

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)

本日のテーマ

JPOSTを使ってプロテオーム解析をする

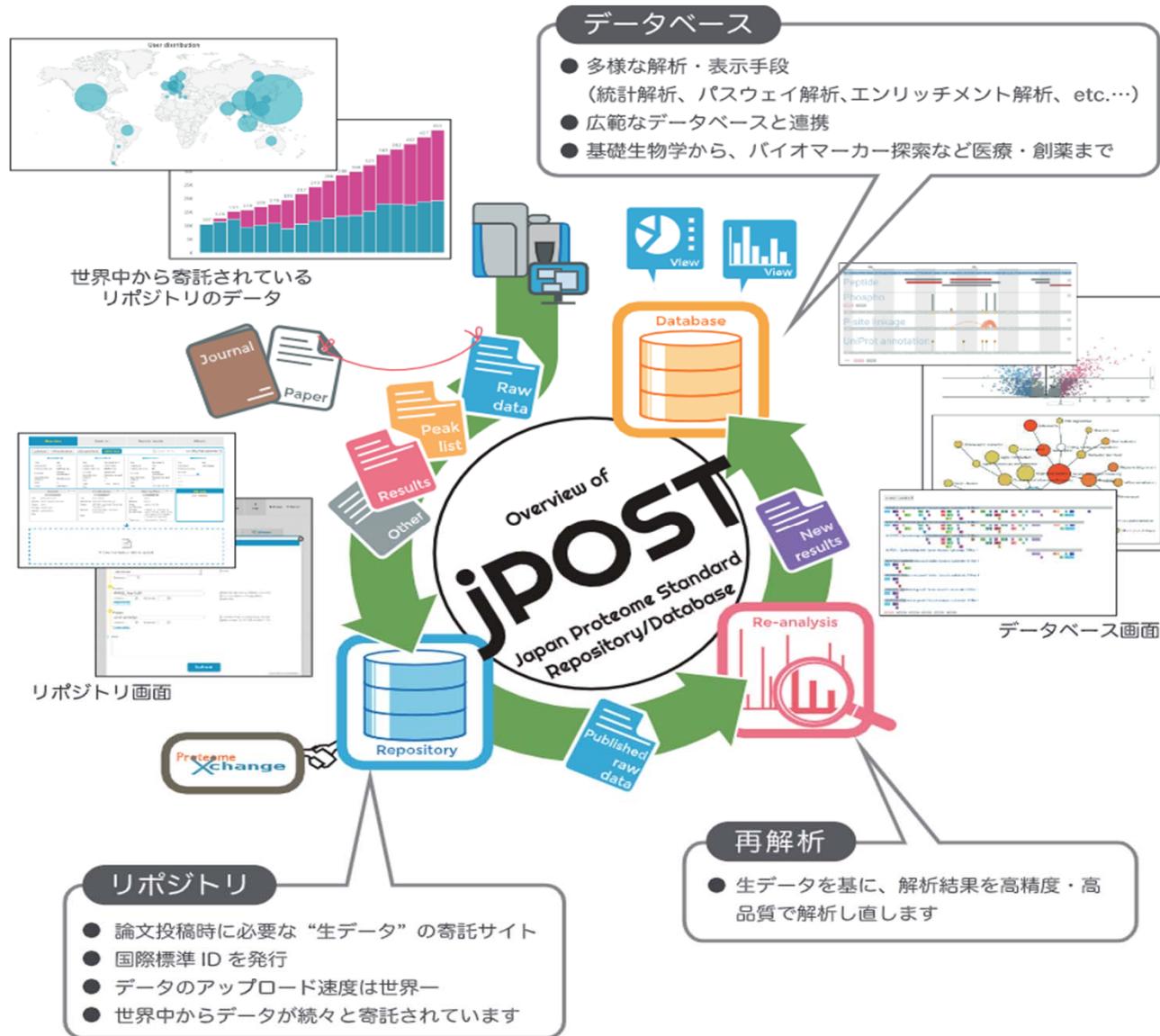
- JPOSTとは？
- 格納されるプロテオームデータとは？
- レポジトリの説明と登録のこつ
- 登録データの再解析について
- 再解析後の高品質なプロテオームデータの蓄積・可視化と応用
- コロナDBの構築・再解析による新たな情報の創出と応用の可能性(リン酸化プロテオームを標的にして)
- JPDM誌の創刊と紹介

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



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

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 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.

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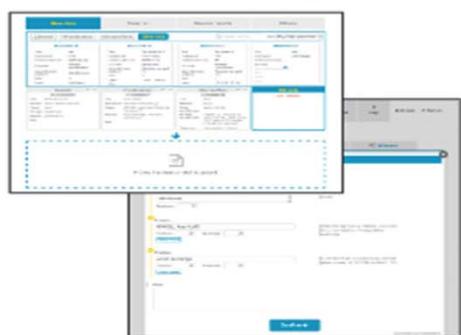
Help
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世界中から寄託されている
リポジトリのデータ



リポジトリ

- 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

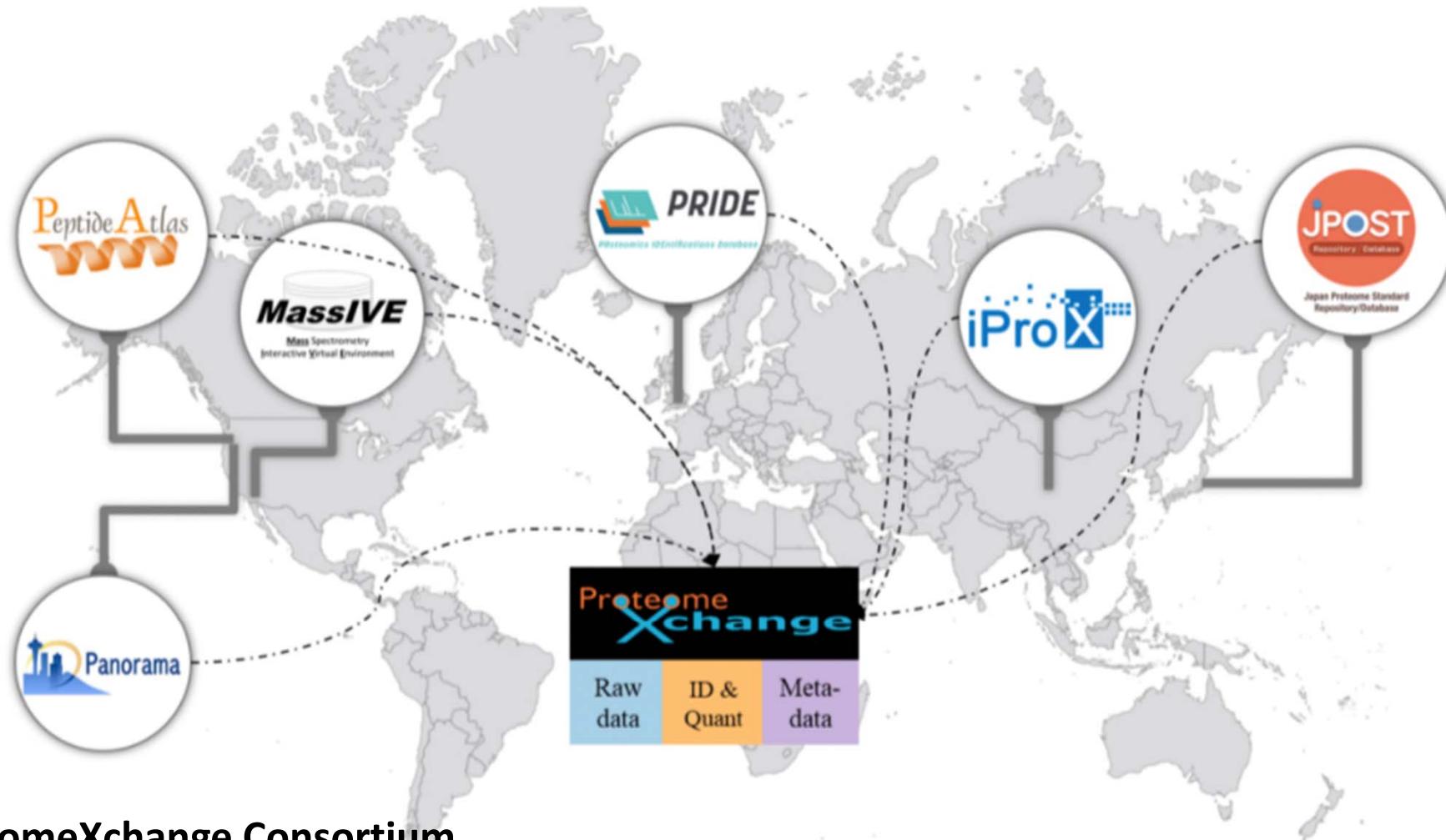
データベース

- 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

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

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

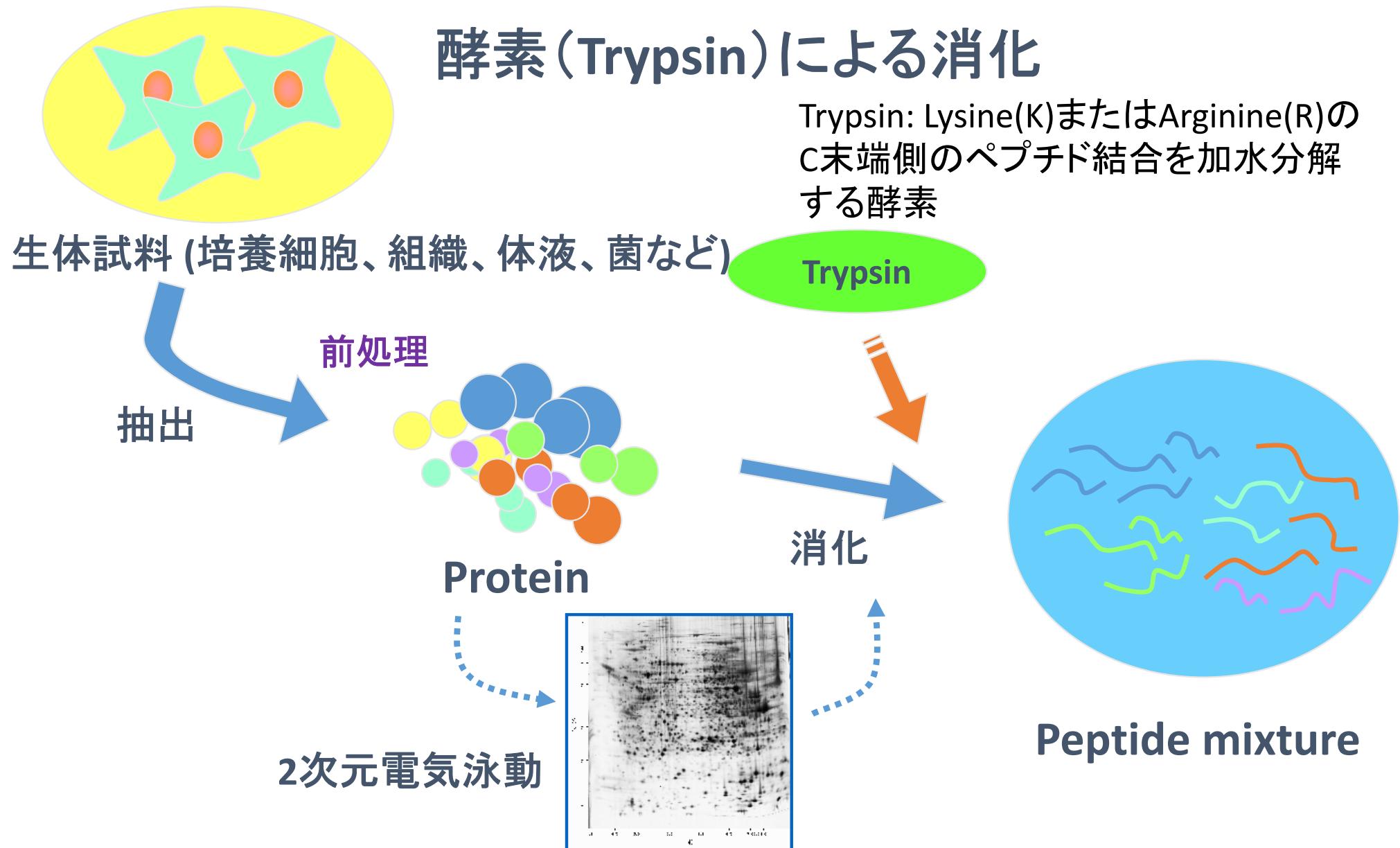
HEK293培養細胞の細胞膜や核や細胞質を構成するすべてのタンパク質等

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。

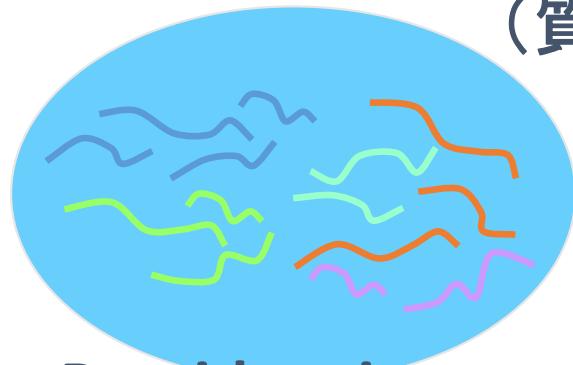
Proteome Analysis Workflow

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)



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

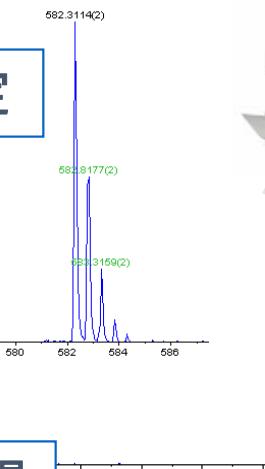


Nano LC
(ペプチド分離)

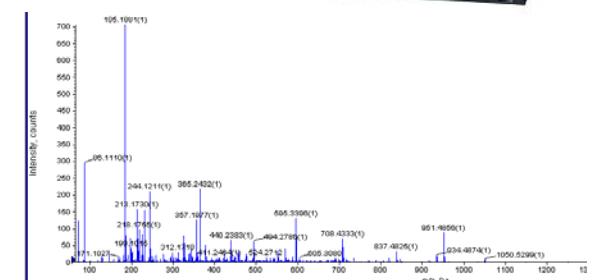
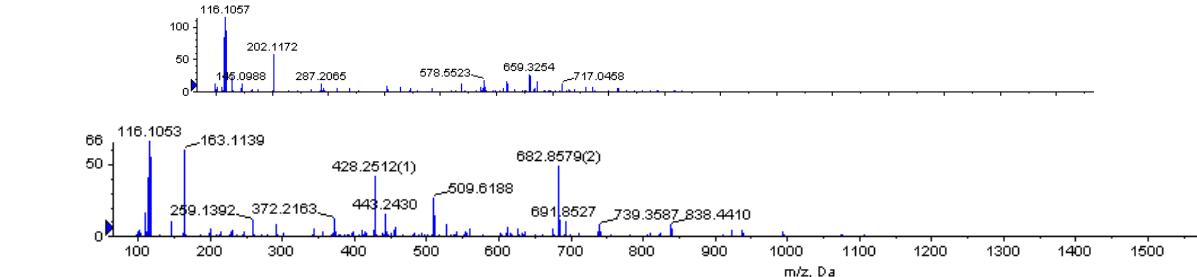
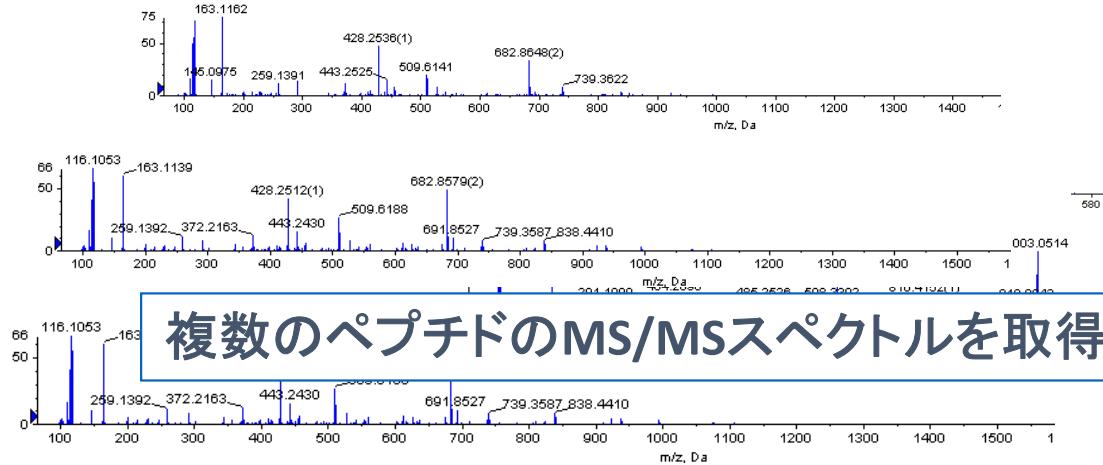


質量分析装置

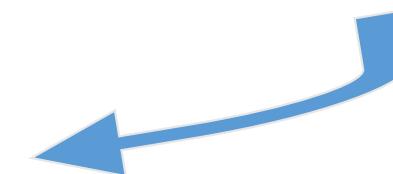
MS測定



複数のペプチドのMS/MSスペクトルを取得



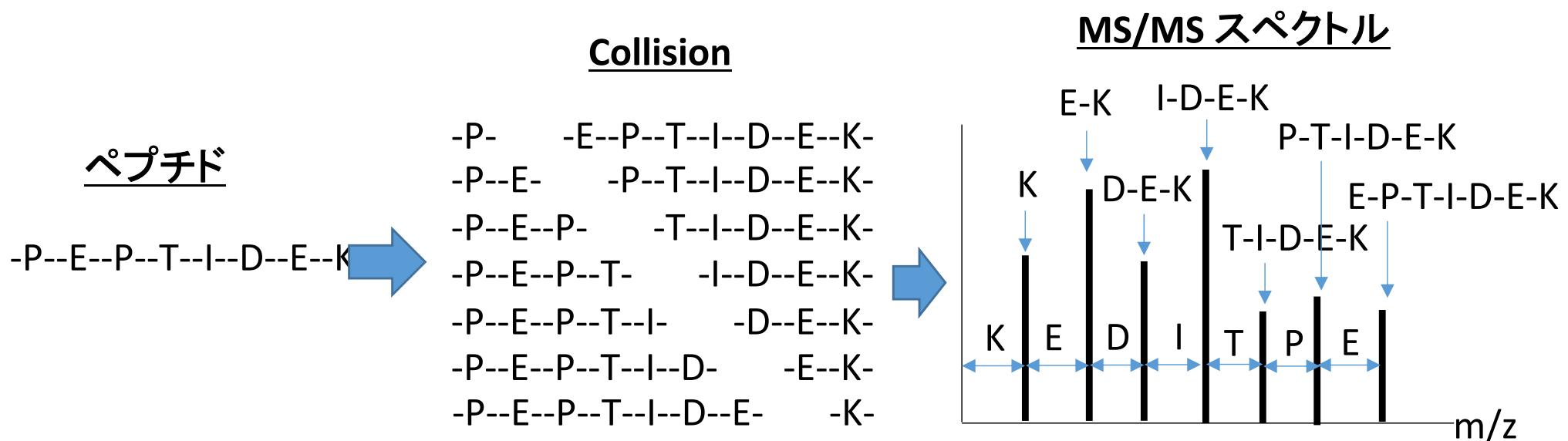
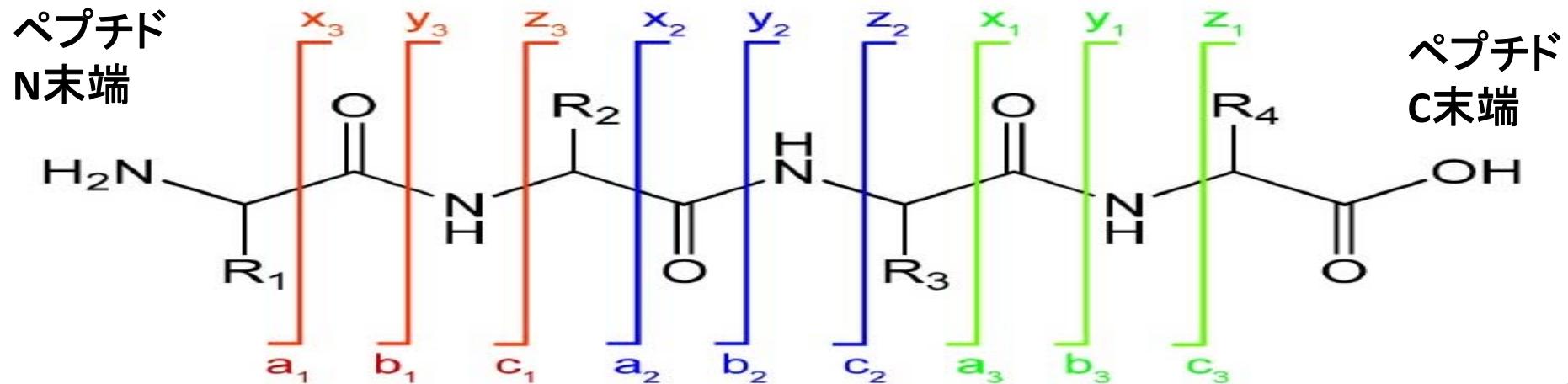
MS/MS測定



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

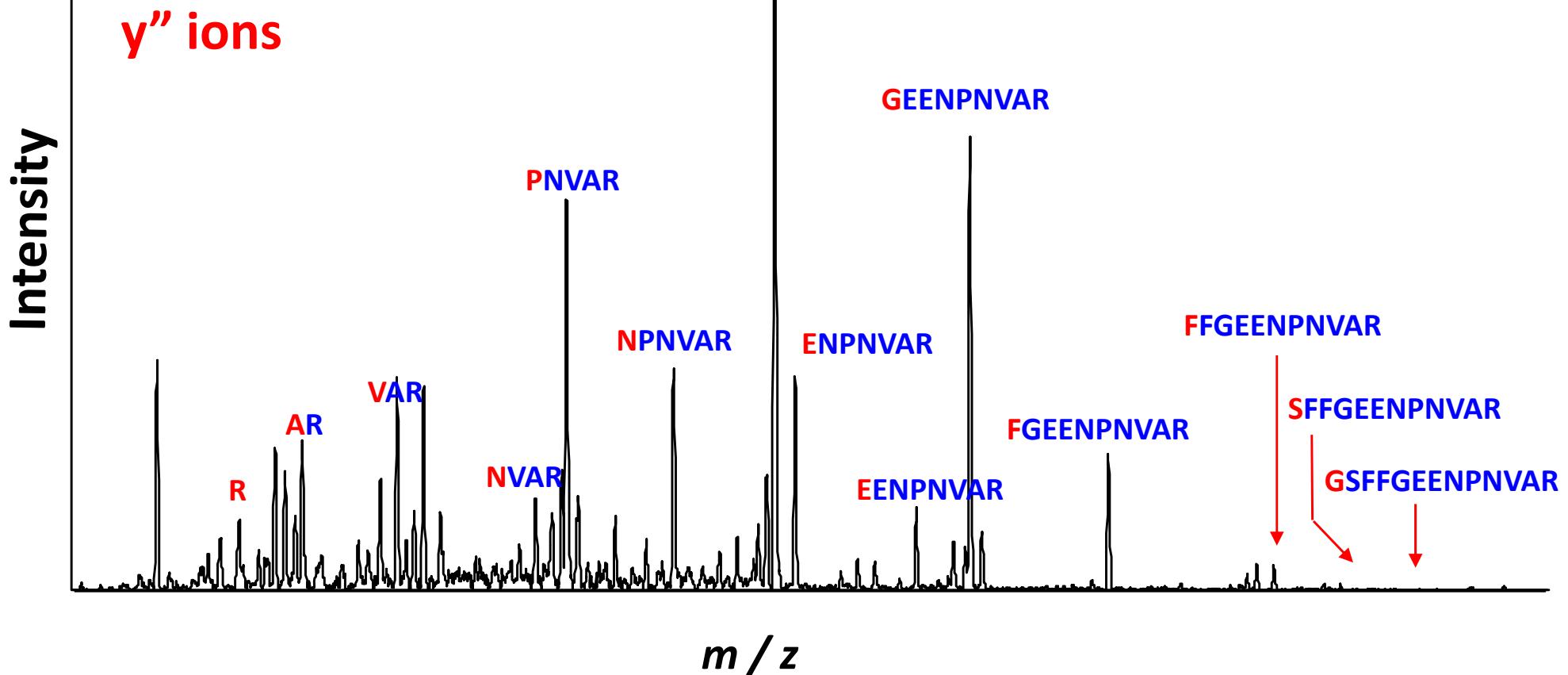
ペプチドのフラグメント化パターン



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

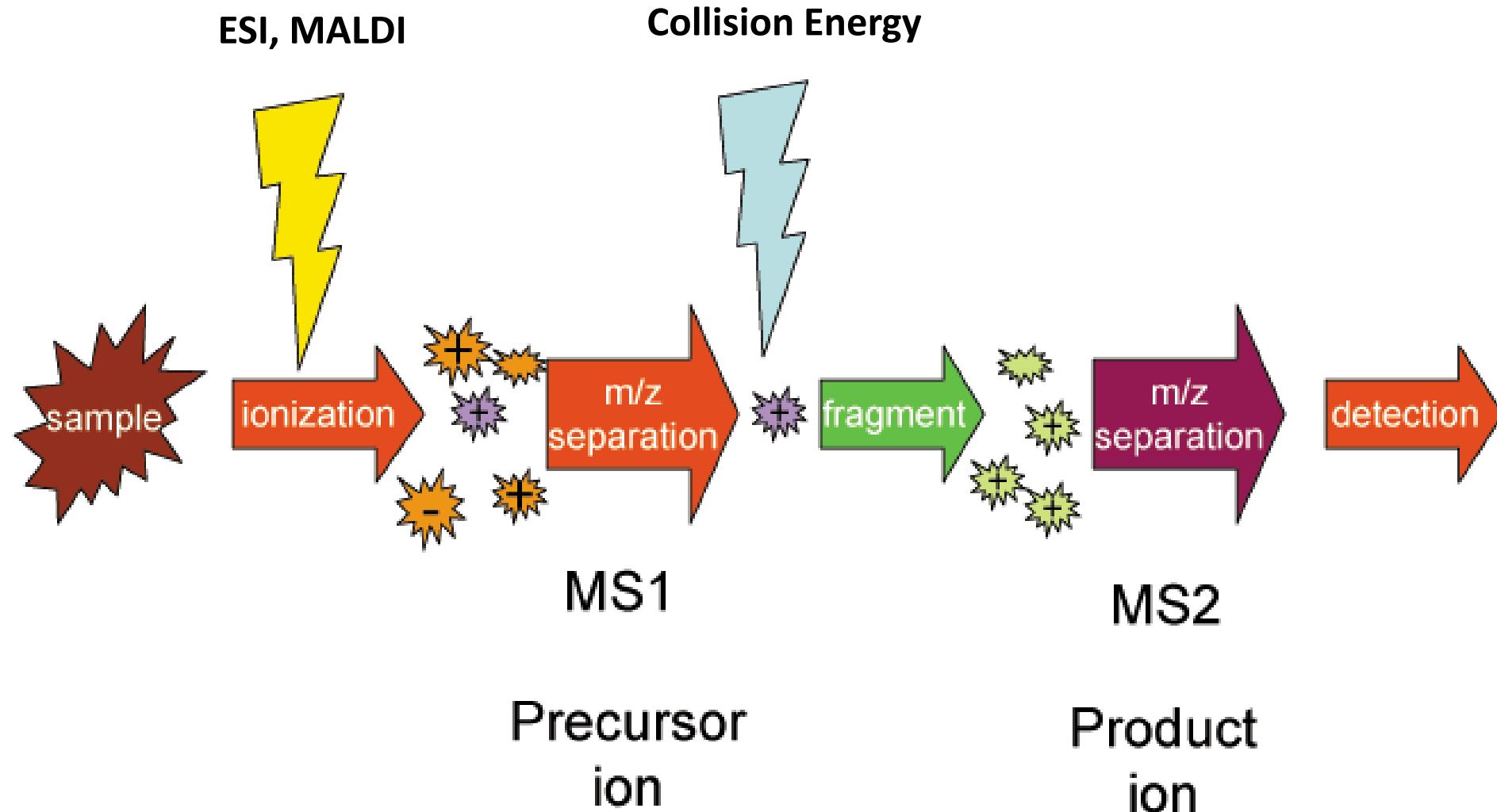
質量分析装置の高感度化・高精度化・迅速化が進み、短時間で同定されるタンパク質の数が飛躍的に増加!!! Mass spectrometers are becoming more sensitive, more accurate and faster, protein numbers identified has increased dramatically.



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？？



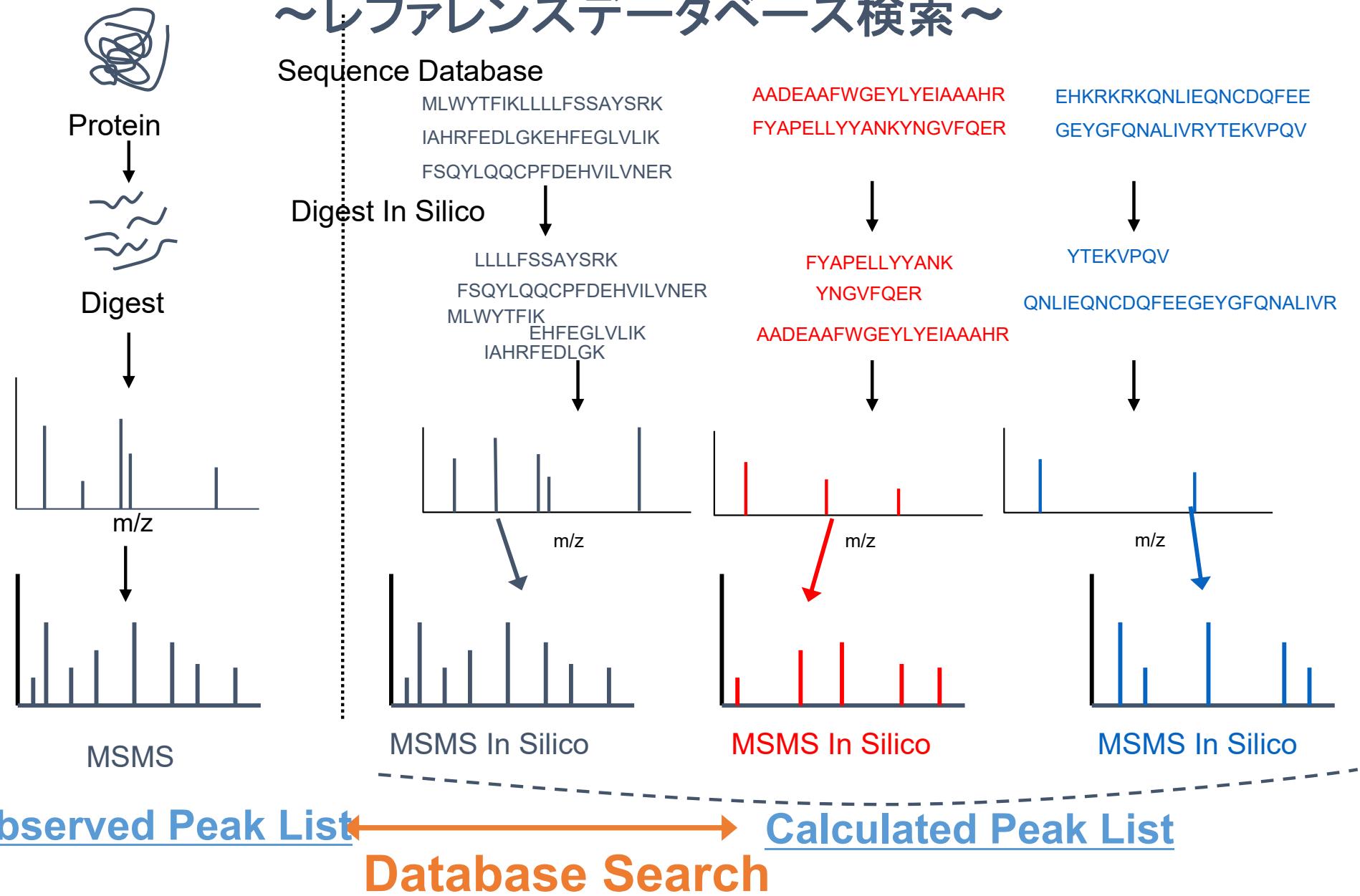
ESI: Electron spray ionization

MALDI: Matrix-assisted laser desorption/ionization

wikipediaより改変

Proteome Analysis Workflow

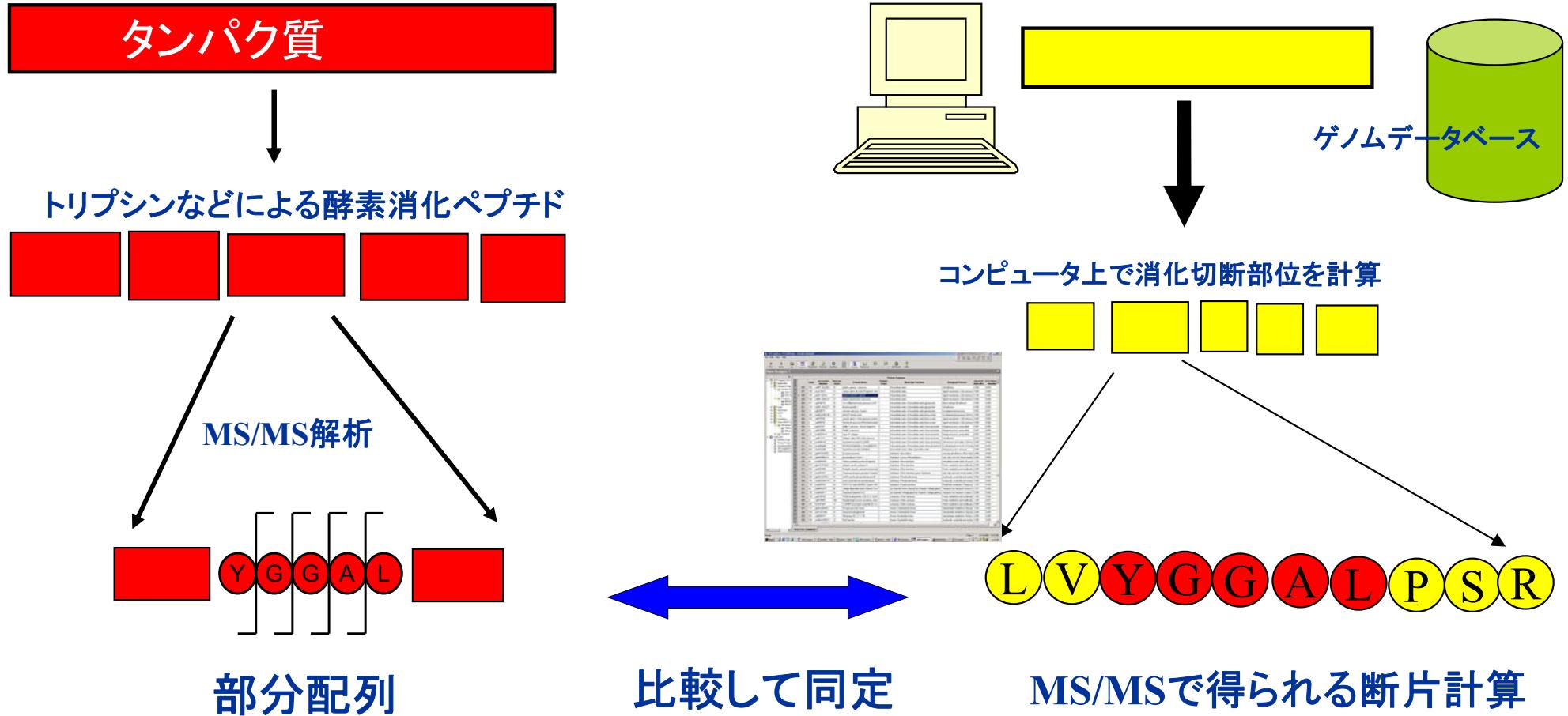
MS/MSスペクトルからタンパク質を同定する
～レファレンスデータベース検索～



Proteome Analysis Workflow

Sequence Tag法

MS/MSによるタンパク質同定の標準法

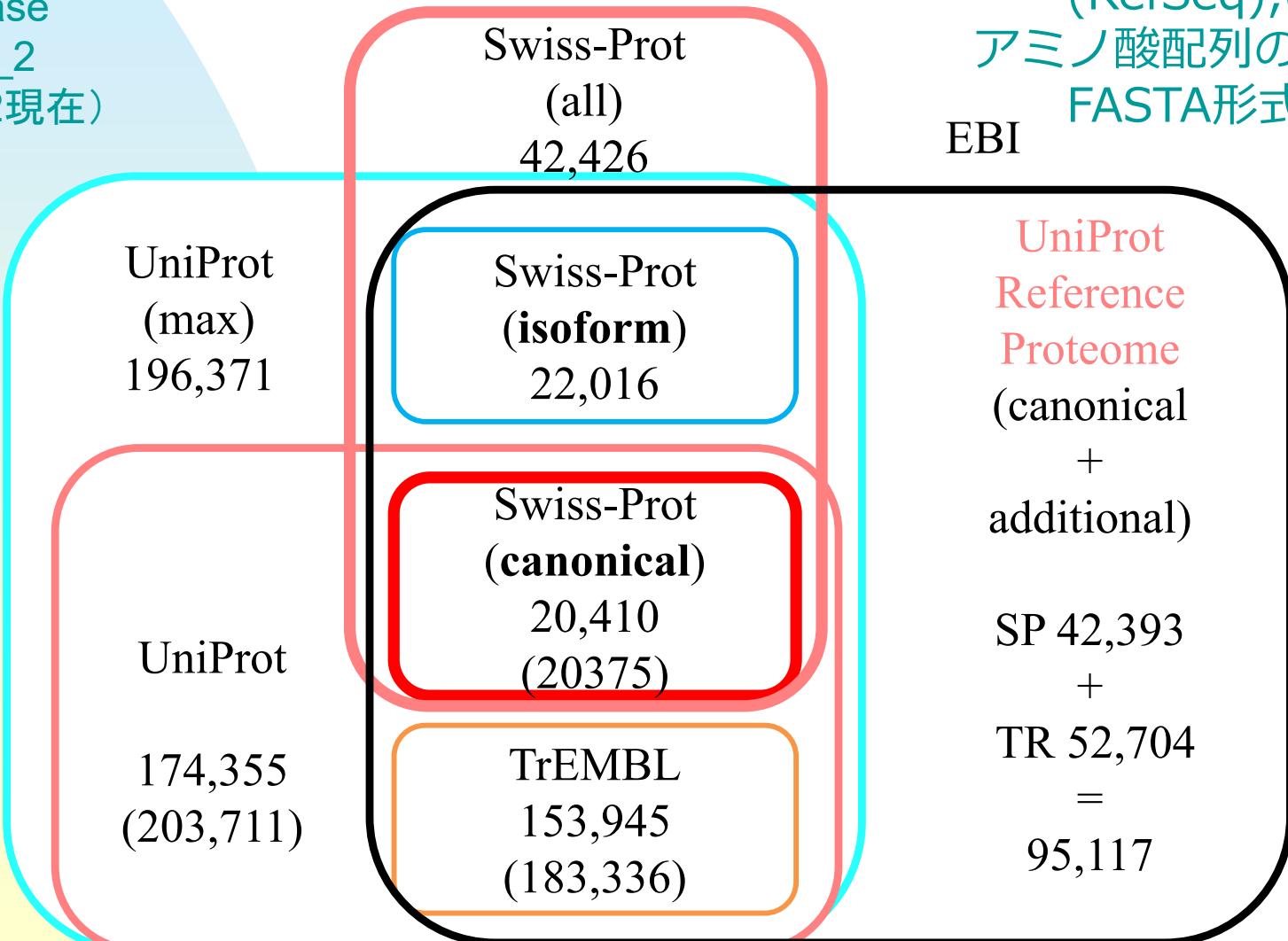


親となるペプチドの質量と分解したアミノ酸部分配列の情報
(シーケンスタグとよばれる)を組合わせてデータベース検索する

Reference Protein Database Sequence collection

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

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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

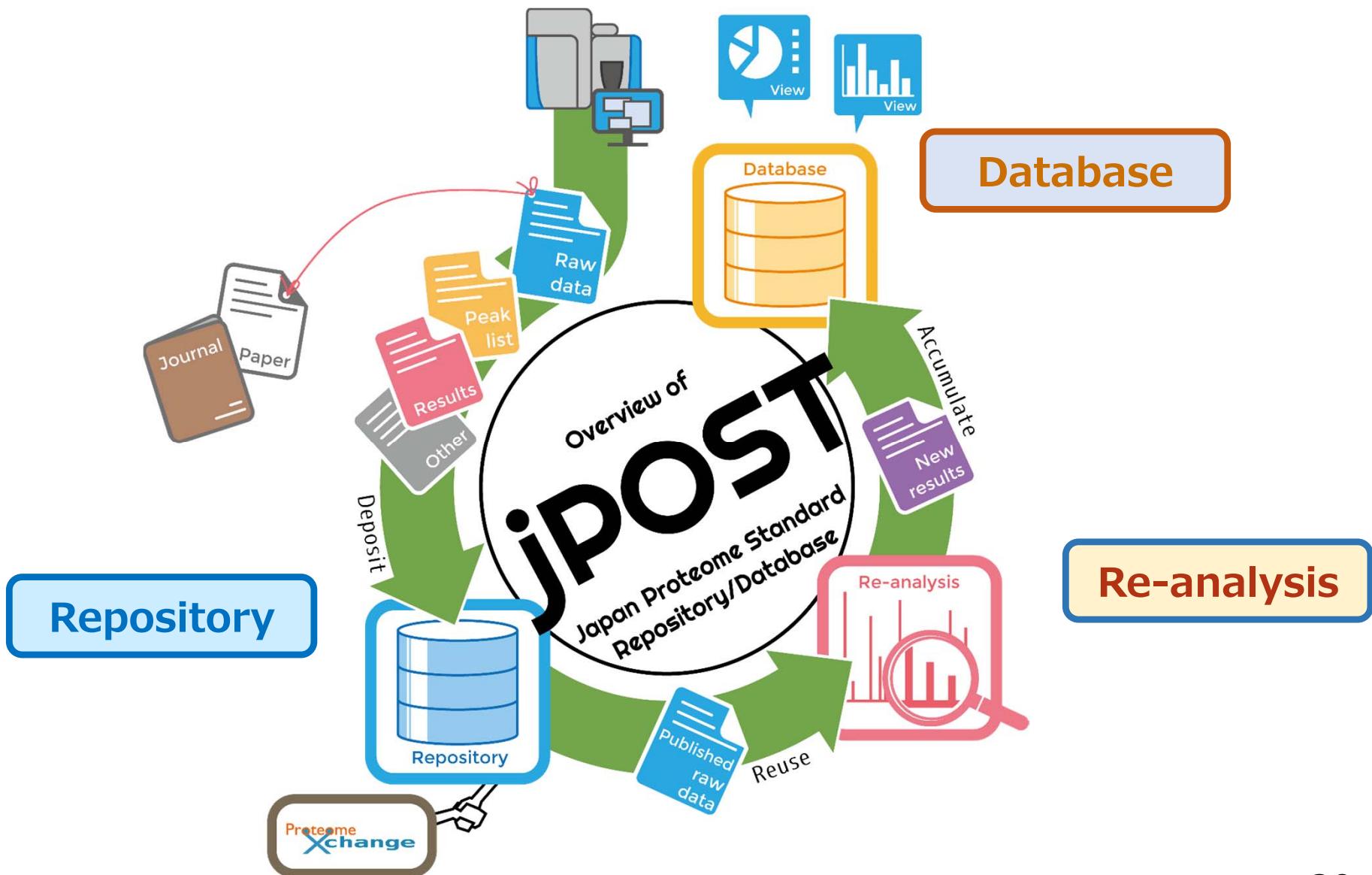
As of January 1, 2018, the Journal of Proteome Research will require SUBMISSION OF RAW DATA to a public repository such as a ProteomeXchange (PRIDE or MASSIVE), or CHORUS, or an equivalent repository when the paper is submitted.

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

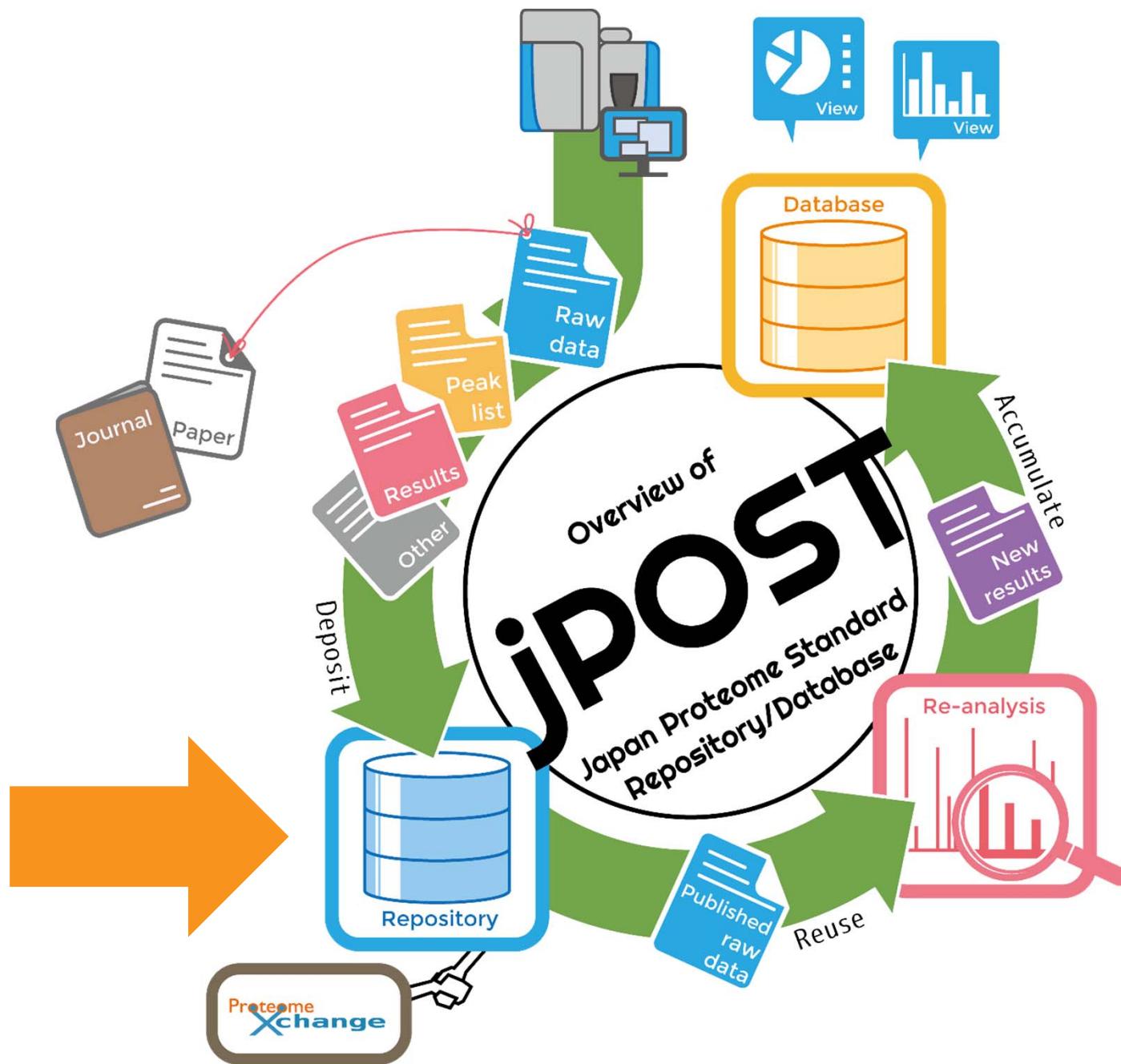


jPOSTの特徴



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



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<https://jpostdb.org>

→ C https://jpostdb.org



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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

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



Reference

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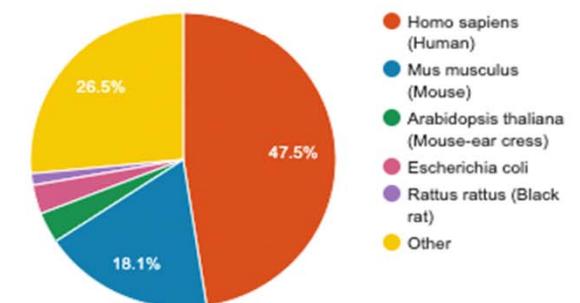
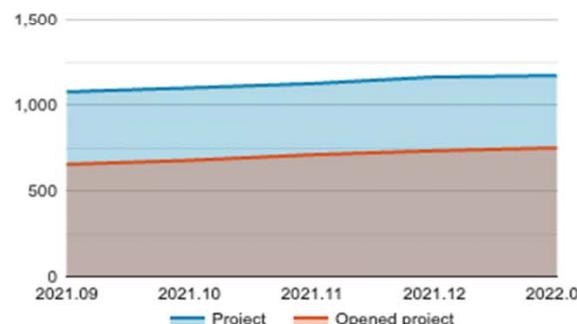
Okuda, S. et al. jPOSTrepo: an international standard data repository for proteomes. Nucl. Acids Res. 45 (D1): D1107-D1111 (2017). doi: 10.1093/nar/gkw1080 [pubmed]

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(Raw 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

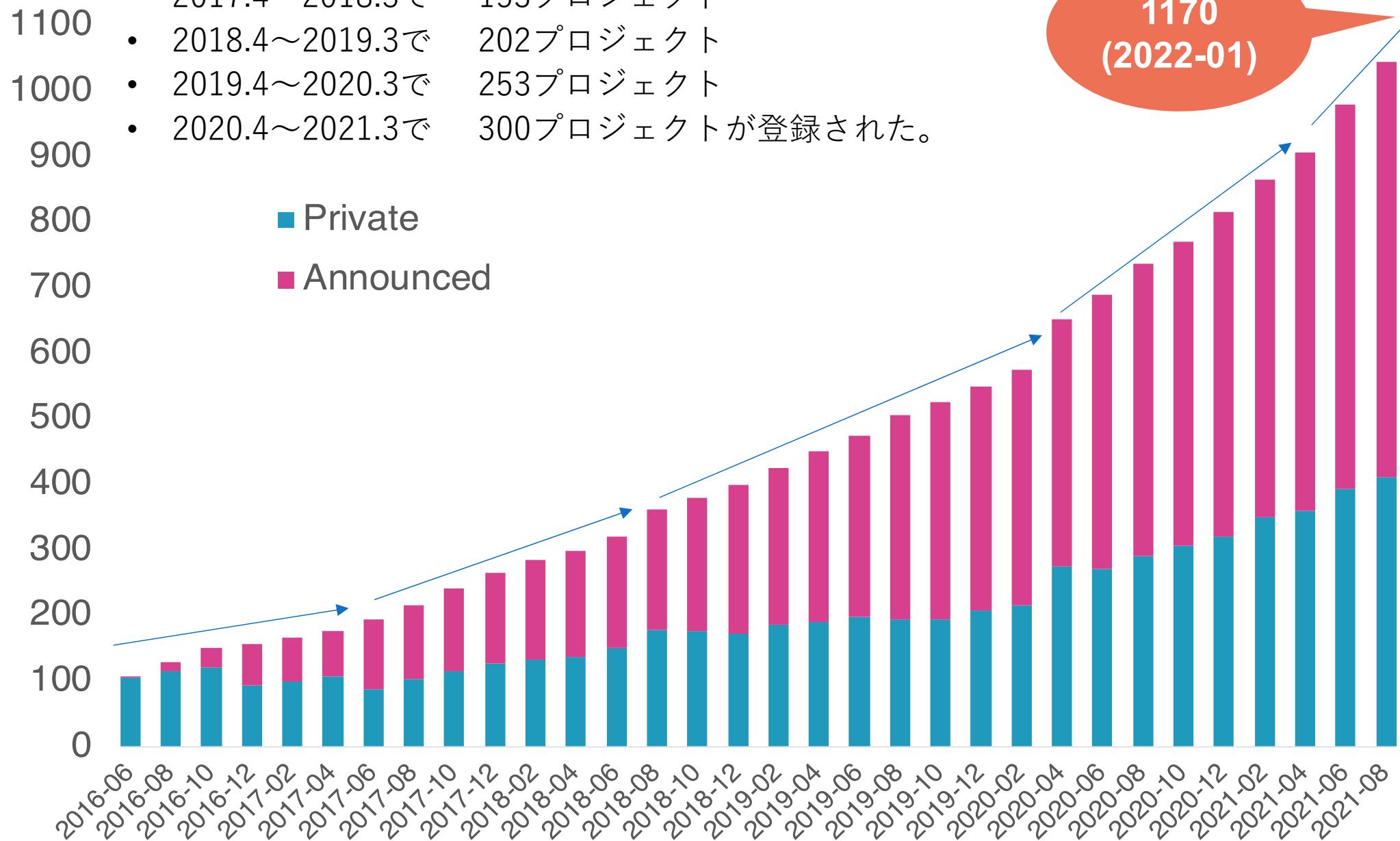
jPOST repository – Current status



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。

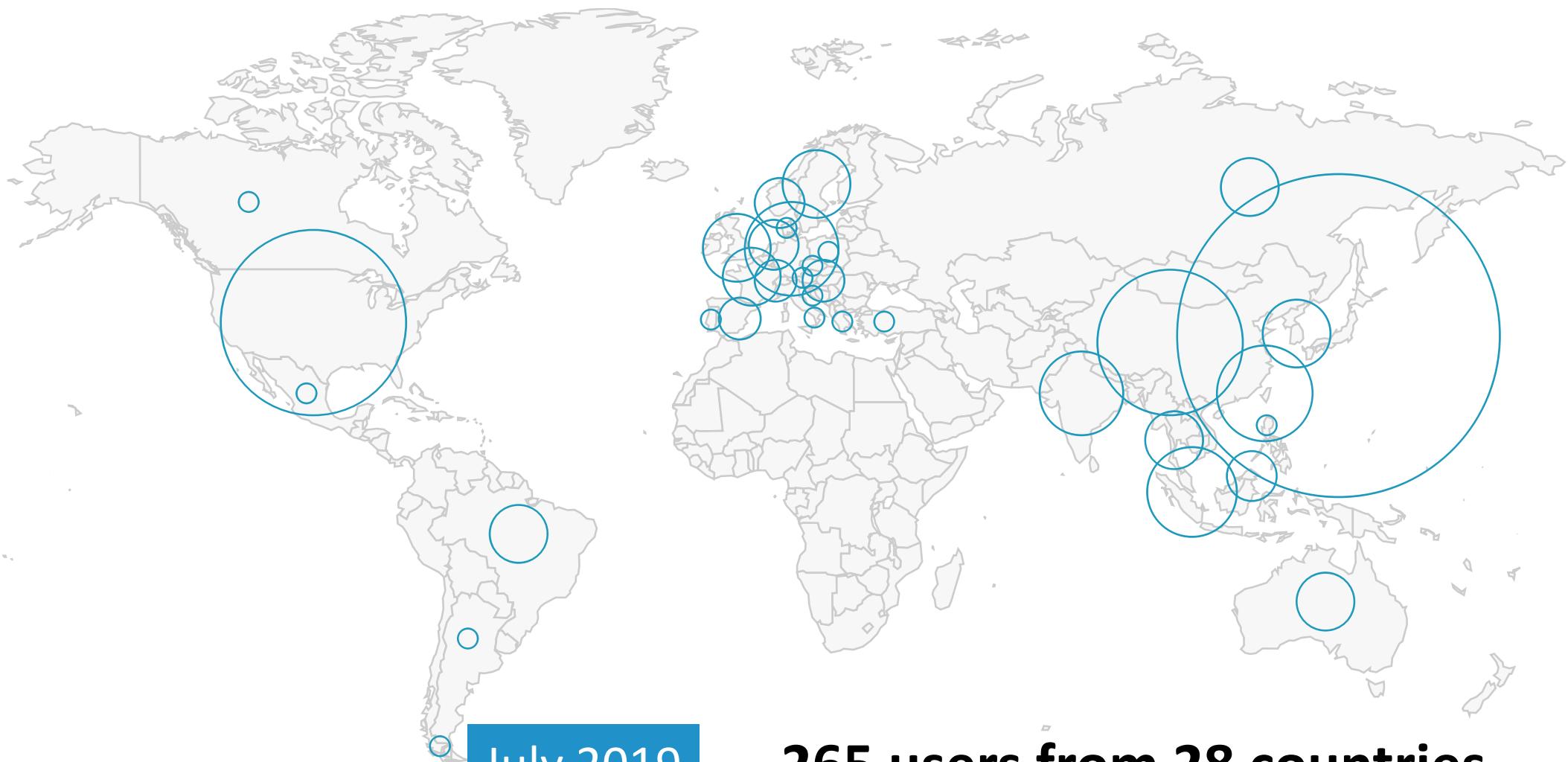
**1170
(2022-01)**



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.

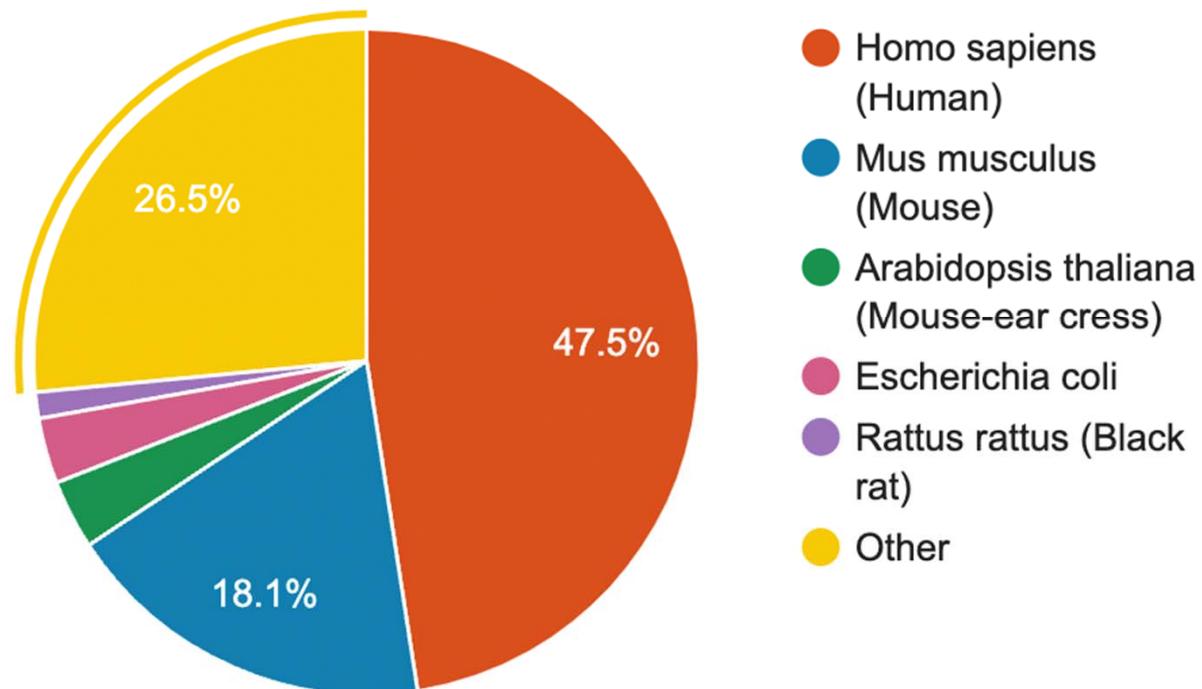
126 species.

Sep 2021

1170 projects are registered. 749 are opened.

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187 species.



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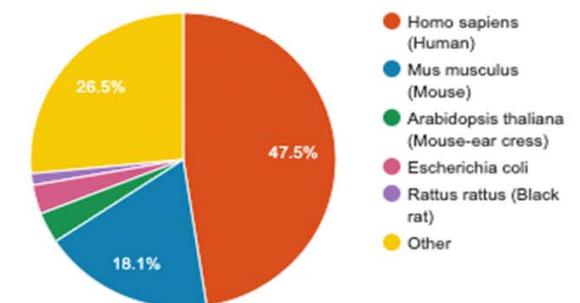
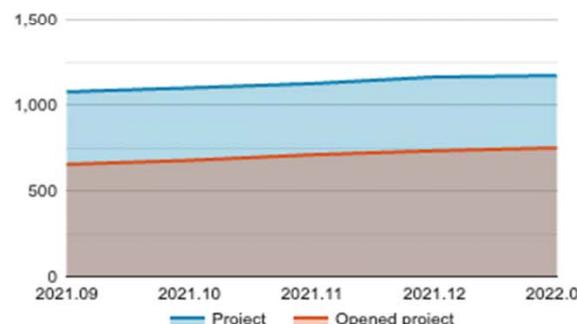
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jPOST repository

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Data

Data list

Free word
 Ontology keyword

phospho

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

JPST 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
JPST001237	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
JPST001437	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
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							Takeshi Tomonaga National Institute of		Detail page	



National Library of Medicine
National Center for Biotechnology Information

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

FULL TEXT LINKS



PMC Full text

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

Chiaki Akifumi 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](https://doi.org/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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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

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.r aw 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.r aw 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.r aw 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)

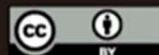


<https://www.youtube.com/watch?v=qXBFfzsCbBs>

TOGO TV

Proteomeデータリポジトリ、
jPOSTrepoにデータを登録する

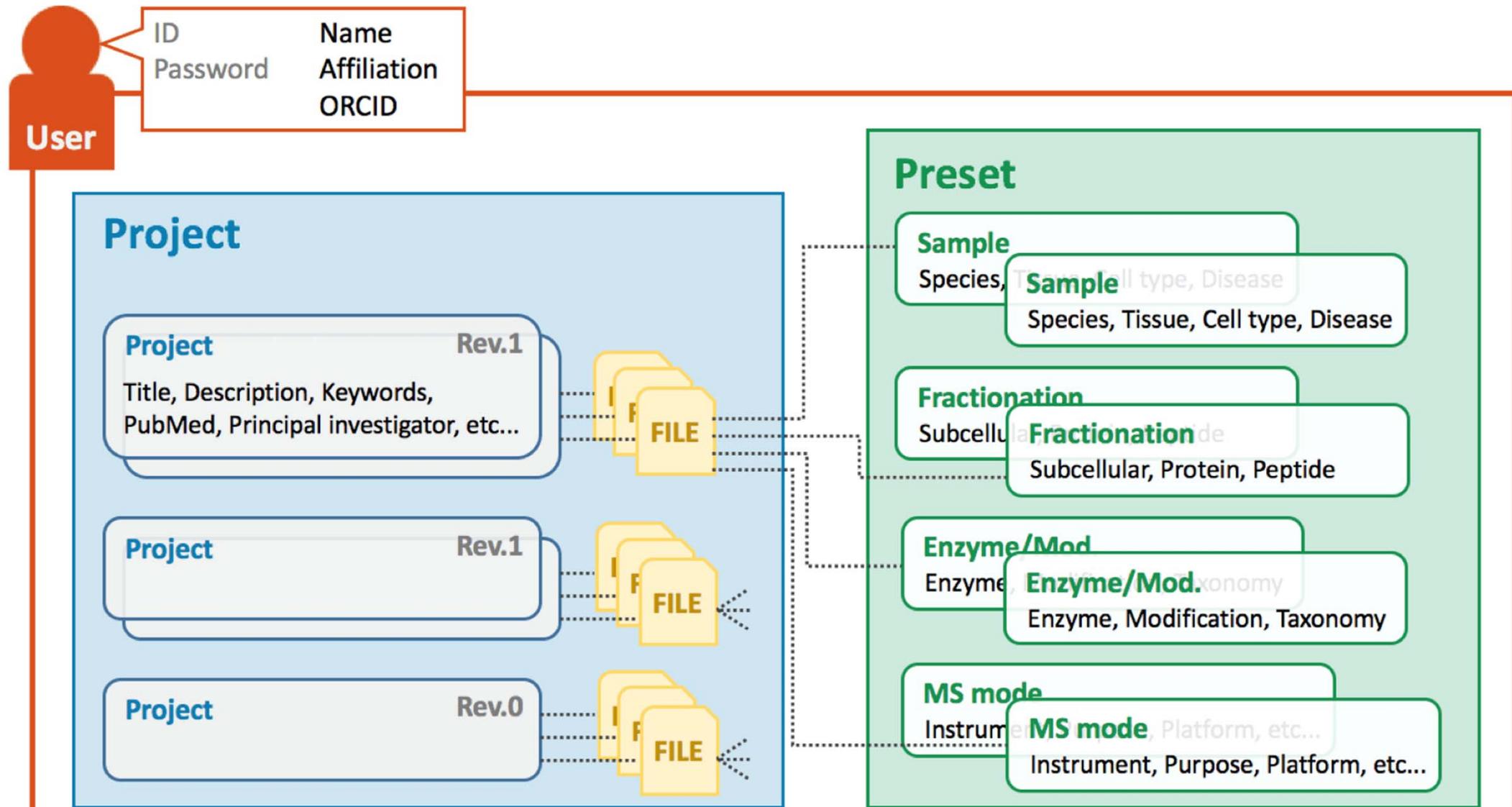
180901版



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。



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: vendor 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。

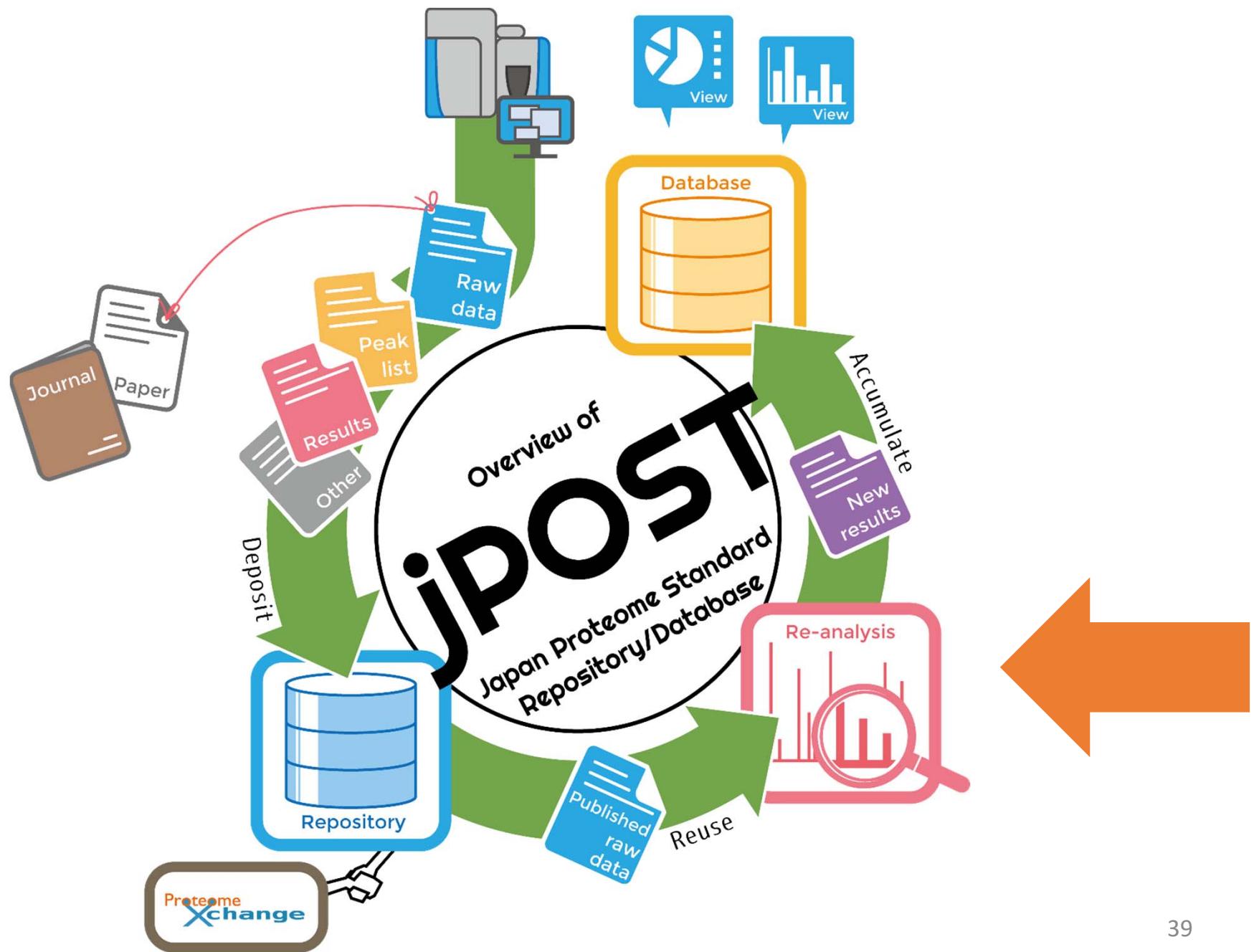
Partial submission

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)

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](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
2. 再解析により、データの統一化が実現される

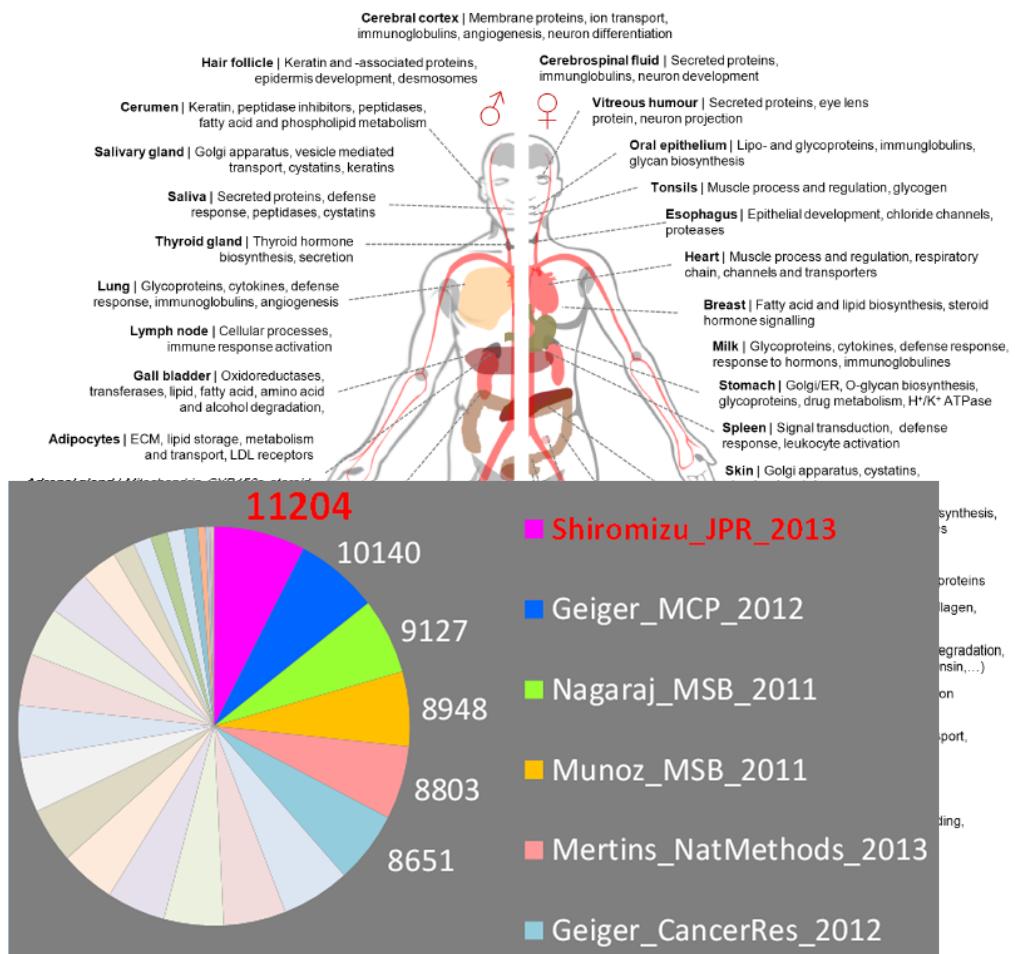
Human Proteome Project (HPP) : large scale MS data

582 | NATURE | VOL 509 | 29 MAY 2014

ARTICLE

doi:10.1038/nature13319

Mass-spectrometry-based draft of the human proteome



HPP
(2010, HUPO)

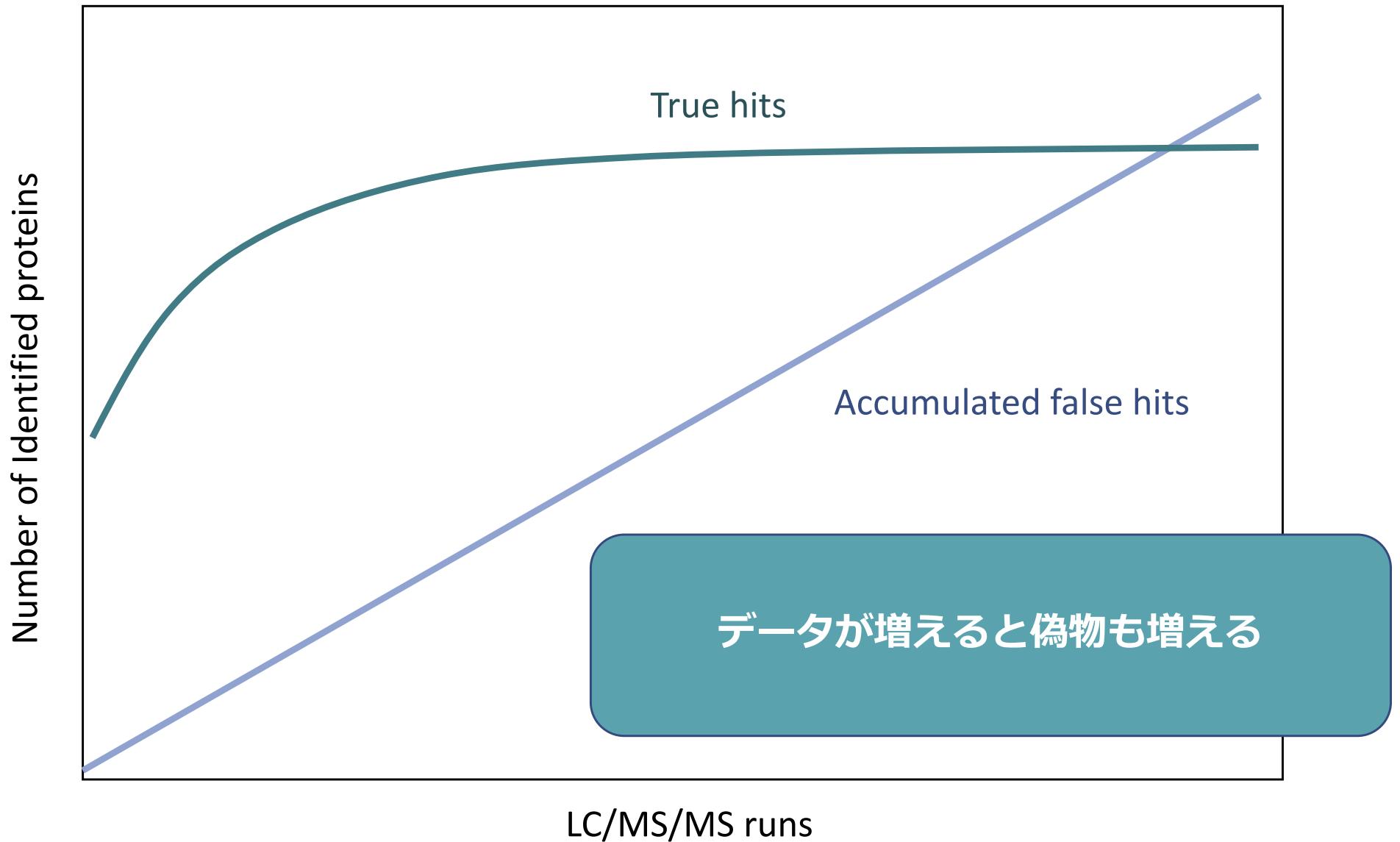
LC/MS/MS analysis: >17,000 times

Proteome data collection

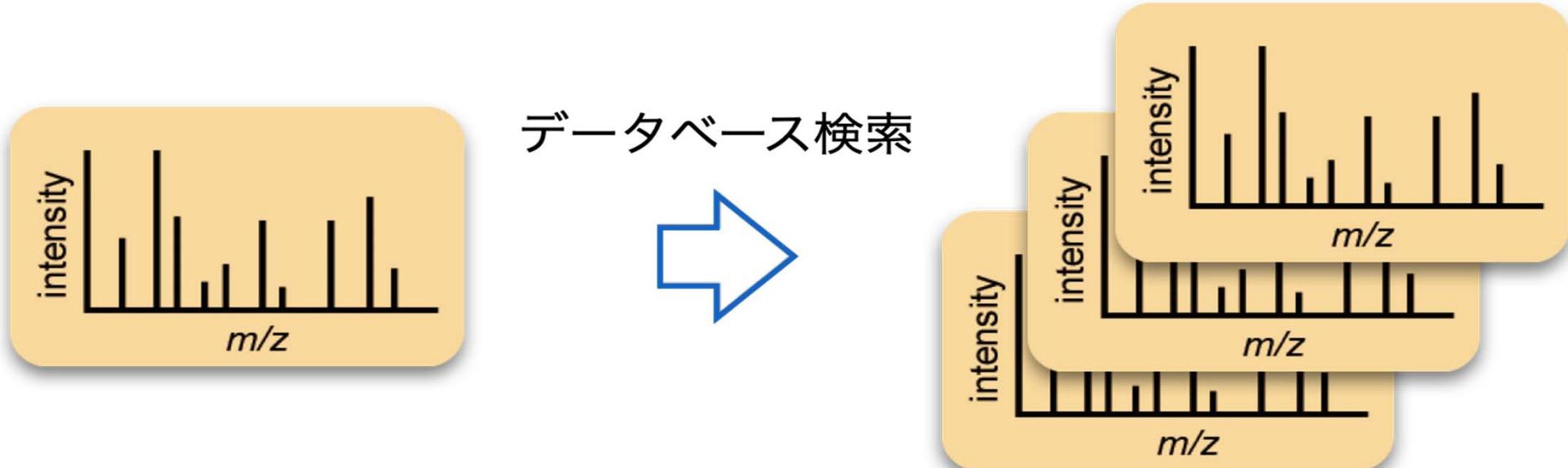
Human proteome map draft
(2014, Nature)

- 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



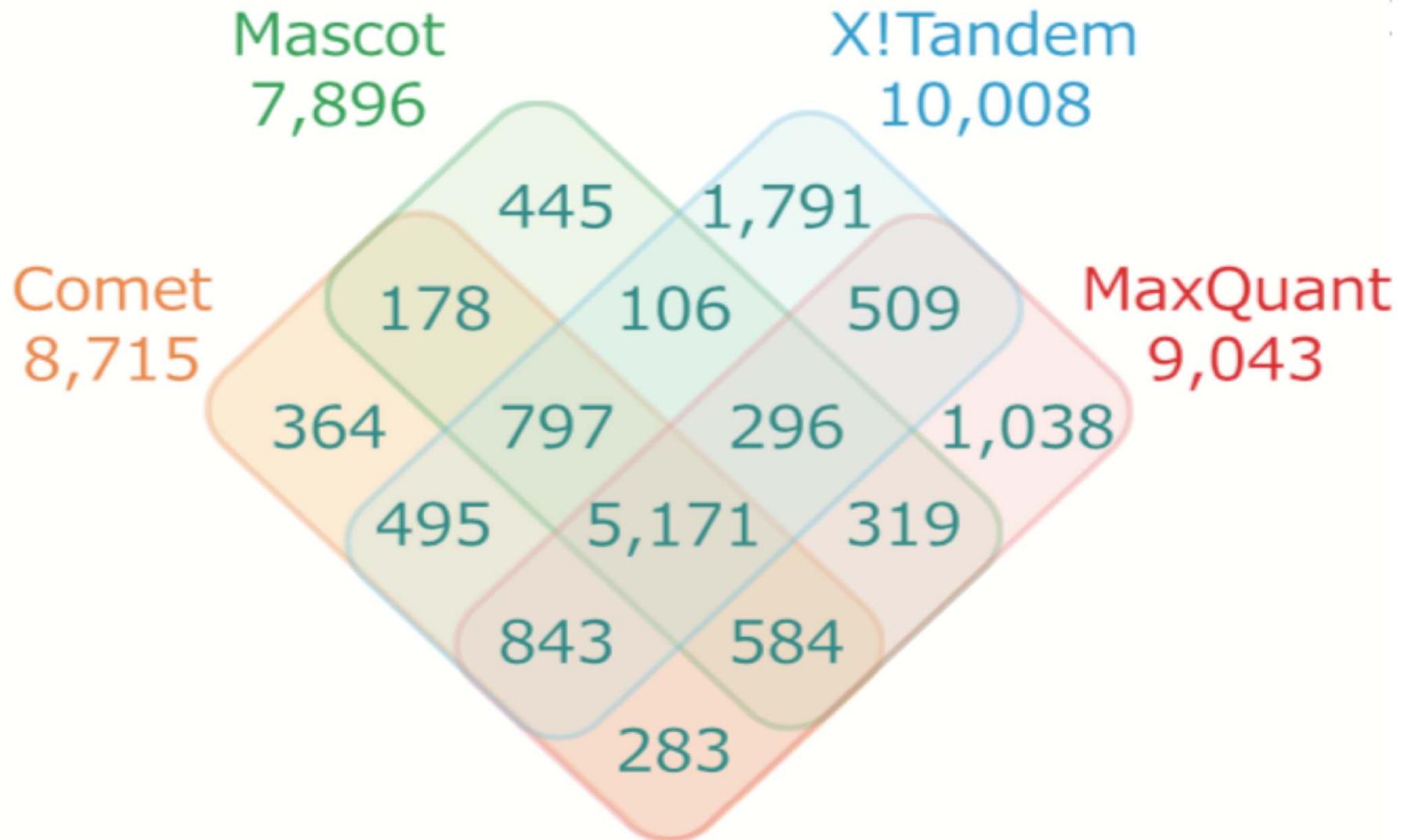
MSから出たピークリスト

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

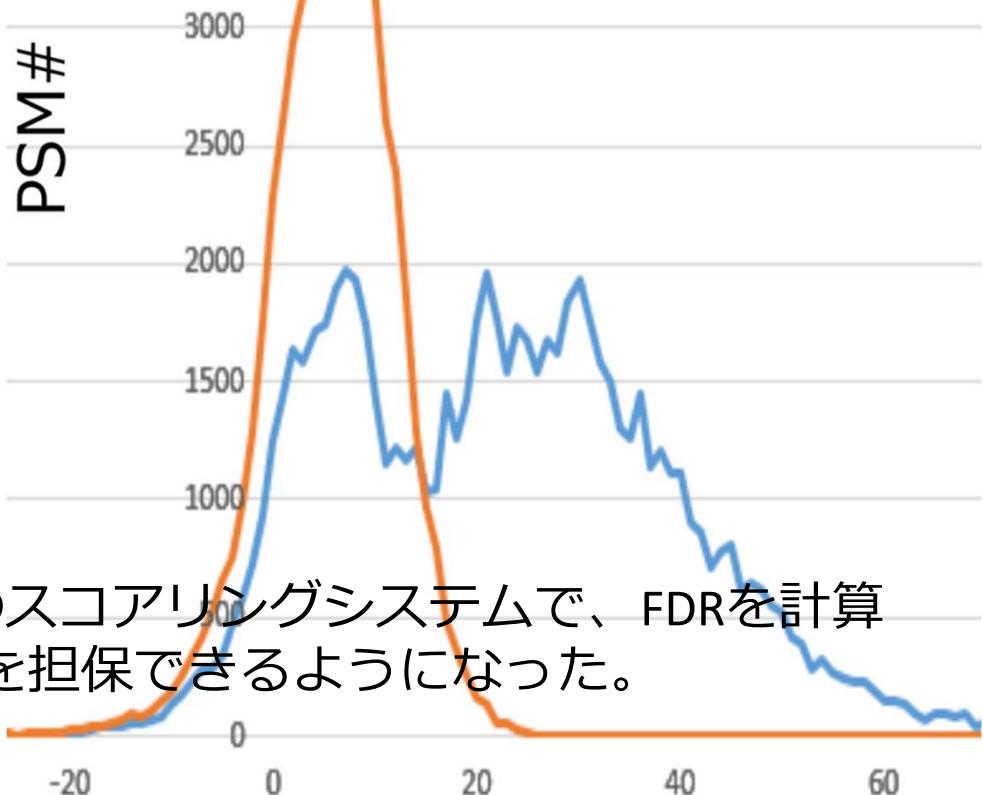


- 新規のスコアリングシステムのもとで、FDRを計算することで、信頼性を担保

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

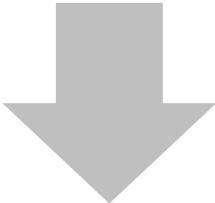
b-ion, y-ion が連続して検出できていれば高スコア

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て、実際のTarget検索での偽陽性の混入率、FDRを評価している。



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。

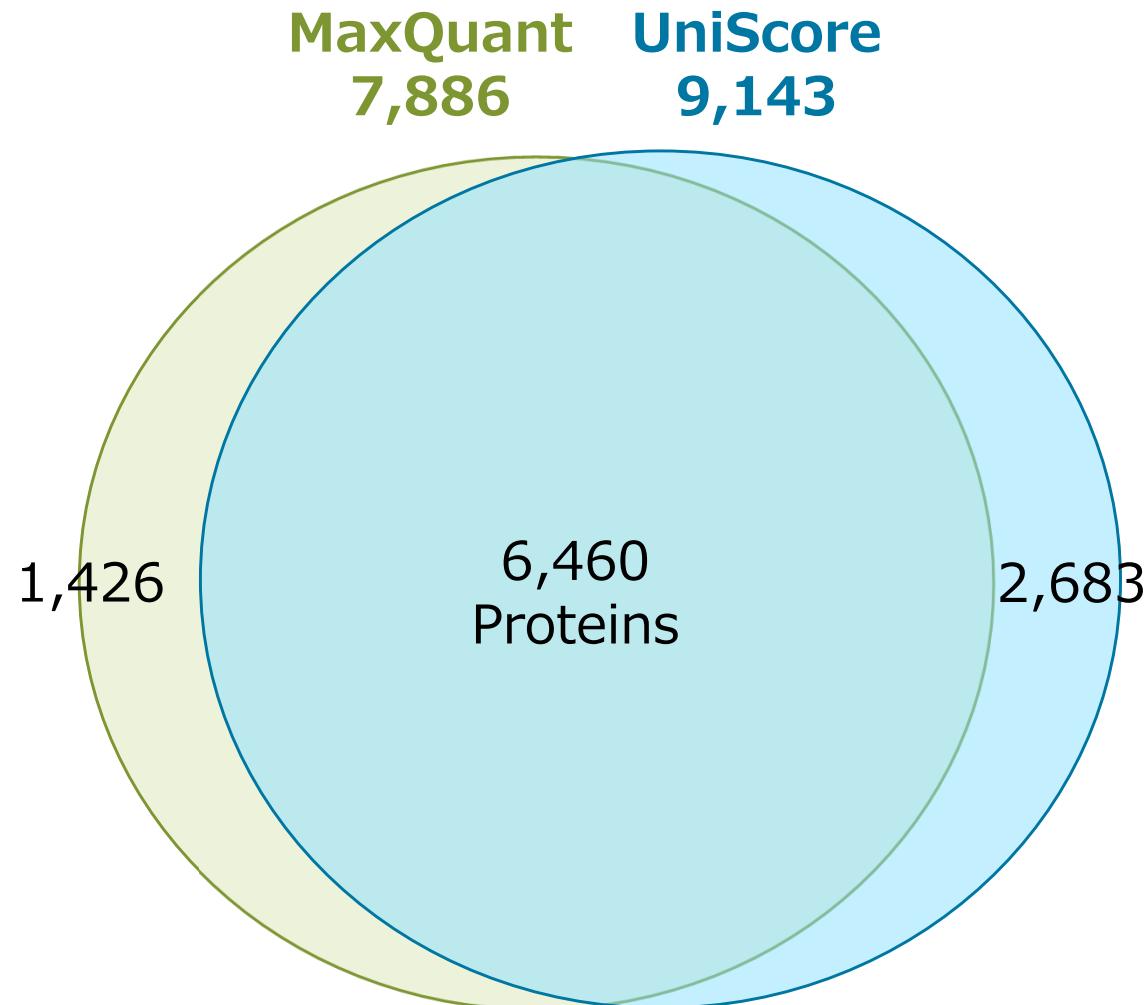
How can we merge the results
from different sources?



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)



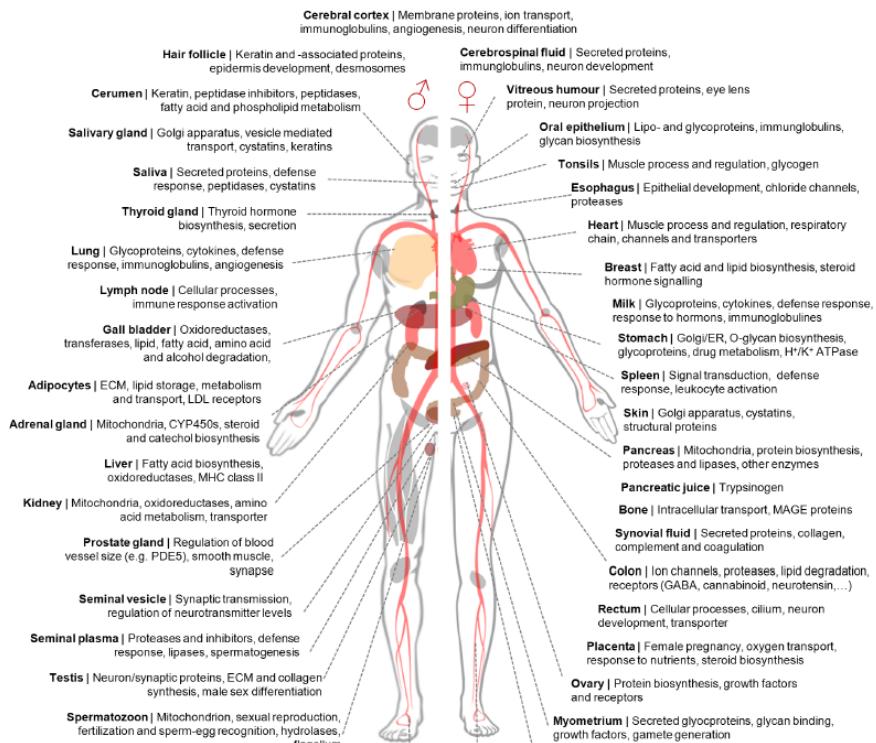
Dataset:JPST000203 – 206
Colorectal cancer samples (used in Wilhelm et al Nature 2014)

Re-analysis : Human Proteome 1st Draft

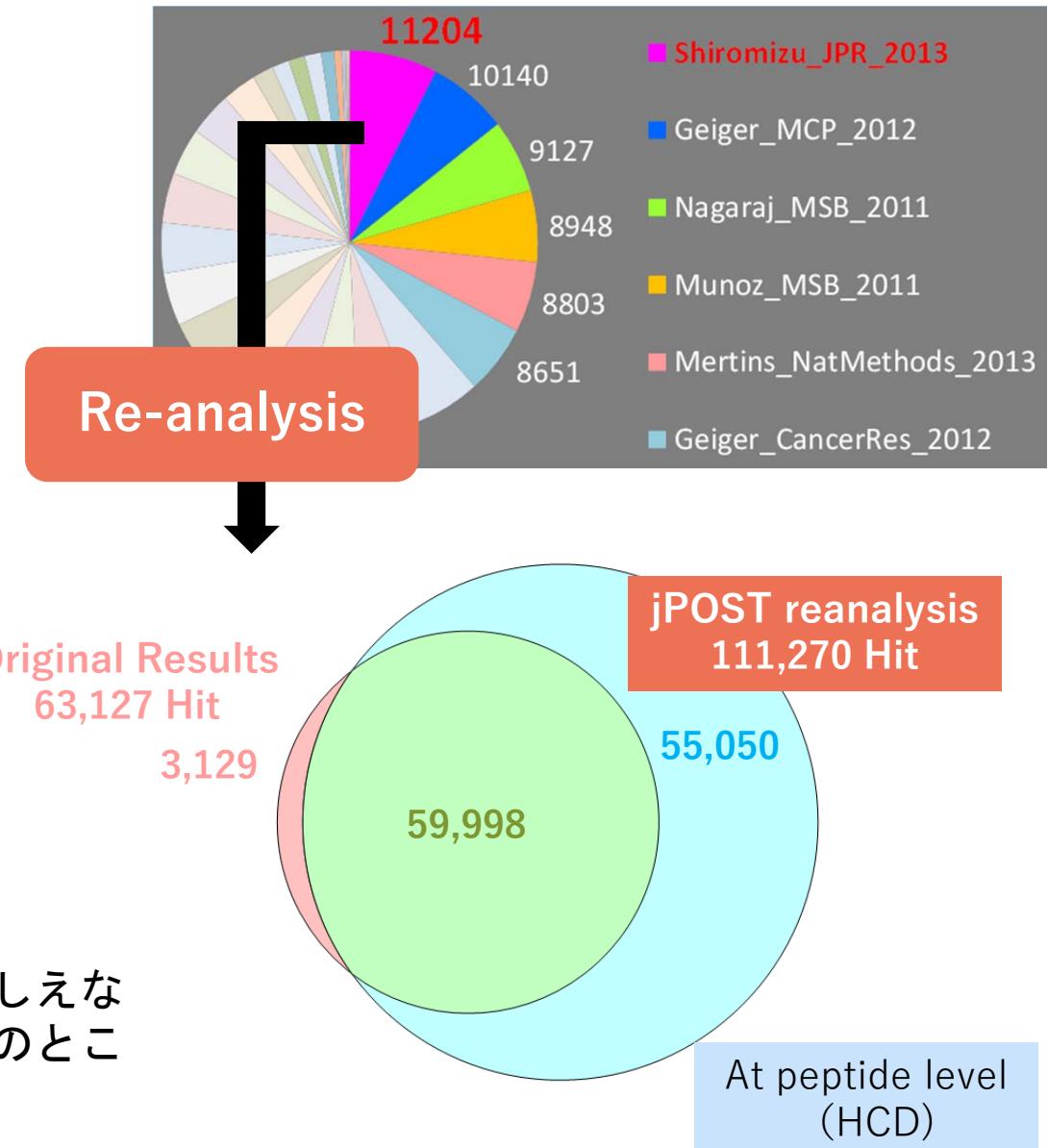
582 | NATURE | VOL 509 | 29 MAY 2014

ARTICLE

Mass-spectrometry-based draft of the human proteome



10447 raw files from Proteome Xchange



同定データには実際にその組織や細胞には存在し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。



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

閲覧のみ

On-going: 40 projects/year

			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)(自安)	jPOSTメタデータ(自動)変換	Interview, マニュアル	Fractionation, 自動後処理	メタデータ作成 Sample	配列データベース作成	フレーザー	サーチテーブルス決定	本サーチ(ピーカビックイング、DBサーチ) - PSM	PSM - ベブチ同定	提出	提出ディレクトリ(SearchResult/Main SearchResult, 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データが混在		
5	JPST000075.1	Q Exactive[MS:1001911]	Homo sapiet	9606	20200318	19	2020/10/01	2020/10/01-			3/18	3/18	3/19					20200331 JPST000791.0 RPXD018465	2020/09/29							
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 JPST000792.0 RPXD018466	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 JPST000793.0 RPXD018467	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 JPST000794.0 RPXD018468	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 sapiet	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 sapiet	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 sapiet	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 sapiet	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 sapiet	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 sapiet	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 sapiet	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 sapiet	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 sapiet	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 sapiet	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 sapiet	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 sapiet	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 sapiet	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 sapiet	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]; Triple1 Arabidopsis thaliana (Mouse-ear		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 sapiet	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 guilliermondii[4929]			8	2020/10/01																			
31	JPST000417.0	Q Exactive[MS:1001911]	Meyeromyza guilliermondii[4929]			8	2020/10/01																			
32	JPST00067.0	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	JPST00081.0	TripleTOF 5600[MS:1000932]	Homo sapiet	9606	20200318	Sciex	10	--	DK	DK	5/5	--	--	--	--	--	3/24	20200323 JPST000810.0 RPXD018484	--	2020/05/06	2020/05/04	iPS				
34	JPST00082.0	TripleTOF 5600[MS:1000932]	Homo sapiet	9606	20200318	Sciex	10	--	DK	DK	5/5	--	--	--	--	--	3/24	20200323 JPST000811.0 RPXD018485	--	2020/05/06	2020/05/04	iPS				
35	JPST00083.0	TripleTOF 5600[MS:1000932]	Homo sapiet	9606	20200318	Sciex	10	--	DK	DK	5/5	--	--	--	--	--	3/24	20200323 JPST000812.0 RPXD018486	--	2020/05/06	2020/05/04	iPS				
36	JPST00085.0	TripleTOF 5600[MS:1000932]	Homo sapiet	9606	20200318	Sciex	9	--	DK	DK	5/5	--	--	--	--	--	3/24	20200323 JPST000813.0 RPXD018487	--	2020/05/06	2020/05/04	iPS				
37	JPST00086.0	TripleTOF 5600[MS:1000932]	Homo sapiet	9606	20200318	Sciex	9	--	DK	DK	5/5	--	--	--	--	--	3/24	20200323 JPST000814.0 RPXD018488	--	2020/05/06	2020/05/04	iPS				
38	JPST00087.0	TripleTOF 5600[MS:1000932]	Homo sapiet	9606	20200318	Sciex	10	--	DK	DK	5/5	--	--	--	--	--	3/24	20200323 JPST000815.0 RPXD018489	--	2020/05/06	2020/05/04	iPS				
39	JPST00088.0	TripleTOF 5600[MS:1000932]	Homo sapiet	9606	20200318	Sciex	9	--	DK	DK	5/5	--	--	--	--	--	3/24	20200323 JPST000816.0 RPXD018490	--	2020/05/06	2020/05/04	iPS				
40	JPST00089.0	TripleTOF 5600[MS:1000932]	Homo sapiet	9606	20200318	Sciex	10	--	DK	DK	5/5	--	--	--	--	--	3/24	20200323 JPST000817.0 RPXD018491	--	2020/05/06	2020/05/04	iPS				
41	JPST00099.0	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	20201002 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 JPST000819.0 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 JPST000819.0 RPXD018469	2020/10/01							
44	JPST000144.0	QSTAR[MS:1000190]	Mus musculus	10090	20200318	TRAp4plex	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 sapiet	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 sapiet	9606	20200318	Sciex																				

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



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



The jPOST logo is a red circle containing the word "jPOST" in white, with a blue dot above the "j". Below the logo is the text "Repository / Database".

Japan Proteome Standard Repository/Database

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

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

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Recent posts

other **jPOST member's co-authored paper about USI has been published.** 2021-06-30 jpost
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event **JCompMS 6th workshop** 2021-05-26 jpost
Workshop details in Japanese

other **jPOST database and repository will**

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

jPOST customizable database 'Slice'



jPOSTの特徴

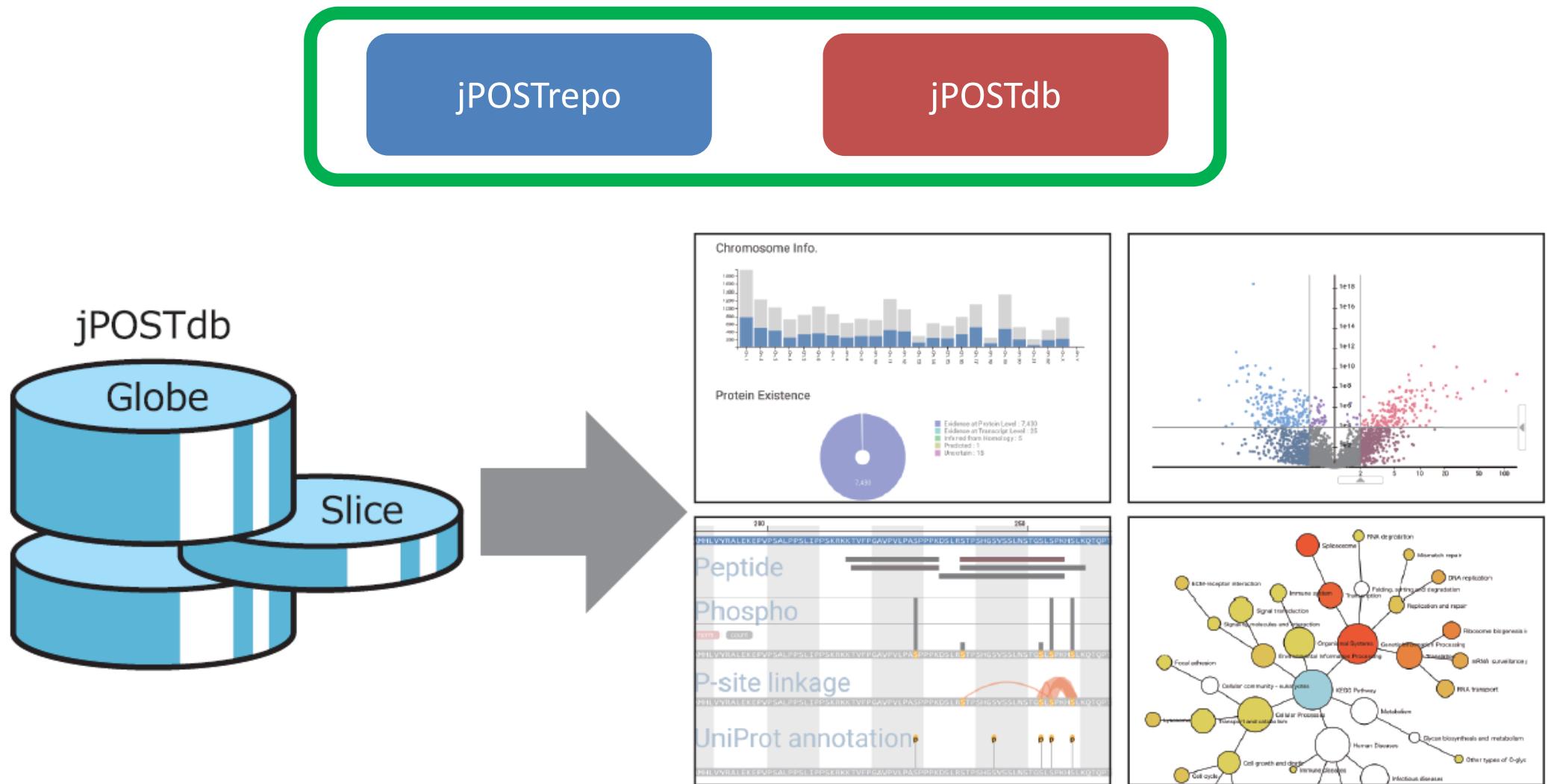


1. フレッシュなデータがどんどん勝手にたまる
2. 再解析により、データの統一化が実現される
3. カスタムDBの作成ツールと可視化ツールの提供

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



<https://jpostdb.org>

→ C https://jpostdb.org



Japan Proteome Standard Repository/Database

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Help

A guide to using the jPOST resources.

jPOST Database

・特徴

The screenshot shows the jPOST Database interface. At the top left is the logo "jPOST DATABASE Repository/Database". To the right are two buttons: "Search" with a magnifying glass icon and "Slice" with a bar chart icon. Below these are three dropdown filters: "Species", "Sample type", and "Cell line", each with a corresponding input field. A "+" button is located next to the "Cell line" filter. Below the filters are three donut charts: "species" (64.1% purple, 24.3% teal, 11.6% yellow), "sample type" (68.4% purple, 17.9% teal, 3.7% yellow), and "cell line" (37.8% purple, 26.7% teal, 8.9% green, 6.7% yellow). At the bottom are tabs for "Dataset (103)" (selected) and "Protein (28573)". A "Keyword" search bar and a "Page size: 10" dropdown are also present.

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	

- ・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

Filters

Species

x Homo sapiens

Tissue

x colon x colorectal cancer cell

Disease

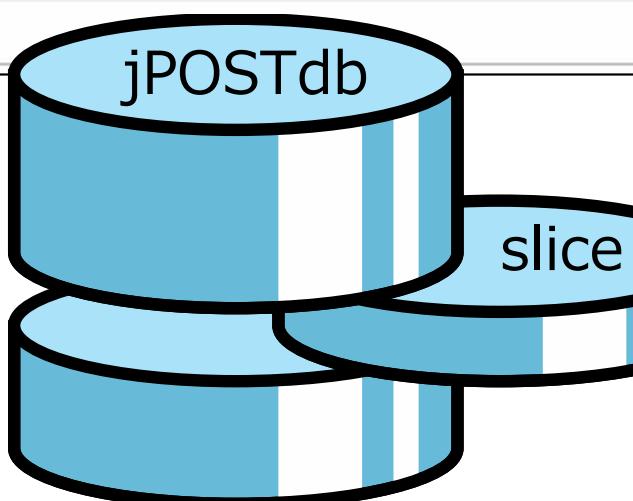
neuroblastoma

breast cancer

carcinoma

adenocarcinoma

Instrument



IPS colon +

Dataset Protein

Showing 1 to 6 of 6 entries

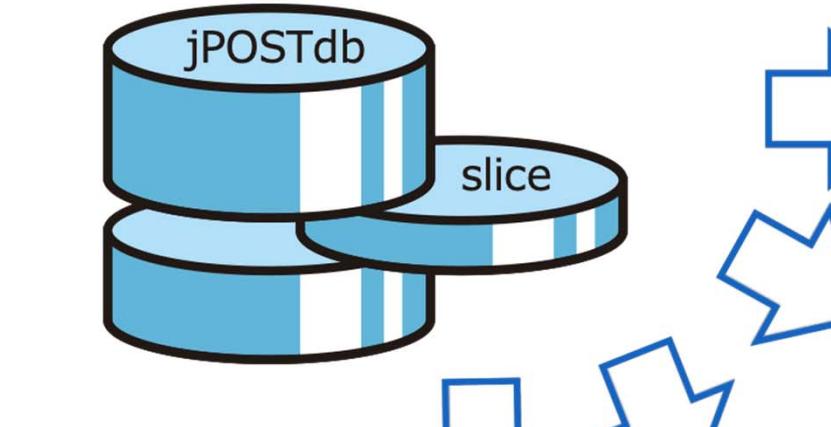
ID	Project ID	Project Title	Project Date
DS203_1	JPST000203	Quantitative proteomics of colorectal cancer tissues	2016-10-18
DS204_1	JPST000204	Quantitative phosphoproteomics of colorectal cancer tissues	2016-10-18
DS205_1	JPST000205	Proteomic data of HCT116 cells	2016-10-18
DS206_1	JPST000206	Phosphoproteomic data of HCT116 cells	2016-10-18
DS210_1	JPST000210	Phosphoproteomics data of colon tissues (tumor and non-tumor)	2016-10-18
DS210_2	JPST000210	Phosphoproteomics data of colon tissues (tumor and non-tumor)	2016-10-18

Show 10⁺ entries

Previous 1 Next

データベース: フィルタリング

jPOST DB 様々な可視化



250
APMLSTVHS~~A~~KNTPSQHSHS~~I~~QHSPERSGSGSVNGSSRYS~~P~~SQNSPIHIPSRRS~~T~~.TIAPOQNAPRDESGRRSSFYPDGGDQETAKTGFLKRF

APMLSTVHS~~A~~KNTPSQHSHS~~I~~QHSPERSGSGSVNGSSRYS~~P~~SQNSPIHIPSRRS~~T~~PAKTIAPQNAPRDESGRRSSFYPDGGDQETAKTGFLKRF

APMLSTVHS~~A~~KNTPSQHSHS~~I~~QHSPERSGSGSVNGSSRYS~~P~~SQNSPIHIPSRRS~~T~~PAKTIAPQNAPRDESGRRSSFYPDGGDQETAKTGFLKRF

P01112 : GTPase HRas
57 48 38 72 6 3 1 14
31 68 72

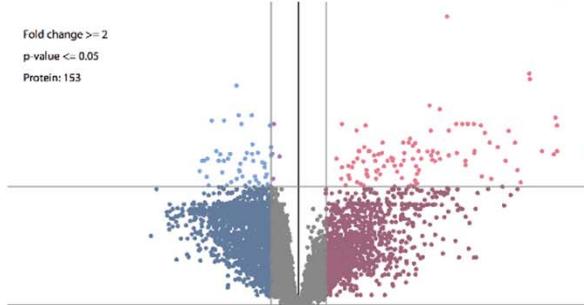
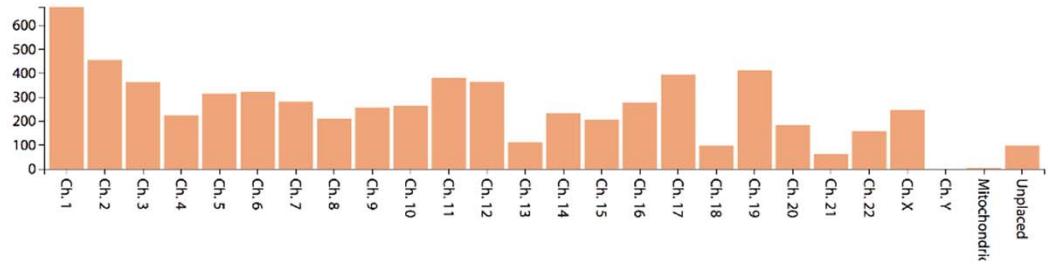
P01116 : GTPase KRas
57 48 72 9 7
68

P01111 : GTPase NRas
57 48 38 31 6 14 90 7 69 1 7 69
31 68 72

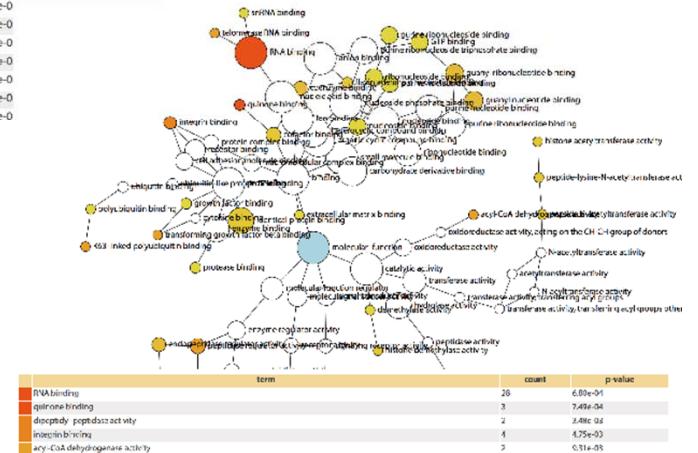
P61224 : Ras-related protein Rap-1b
95 48 23 1 88 7 55 18 24 144 133 3
139 72 1 12 1 5 21 60 2

P62834 : Ras-related protein Rap-1A
95 48 139 72 88 4 3 14 21 60 2 18 24 41 133

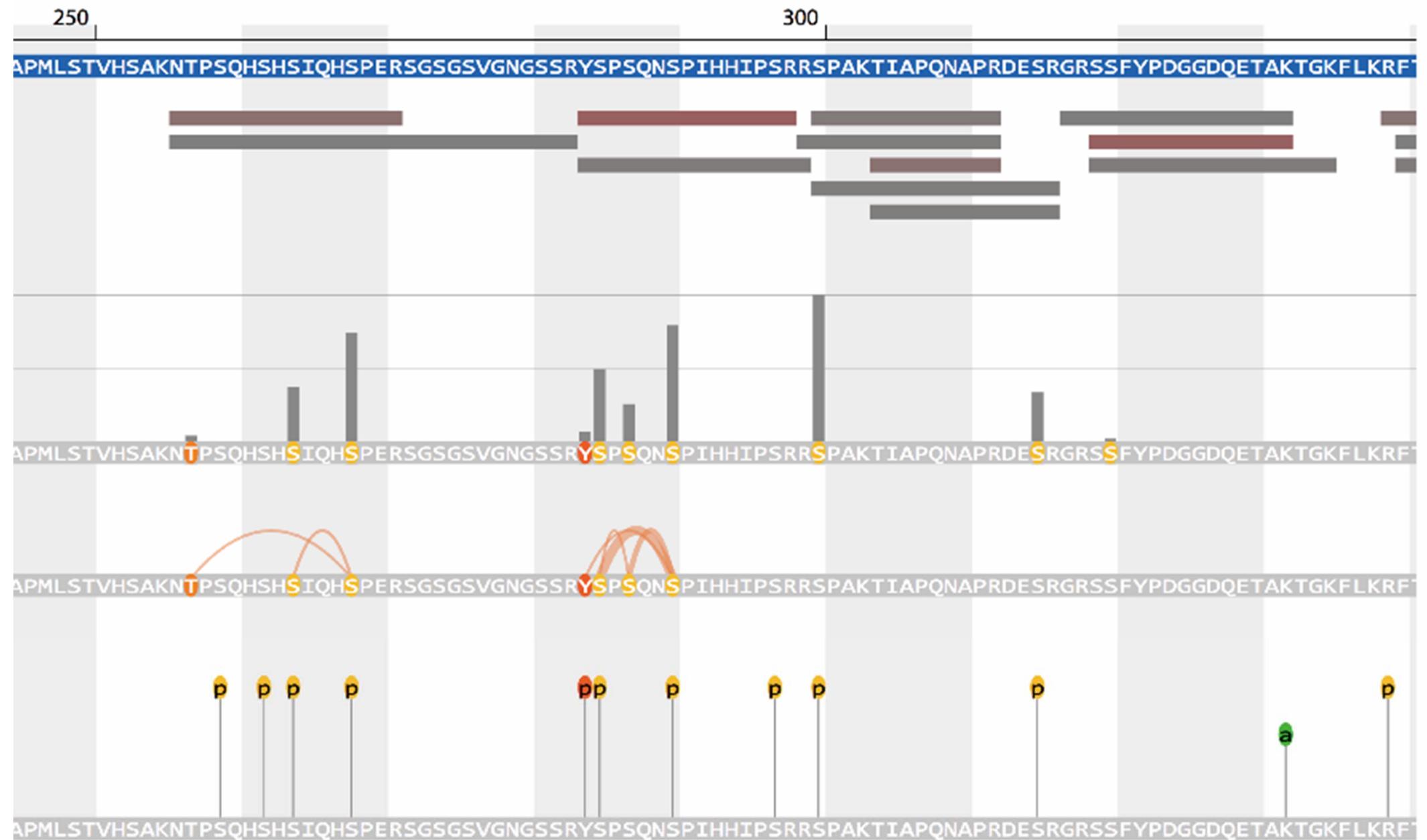
name color trypsin exon guide edit



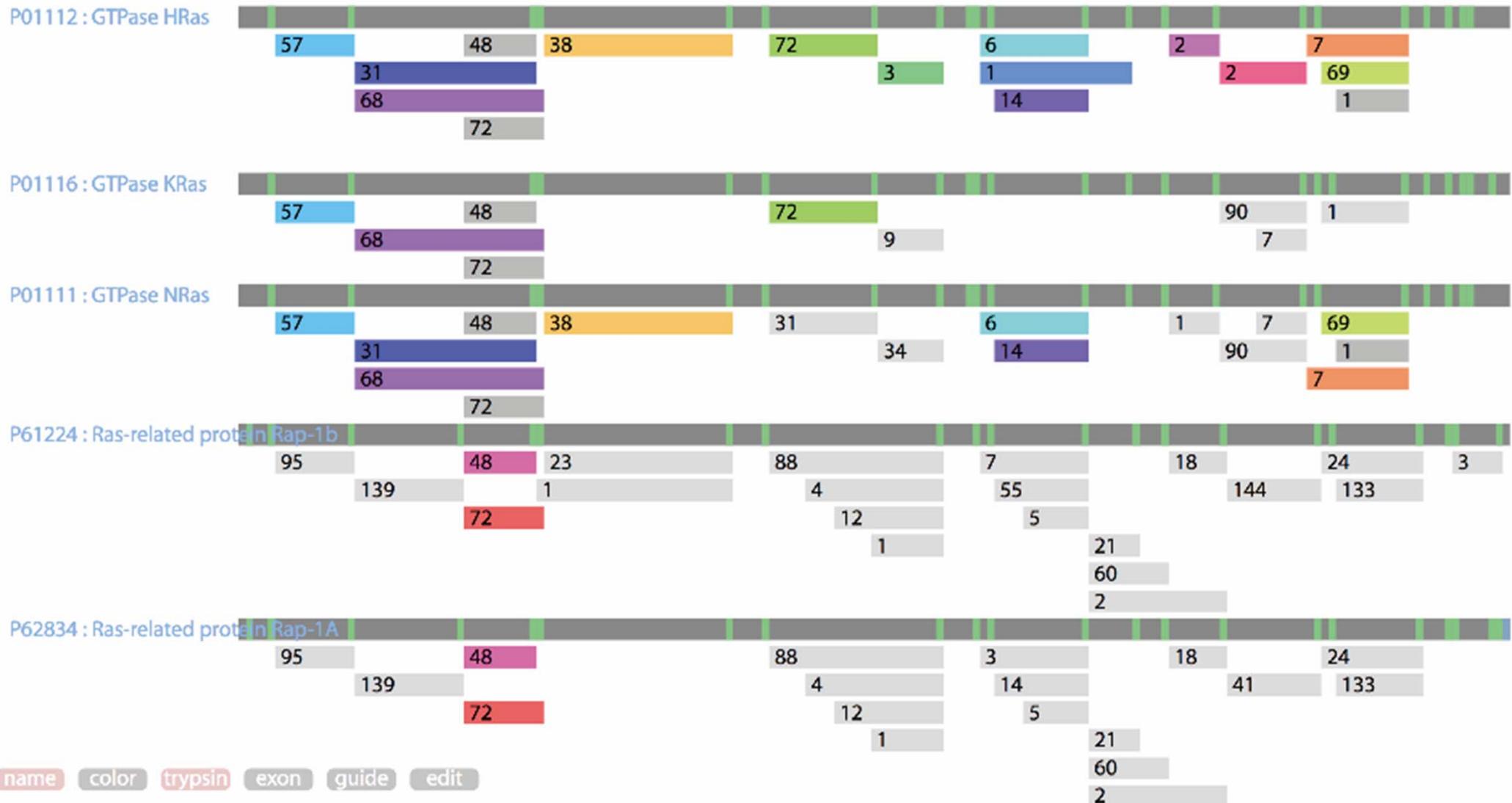
UniProt ID	log2FC	p-value
P02751	10.6	2.14e-0
Q14764	9.41	1.08e-0
P24821	9.41	2.06e-0
Q9NZM1	9.35	8.88e-0
P12111	9.29	2.23e-0
Q6YHK3	8.86	2.06e-0
P08473	8.42	3.37e-0



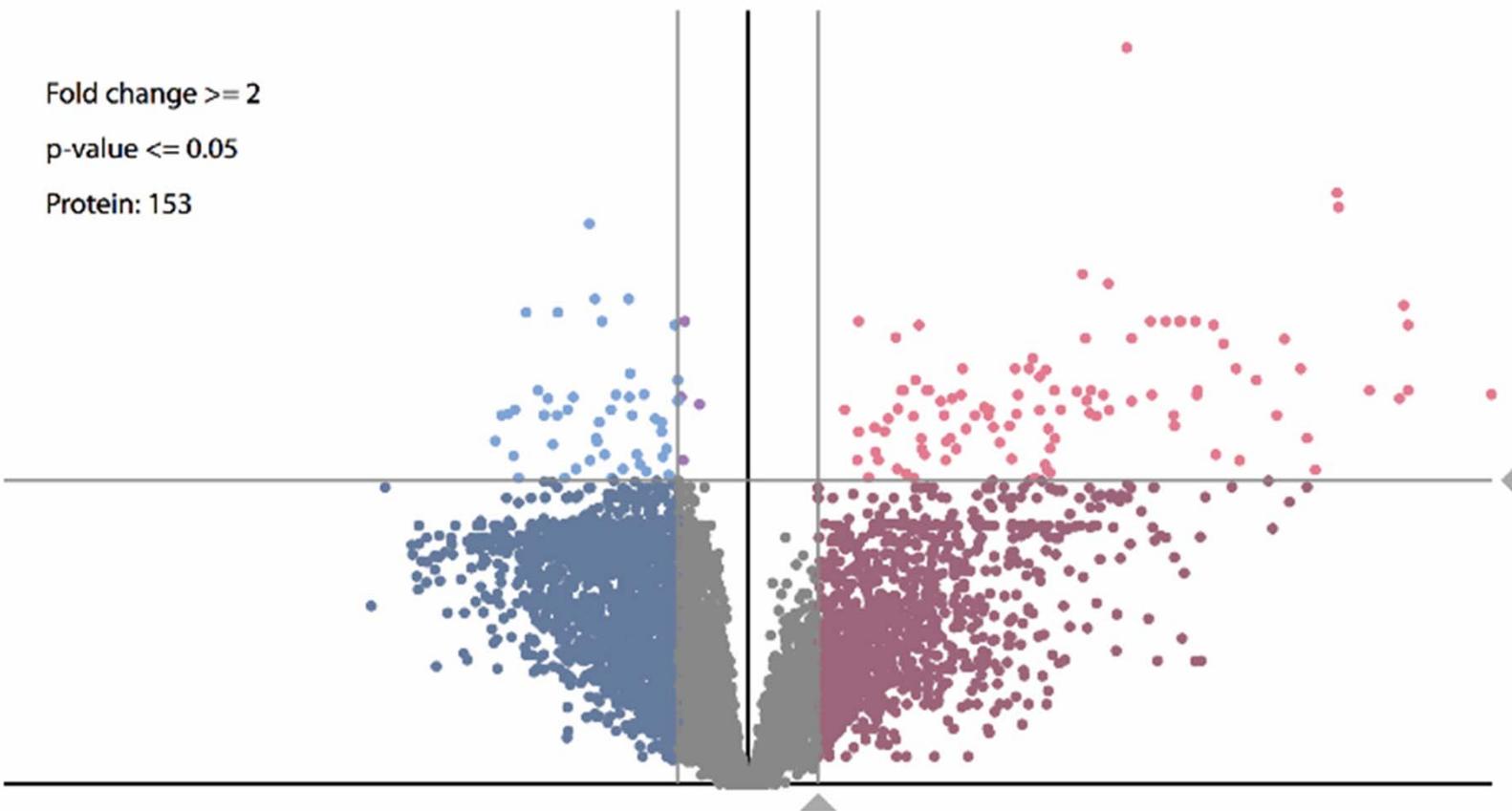
jPOST DB Protein Browser



jPOST DB Peptide Sharing

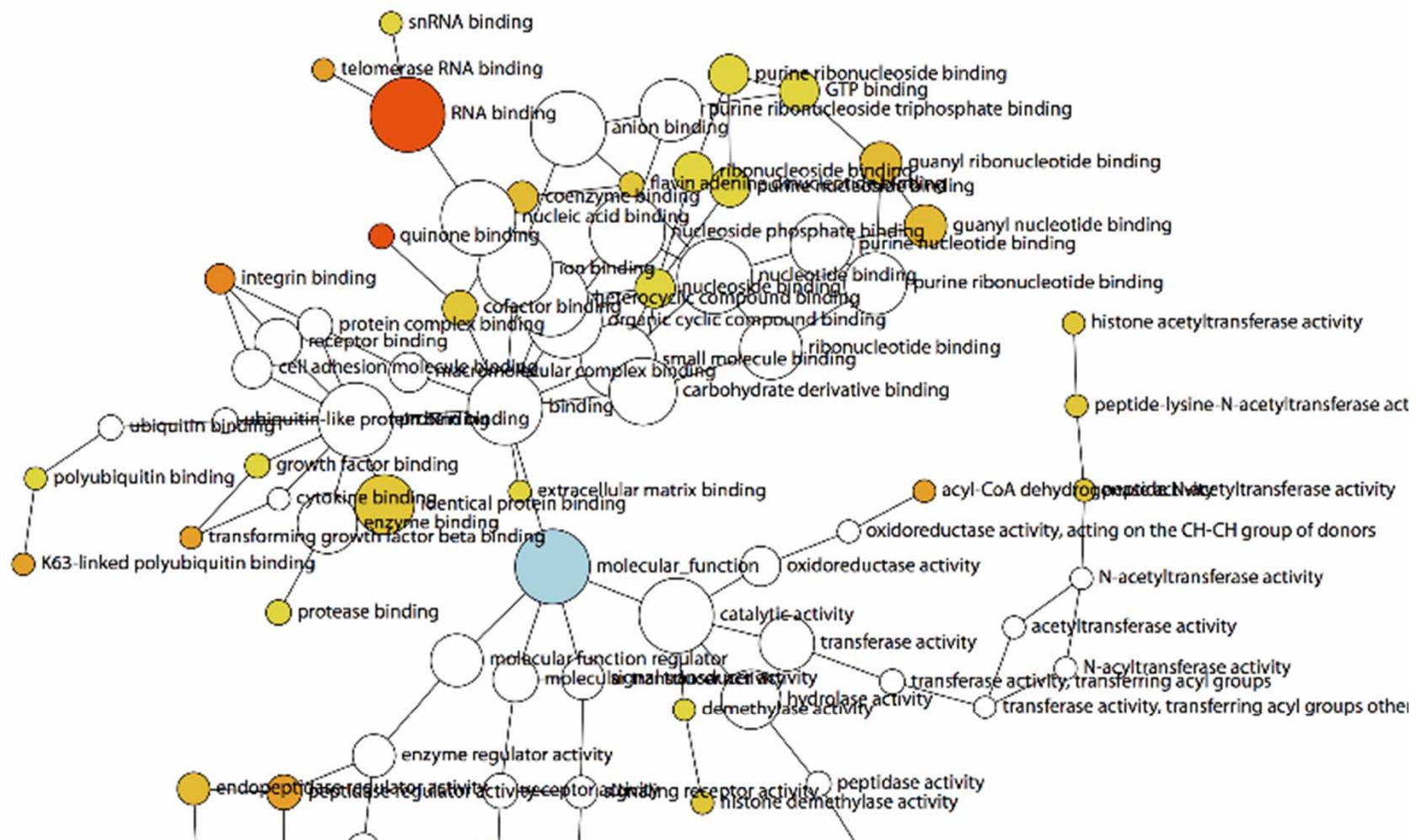


jPOST DB 発現変動解析



	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

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

- Protein | Malate dehydrogenase, cytoplasmic
- Gene | MDH1
- Organism | Homo sapiens (Human)
- Status | Reviewed - Annotation score: 88888 - Experimental evidence at protein level!

Display

Entry

Post-translational modificationⁱ

ISGylated. 1 Publication

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

Keywords - PTMⁱ
Acetylation, Methylation, Phosphoprotein, Ubl conjugation

Proteomic databases

EPD ⁱ	P40925
jPOST ⁱ	P40925
PaxDb ⁱ	P40925
PeptideAtlas ⁱ	P40925
PRIDE ⁱ	P40925
ProteomicsDB ⁱ	55384 55385 [P40925-2]
TopDownProteomics ⁱ	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 MSEPIRVLVITGAQDIAYSLLYSIIQNGSVFGKDDPIILVLLDITPMGMVLDGVLMELODCALPLLKDVIAITDKEDVAFKLDVAILVGSMPRREGMERKDILLKANVKIFKSQGAALDKYAKSVKVIVVGNPANTNCLTASKSAPSIPKENFSCLTRLDHNRAKAQIAALKLGVTANDVKVNTIIMGNHSSTOYPDVNHAKVKGOKEVGVYEAALKDDSWLKGEGFVTTVOORGAVIKARKLSSAMSAAKA1CDHVRIWFGTPEGEFVSMGVISODGNSTYGVPDOLLYSPFPVVNIKNTWKFVEGLPINDFSREKMDLTAKELTEKEESAFEFLSSA

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: Isoform Variant

-- Add view -- ▾

Peptide Sharing

shared in isoforms ▾

P40925

<https://jpostdb.org>

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Japan Proteome Standard Repository/Database

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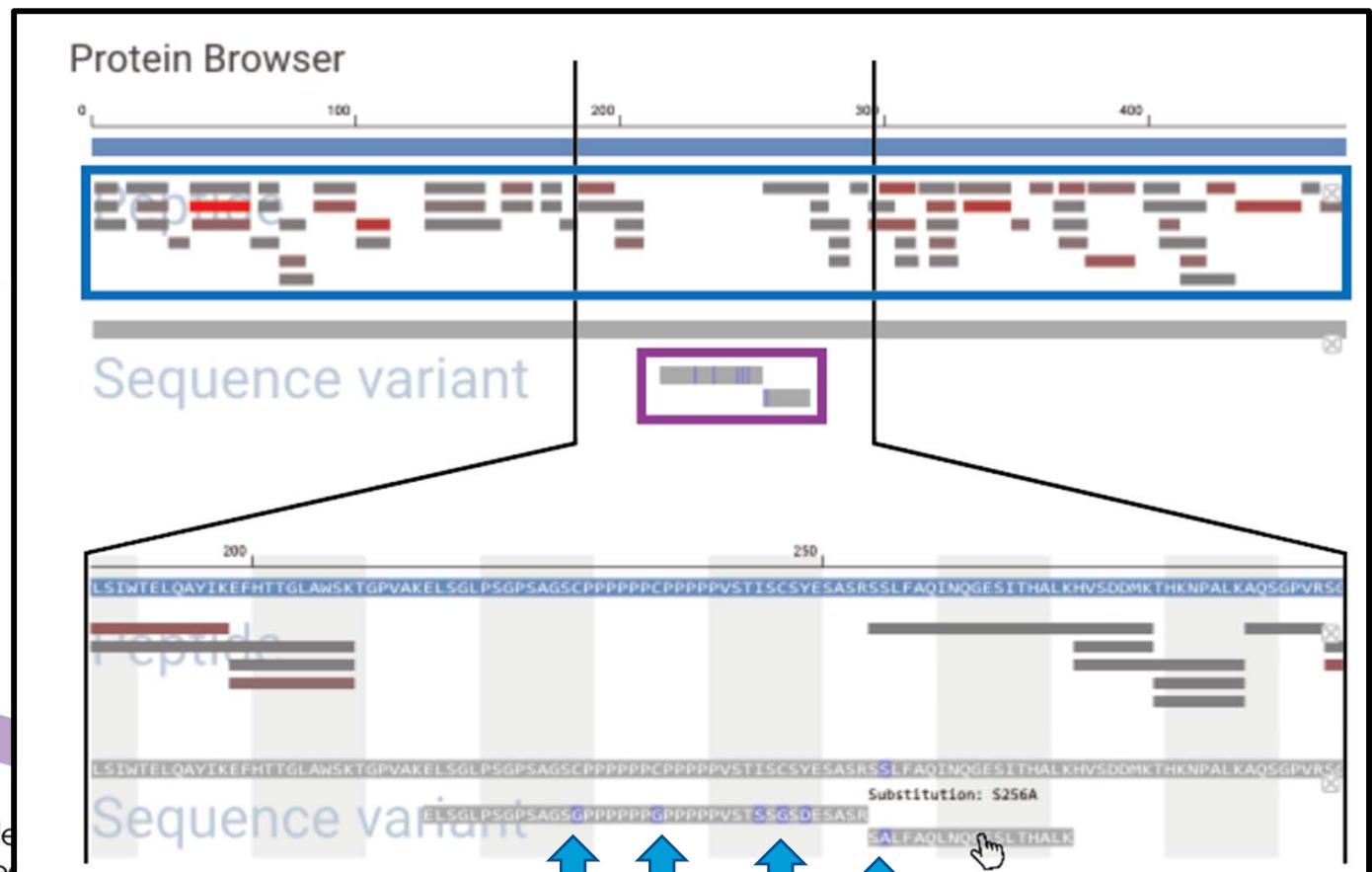
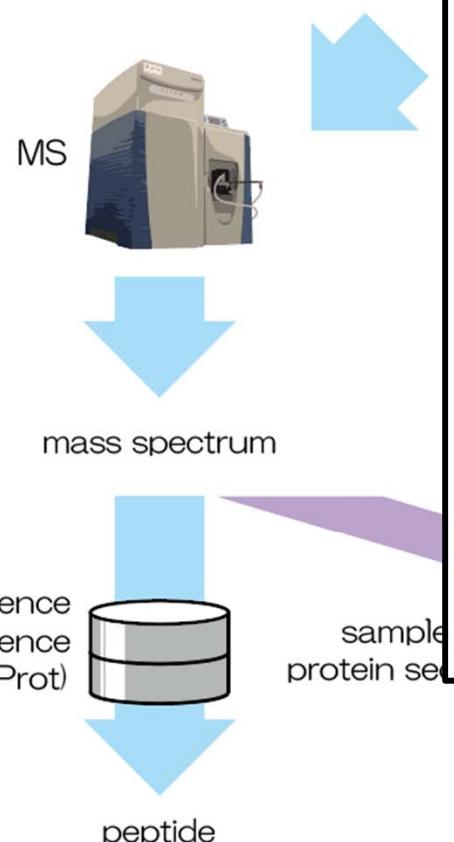
Help

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

Proteomics



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
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Molecular Cell

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

other
jPOST will publish the re-analysed proteome

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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 protein

PXD018804 Extensive proteomic dataset of V

PXD018594 Shotgun proteomics of Vero E6 c

PXD018357 Inhibition of growth factor signa

PXD018117 A SARS-CoV-2-Human Protein-Pro

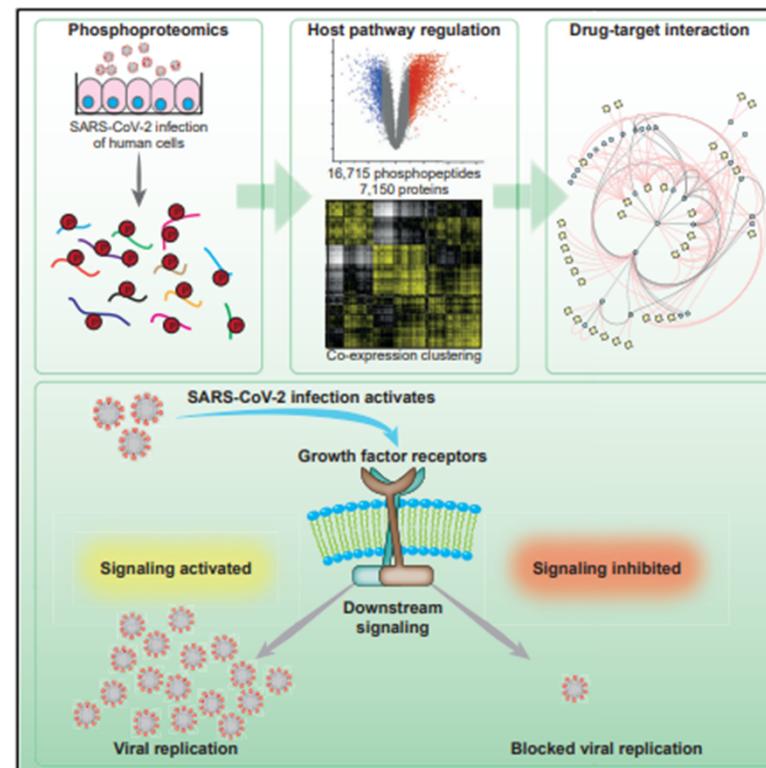
PXD018581 Proteomics of SARS-CoV and SAI

PXD018241 Characterisation of the transcript frame deletion in the spike glycoprotein

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, Tascher G, Ciesek S, Münch C, Cinatl J. (2020) Growth Factor Receptor Signaling Inhibition Prevents SARS-CoV-2 Replication. Molecular Cell, 80(1):164-174.e4(20).	
Keyword List	

Graphical Abstract



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.

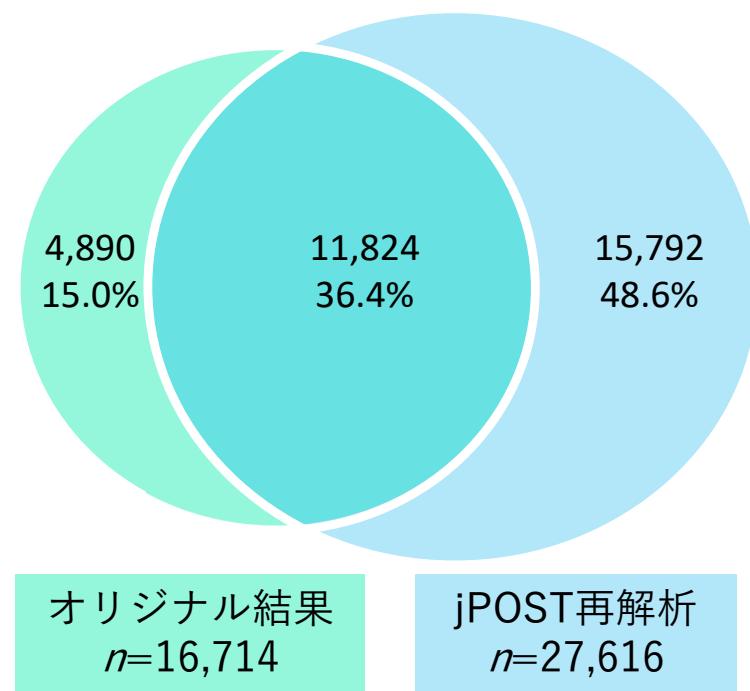
Highlights

- 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

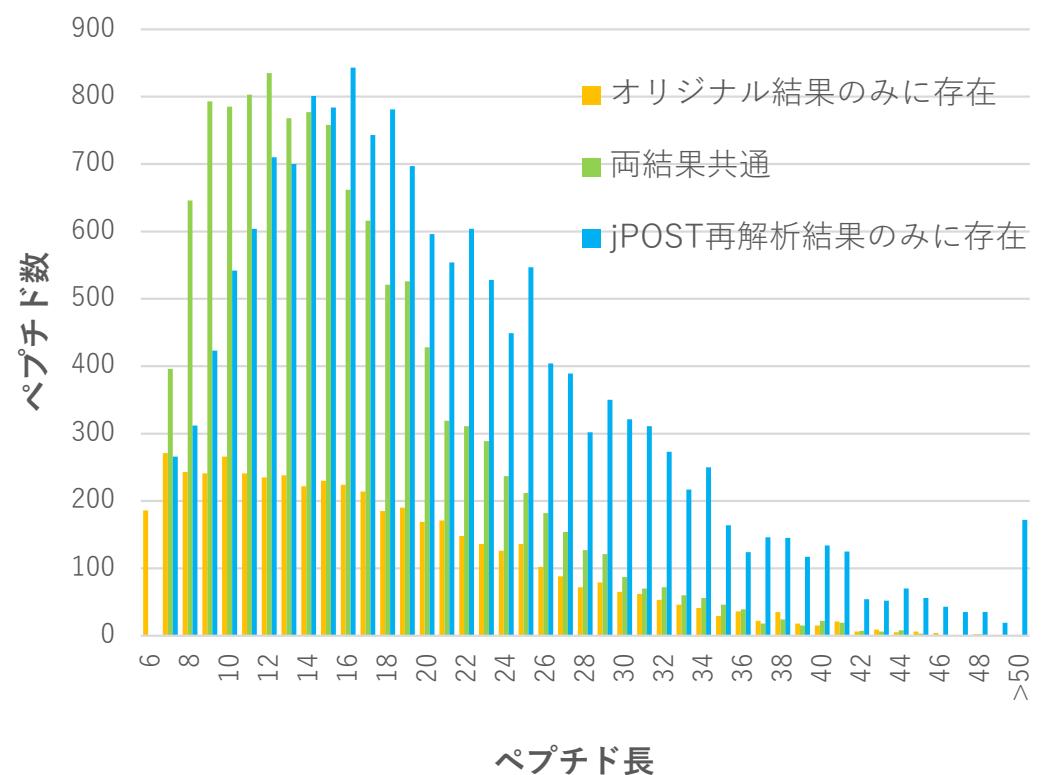
Re-analysis of COVID-19 paper

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

同定リン酸化ペプチド数の比較



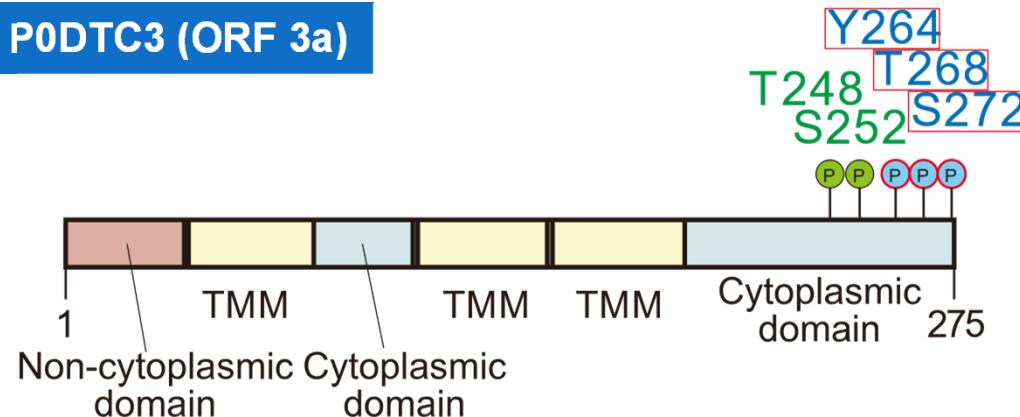
両解析結果のペプチド長ごとの比較



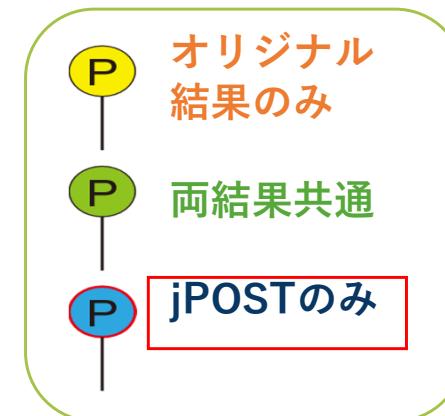
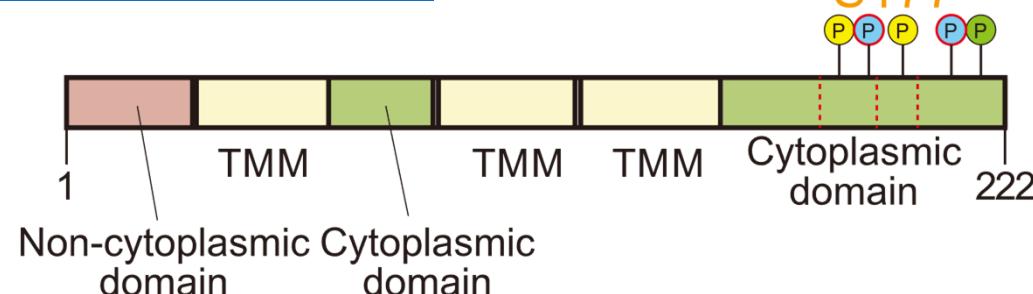
Phosphorylated sites on SARS-CoV-2 proteins

同定されたリン酸化サイトの比較

P0DTc3 (ORF 3a)



P0DTc5 (M) (ORF 5)



T172 vs S173

EITVATSR

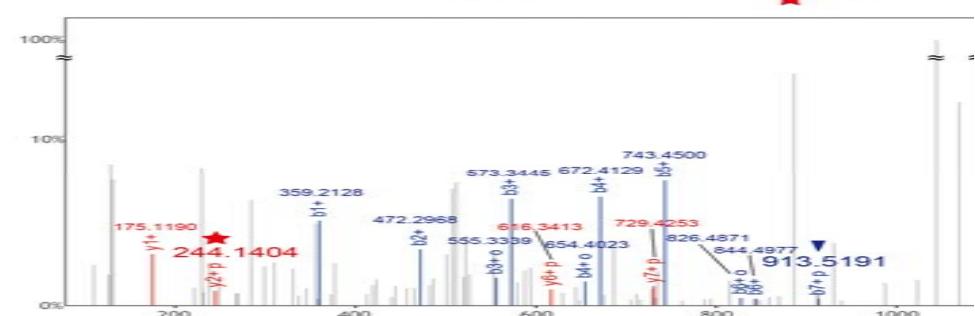
b+	#	Seq	#	y+
359.2128	1	E	8	
472.2968	2	I	7	827.4022
573.3445	3	T	6	714.3182
672.4129	4	V	5	613.2705
743.4500	5	A	4	514.2021
844.4977	6	T	3	443.1650
1011.4960	7	S	2	342.1173
	8	R	1	175.1190

[Click] to move table

Add to N-term: 229.1629

Variable Modifications:

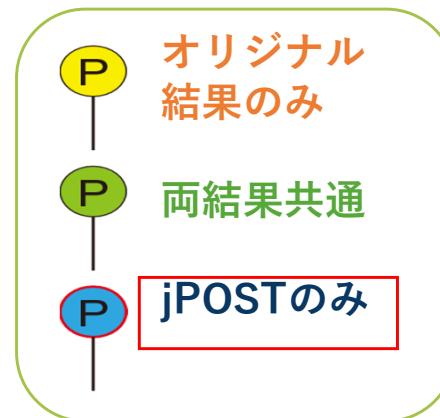
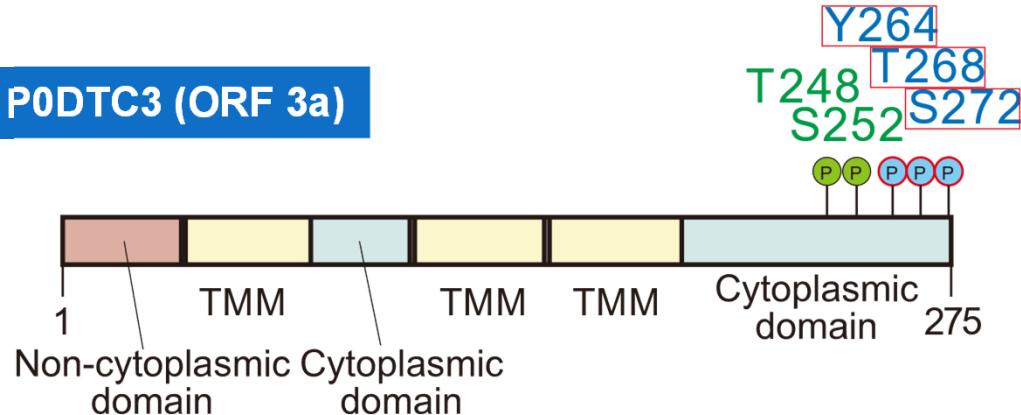
S: 79.9663 [7]



Phosphorylated sites on SARS-CoV-2 proteins

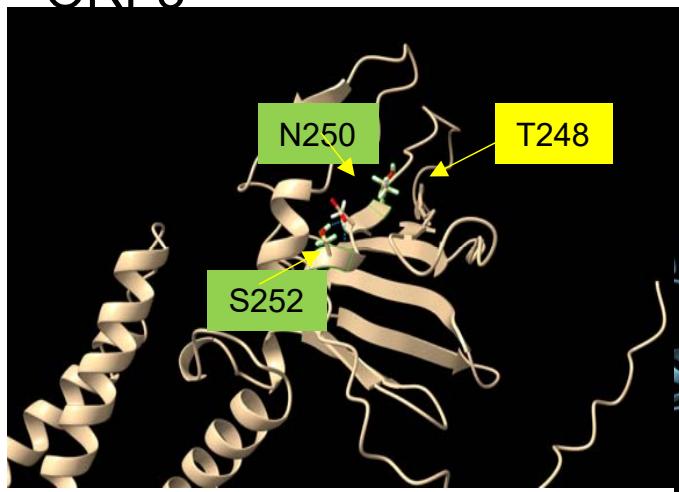
同定されたリン酸化サイトの比較

P0DTc3 (ORF 3a)

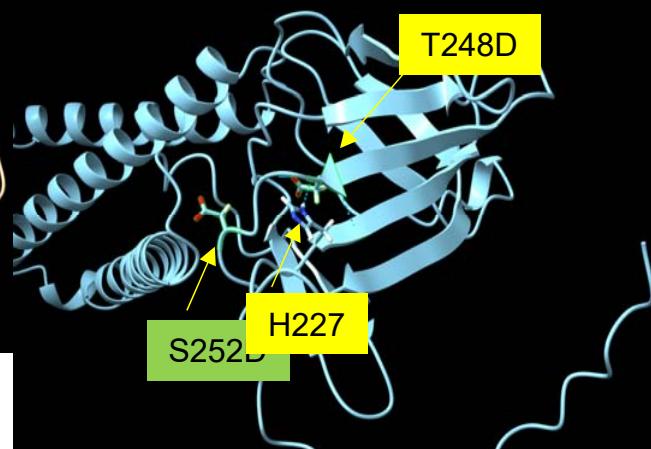


Alpha-Fold 2
にてリン酸化サイト
をDでミックルして
構造解析してみた。

ORF3

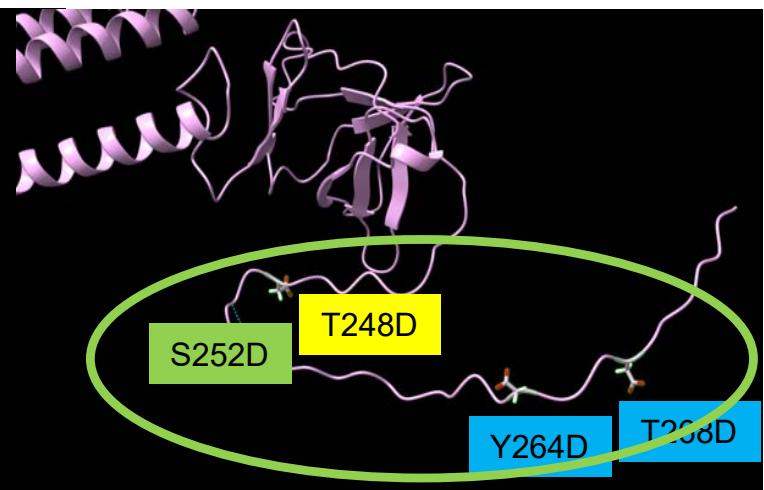


ORF3 T248D,
S252D



βシート構造の位置が
大きく変わる

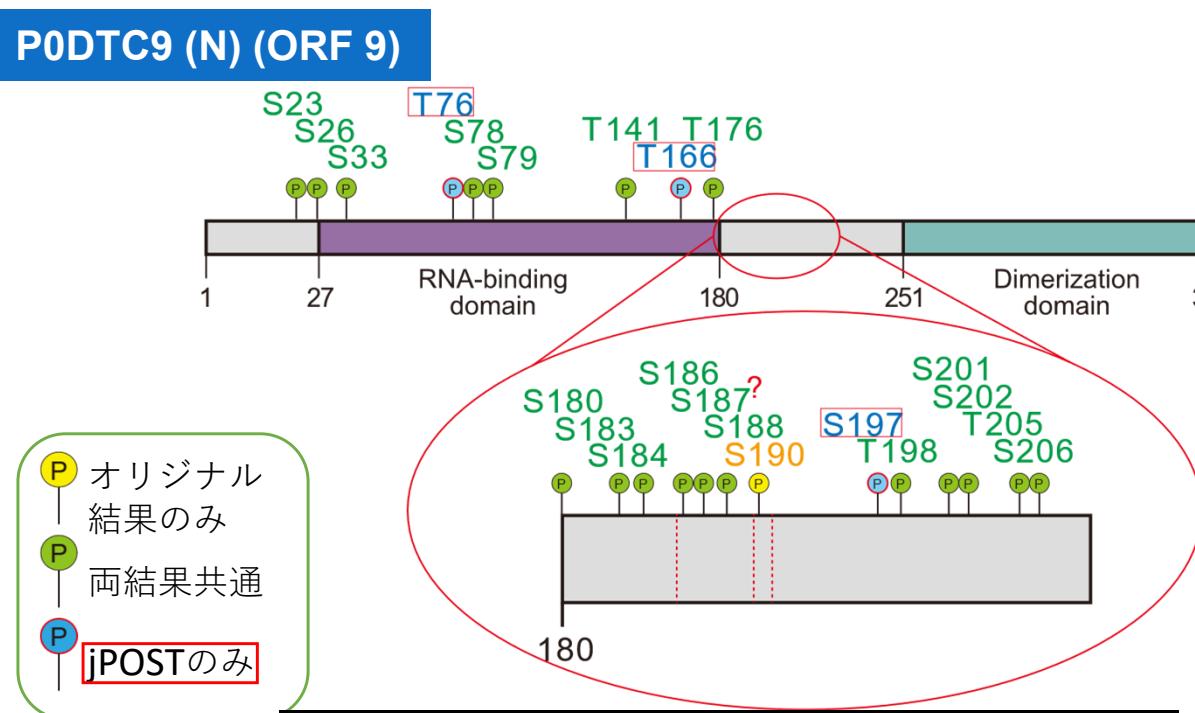
ORF3 T248D, S252D, Y264D,
T268D



Cytoplasmic domainのC末端
がfoldしなくなる

Phosphorylated sites on SARS-CoV-2 proteins

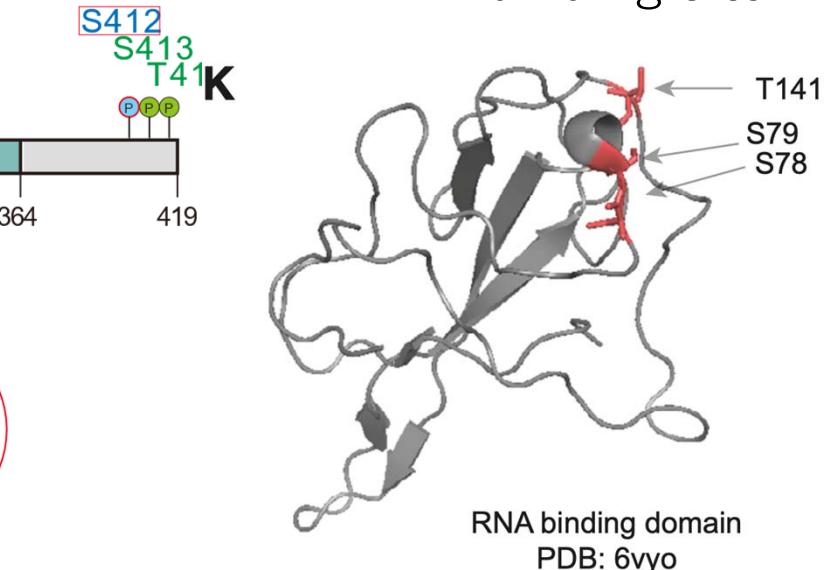
P0DTC9 (N) (ORF 9)



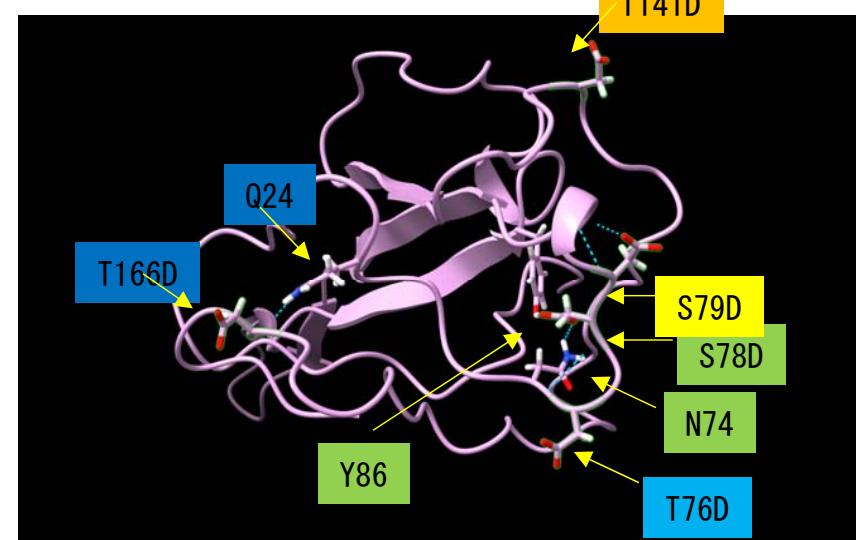
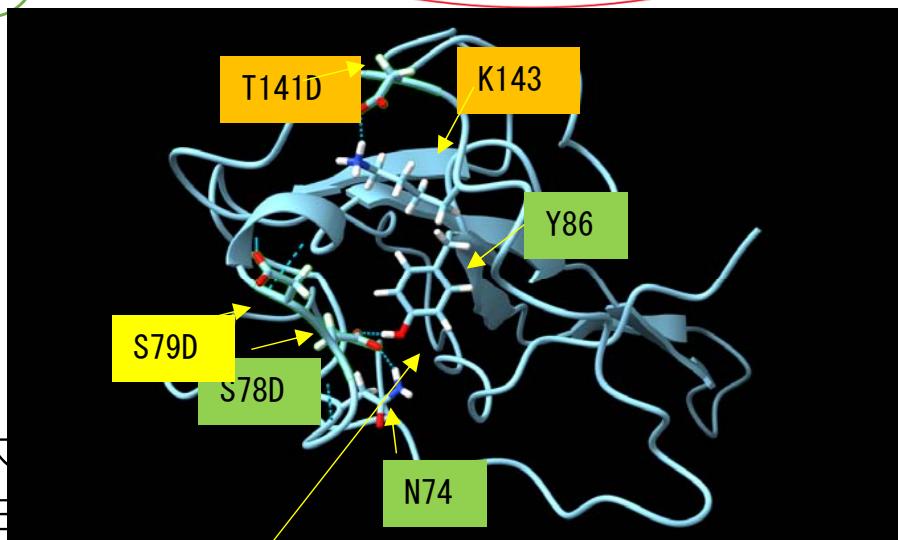
北海道医療大
北川孝雄先生
解析御協力

S78DがY86と水素結合するようになる

RNA binding site



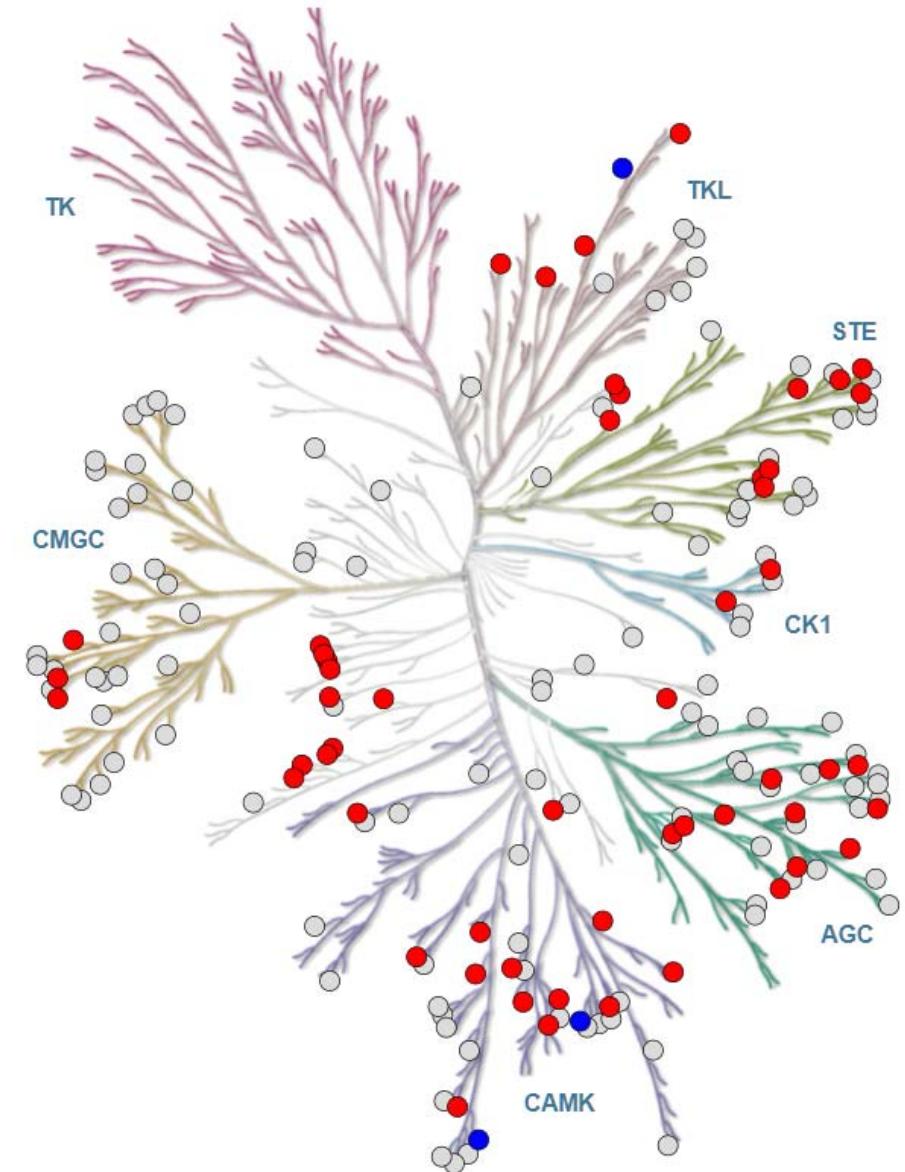
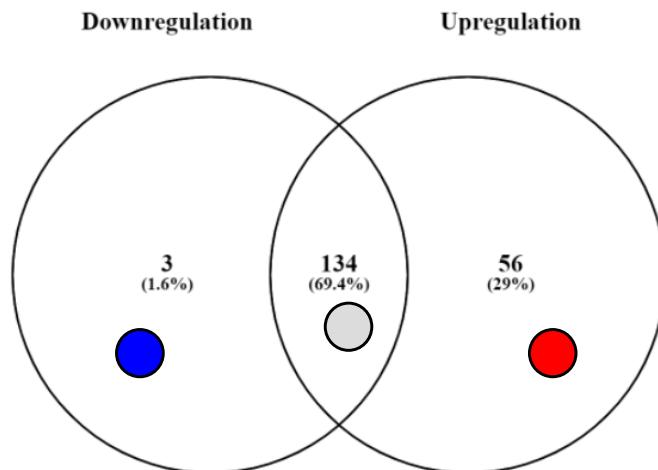
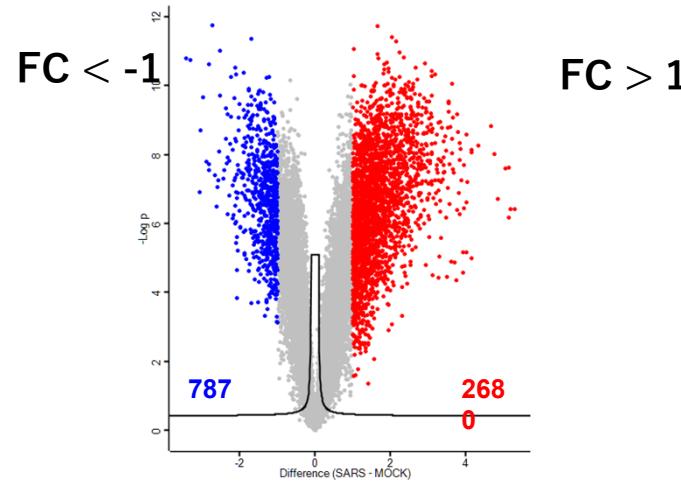
RNA binding domain
PDB: 6vyo



S78DがY86と水素結合するようになる

Prediction of activated Kinases in SARS-COV2 infected Cells

Significant: $\text{Log}_2(\text{TMT of p-sites}) > |1|$, FDR < 5%



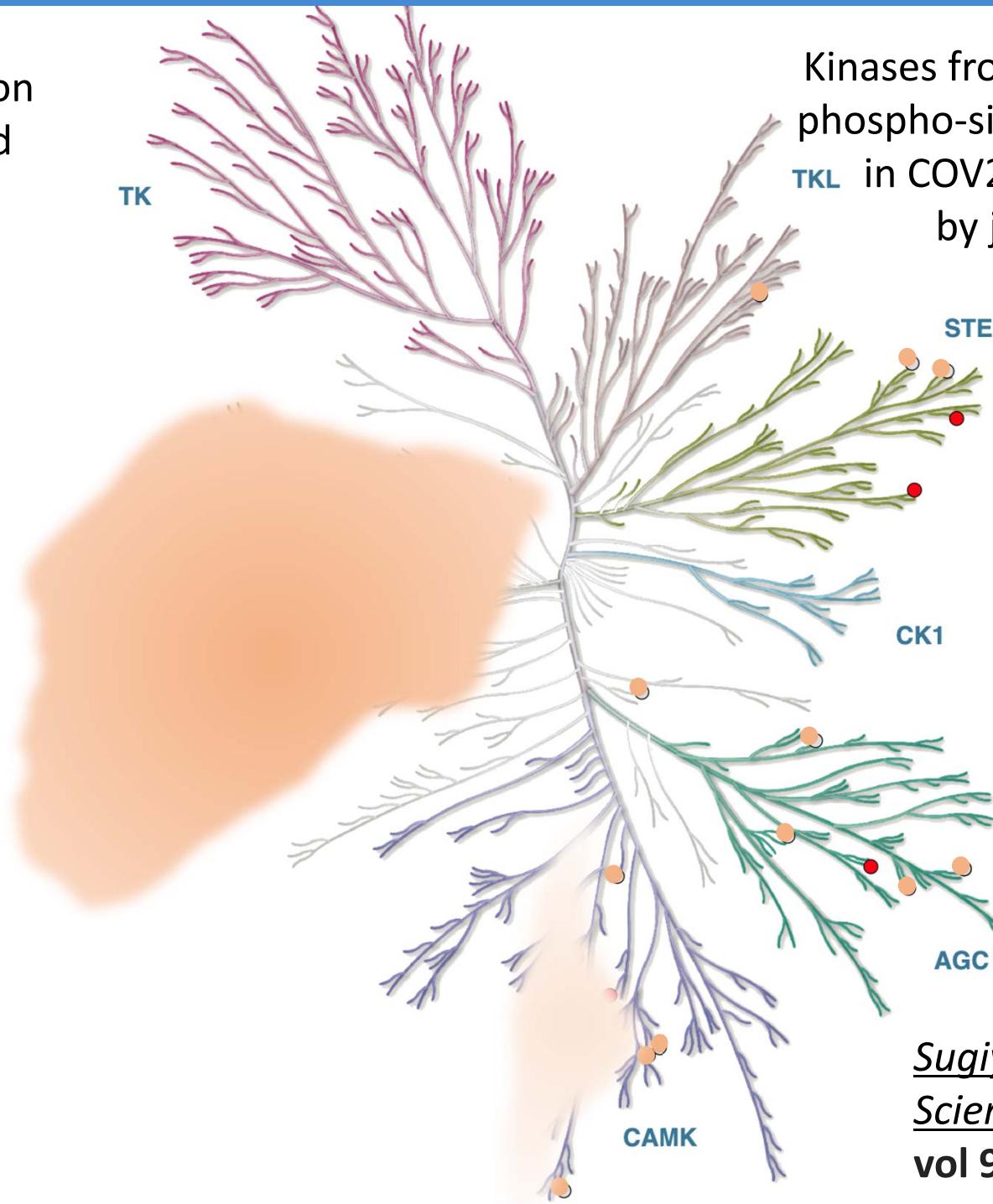
Prediction of activated Kinases in SARS-COV2 infected Cells

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



<https://jpostdb.org>

The screenshot shows the jPOST website homepage. At the top, there is a blue header bar with the URL <https://jpostdb.org>. Below the header, the jPOST logo is displayed, featuring a red circle with the text "jPOST" and "Repository / Database". To the right of the logo, there is a search bar and navigation links for "AQ", "Contact", and a feed icon. A large, bold Japanese text block is centered on the page, reading: "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." Below this text, there is a section titled "Recent posts" with a "Recent post" card. The card contains a snippet of text about a co-authored paper, the date (2021-06-30), and the author (jpost). A detailed explanatory text block follows, discussing the Universal Spectrum Identifier (USI) and its role in proteomics data access. At the bottom of the page, there is another large Japanese text block: "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!" and a smaller explanatory text block about ProteomeXchange resources.

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。

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 ProteomeX (PX) repositories. It has been discussed for time in the HUPO Proteomics Standards Init which jPOST member Prof. Kawano has con greatly. The USI facilitates access to the hu 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

ntaining re-analysis
a for proteome data

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

T resources.

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

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つており、誰でもDLが可能である。
- リポジトリー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、フリーナ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/>



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

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)

JPDM (Journal of Proteome Data and Methods) website homepage. It features a header with the logo of the Japanese Society of HUPO (JProS). The main menu includes 'Instruction to authors', 'Guide to reviewers', 'Editorial board', 'FAQ', 'Ethics policies', and 'License to publish form'. Below the menu, there are sections for 'About JPDM' and 'News'. The 'About JPDM' section contains a brief description of proteomics and the launch of the journal. The 'News' section indicates the website was opened on 2018.11.6.

ウェブサイト
<https://www.jhupo.org/jpdm/>

ScholarOne Manuscripts™ J-STAGE powered by SCHOLARONE MANUSCRIPTS™ JProS. The interface shows a 'Submission' process. Step 1: Type, Title, & Abstract. The user is selecting 'Type' from a list: CHOICE TYPE. Options include Data Descriptors, Protocols, Data Processing Notes, and Reviews. A note says '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 ...](#)'.

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

JPDM (Journal of Proteome Data and Methods) website. The 'Instructions to Authors' page includes sections on 'AIMS & SCOPE', 'Guide to Reviewers', 'Journal & Ethics Policies', and 'Frequently Asked Questions (FAQs)'. The 'AIMS & SCOPE' section describes the journal's focus on publishing standardized accounts of original proteomics data and datasets, as well as the protocols used to derive and utilize them. The 'Guide to Reviewers' section provides advice for reviewers on preparing and submitting their reviews. The 'Journal & Ethics Policies' section covers author responsibilities and data submission guidelines. The 'FAQs' section answers common questions about open access, data submission, and publication costs.

Instructions to Authors

Guide to Reviewers

Ethics Policies

FAQ

JPDM (Journal of Proteome Data and Methods) website. The 'License to Publish' form includes fields for 'Manuscript Number', 'Journal Name (the "Journal")', 'Article Title (the "Title")', and 'Authors (the "Author(s)")'. A note states: 'The Japanese Proteomics Society (the "Society") will consider publishing the Article in the Journal pursuant to the terms below.' A list of conditions for publication rights follows:

- 1) Publish, disseminate, copy, display, store, commercially exploit and otherwise use the Article, including any supplementary material, in all forms and all media (now or at any future time);
- 2) Create any translations, extracts or derivative works based on the Article and exercise all of the rights set forth in (1) in any such translations, extracts or derivatives; and
- 3) Sublincense 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

> Instruction to

About JPD

Proteomics is a rapidly growing field, which has led to increased interest in data and datasets needed for analysis. Therefore, better user interfaces and facilitate better protocoles and procedures are proposed to launch a new journal, *Journal of Proteome Data and Methods*.

Article list

J-STAGE : Journal of Proteome Data and Methods

Journal of Proteome Data and Methods

Journal home Journal of Proteome Data and Methods

J-STAGE home / Journal of Proteome Data and Methods

Search Search within t

Journal issue



Volume 3 (2021)

Volume 2 (2020)

Volume 1 (2019)

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.

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)

JPDM: A New Journal to Internet: Sharing Proteomics Data as the Open Access Journal

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eadly growing research area relating to all of bioscience fields. Advances in proteomics techniques coupled with bioinformatics had opened the way to produce large amounts of data from the whole organism etc. under the several set of conditions. Now, these advances have given us complex proteomics data and datasets coupled with detailed metadata need to become more Findable. A new journal needs to promote data sharing in the scientific community. To address these challenges and facilitate data sharing, the JPPrOS (Japan Proteome Resource) decided to launch a new data journal – the **Journal of Proteome Data and Methods** (JPDM).

JPDM is a peer-reviewed, fully open access and online only journal, provided via the J-stage platform. JPDM publishes three types of articles: "Protocol", "Data processing notes", and "Reviews". The main content of the journal is the detailed metadata on the samples to be analyzed, the sample preparation, the data analysis are provided, not the functional data for attempting to address hypothesis and insight. We ask authors to fill in a **dataset summary table** to provide the basic information described in the JPDM article is of value to the greater scientific community. These requirements are done in a simple and easy way and consequently more useful to others. JPDM tightly collaborates with Japan Proteome Data Bank (jPOST), one of the partner repositories in ProteomeXchange consortium (PX). When data is deposited in jPOST, the journal sends a feedback to the PX repository then post detailed metadata in JPDM, the journal sends a feedback to the PX repository by providing detailed metadata. Since JPDM is a data journal that means data can still be posted to ordinary journals.

JPDM publishes articles in three categories: "Protocols", "Data processing notes", and "Reviews". Protocols are detailed descriptions of methods and procedures used in the laboratory. Data processing notes are detailed descriptions of computational tools and methods used in the laboratory. Reviews are articles in other three categories (Protocols, Data processing notes, and Reviews) that may have never left the lab, or that normally goes unpublishe

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。

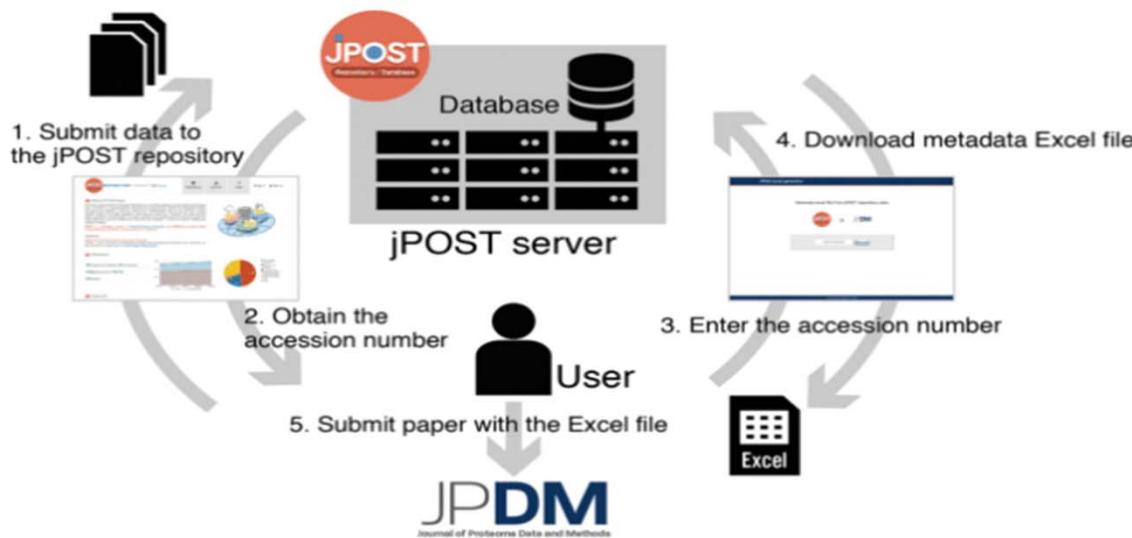
詳細なメタデータに対応するサプリメンタルデータの登録を
JPDMのEditorial サポートメンバーが素早くお手伝いいたします。
どうぞ、気楽に投稿してください！

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。



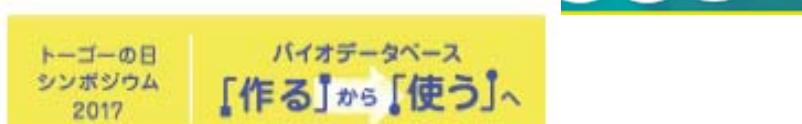
jPOSTrepo: an international standard data repository for proteomes
S. Okuda et al., Nucleic Acids Res., 45:D1107-D1111 (2017).

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

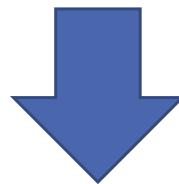
2019 annual report of the jPOST repository
Y. Watanabe, S. Okuda, J. Proteome Data and Methods, 2:1 (2020).

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！



バイオサイエンス
データベースセンター



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ェ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