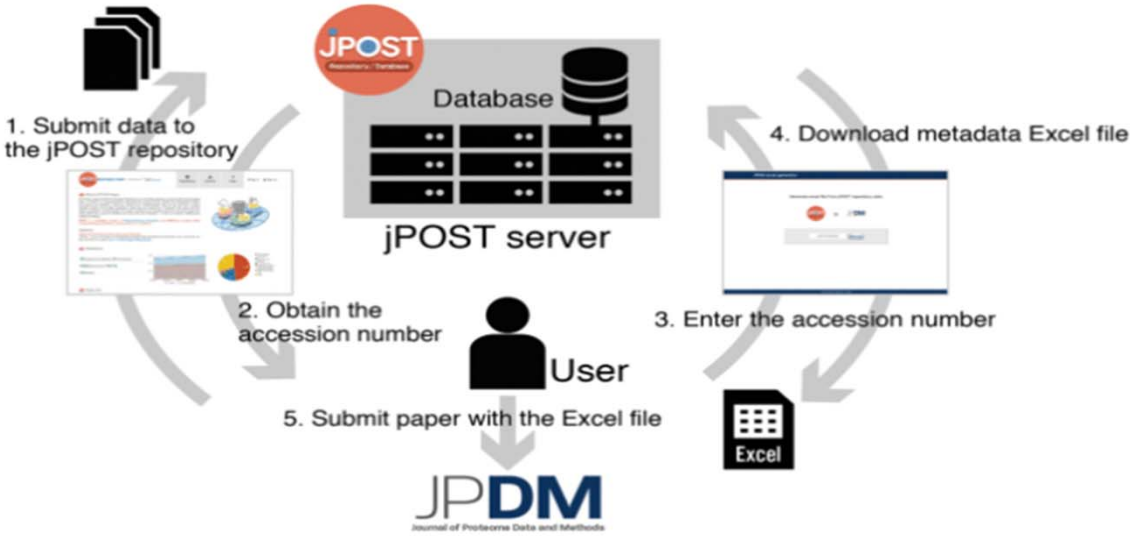
詳細なメタデータに対応するサプリメンタルデータの登録をJPDMのEditorial サポートメンバーが素早くお手伝いいたします。

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！

JST NBDC バイオサイエンス データベースセンター

JPOST Repository/Database
Japan Proteome Standard Repository/Database

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エットサイエンティスト
の皆様、お問い合わせください。

jpostdb@gmail.com