プロテオーム解析における 質量分析技術と応用研究例

Mass Spectrometry-based Proteomics and its Applications

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Today's topics

1. Mass spectrometry-based proteomics
2. Phosphoproteomics study on cancer cells treated with molecular targeted drug
3. LC-MS in CoMIT Omics Center (COC)

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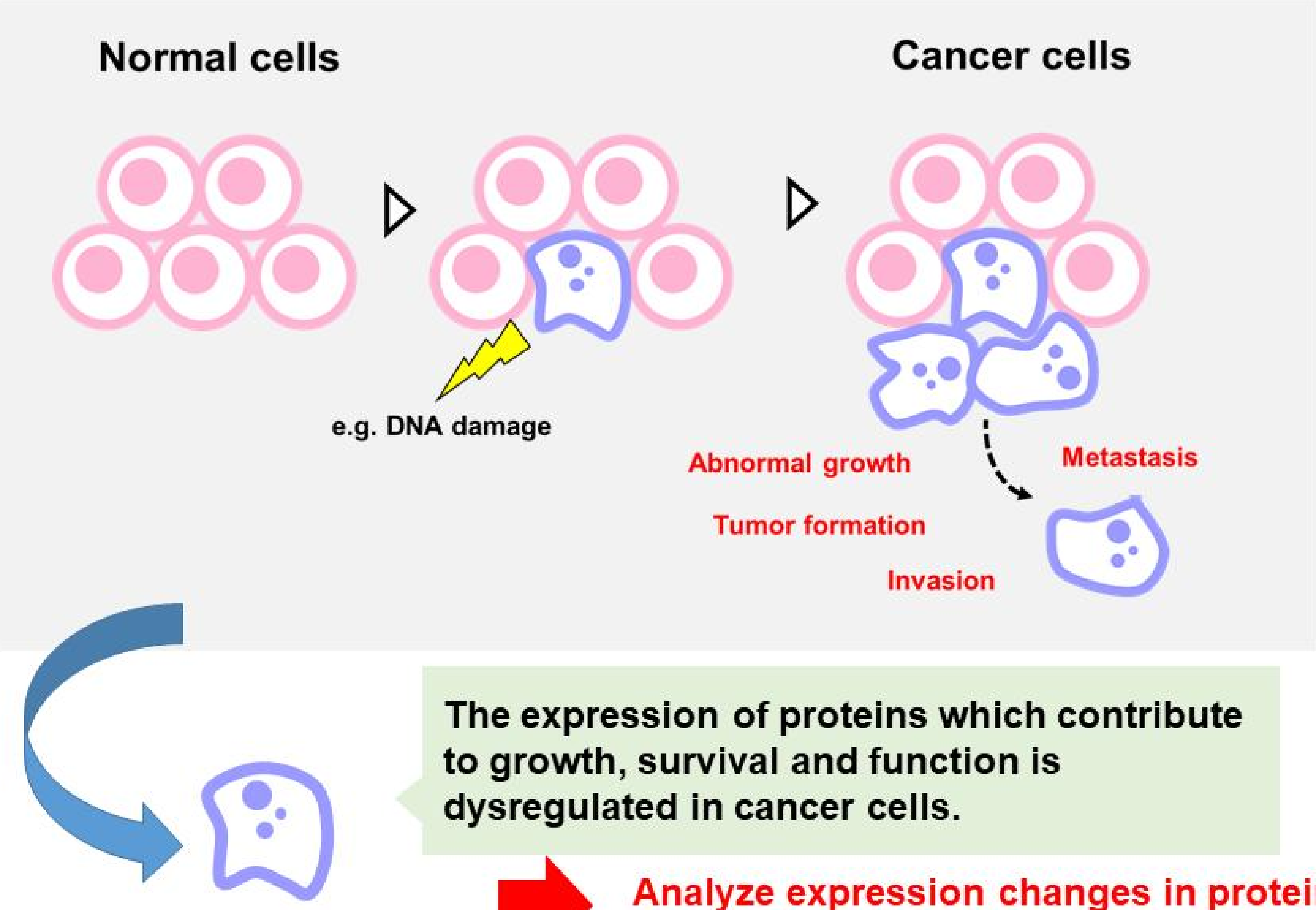
Normal cells vs. cancer cells



The expression of proteins which contribute to growth, survival and function is dysregulated in cancer cells.

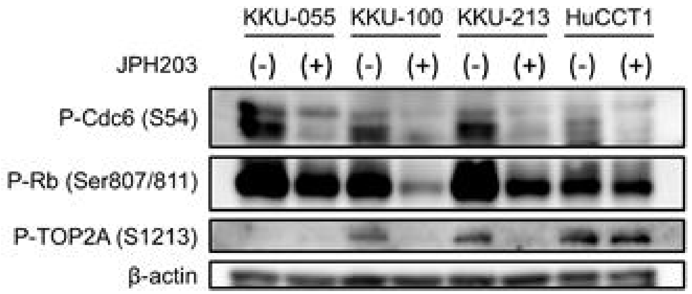
Analyze expression changes in proteins associated with diseases

How to analyze protein expression

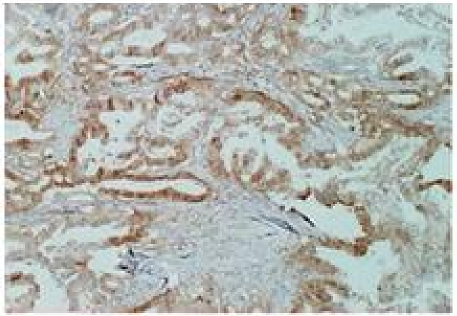
Western blotting, immunocytochemistry Immunohistochemistry, ELISA

- Detect target proteins using antibodies
- Can quantify expression of targeted proteins and reveal their localization
- Need specific antibodies

Western blotting



Immunohistochemistry

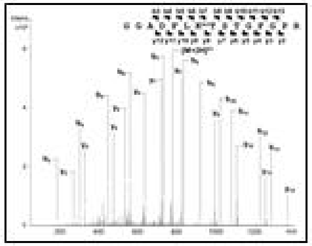


Kaira *et al.* (2012)

Mass spectrometry-based proteomics (Shotgun proteomics)

- Identify proteins using mass spectrometer
- Can quantify expression of thousands of proteins
- Don't need antibody (need protein sequence database)

Mass spectrometry-based proteomics



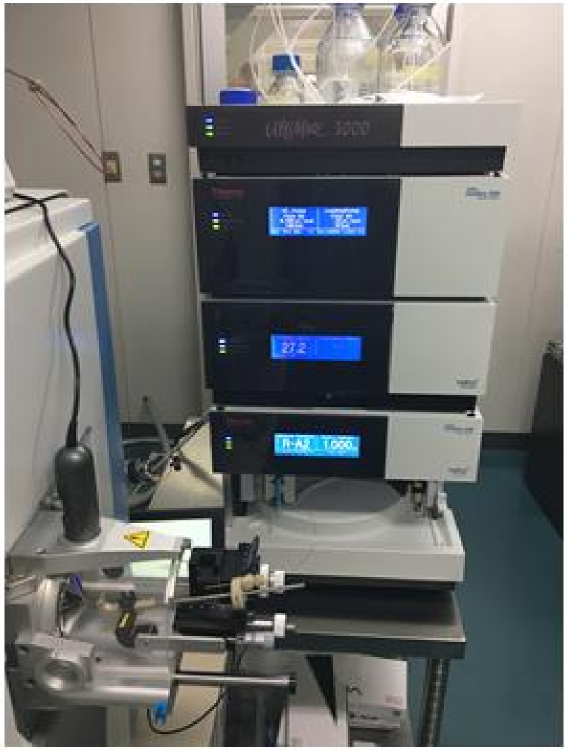
Genome = Gene (遺伝子) + Ome (全体)
Proteome = Protein (タンパク質) + Ome (全体)

Mass spectrometer

Mass spectrometer combined with nano liquid chromatography system (nLC-MS)

Mass spectrometer
(Q Exactive^{TM} mass spectrometer)

Nano liquid chromatography system
Ultimate^{TM} 3000 HPLC system

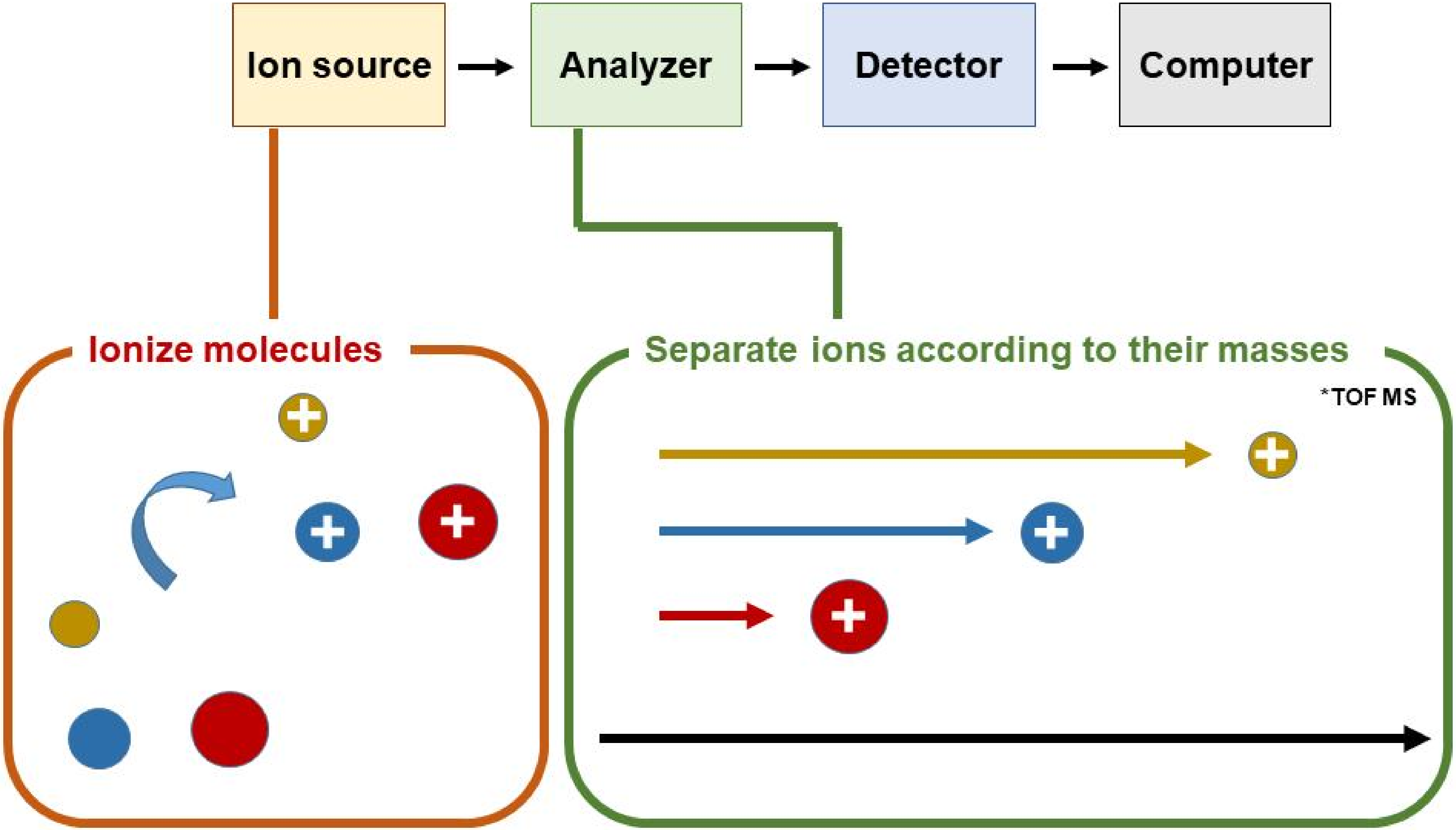


Mass spectrometer can measure the mass of molecule
(Resolution: 140,000 [maximum] Q-Exactive)

Mass spectrometer
(Exploris^{TM} 480)

Mass spectrometer can determine mass of molecule

Construction of mass spectrometer



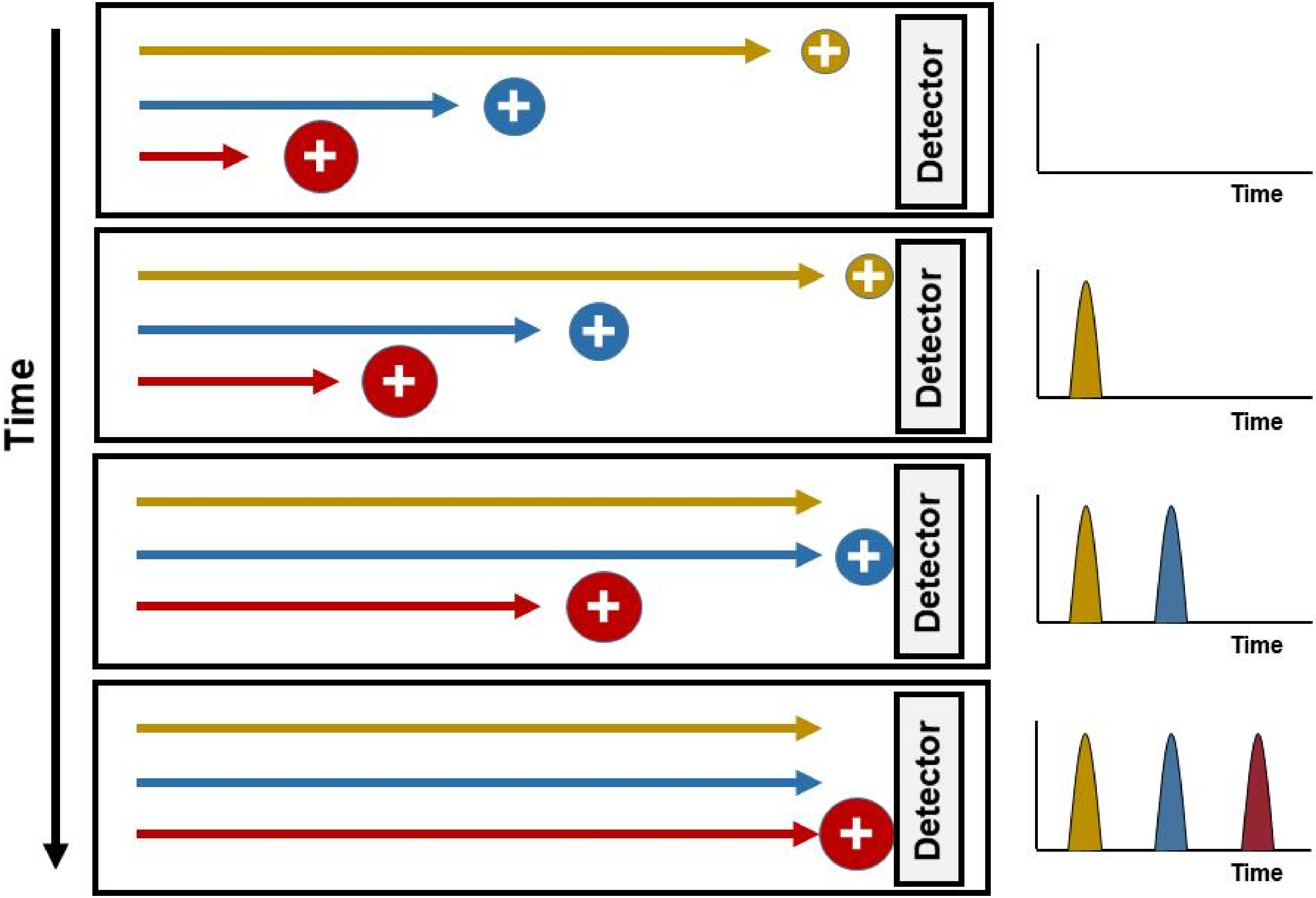
Ion source → Analyzer → Detector → Computer

Ionize molecules

Separate ions according to their masses

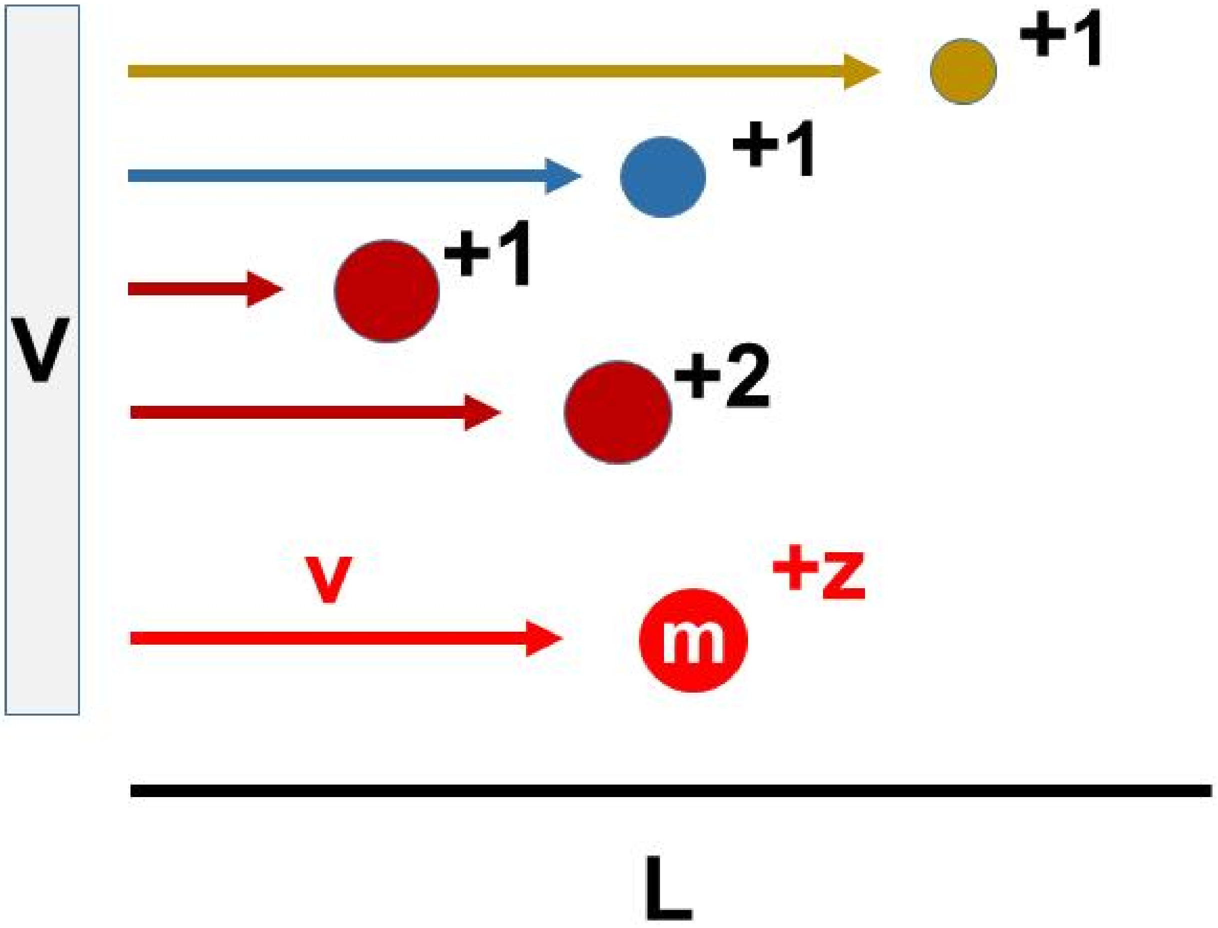
*TOF MS

Time-of-flight mass spectrometer



m/z

m/z: mass/charge number



$$zeV = \frac{1}{2}mv^2$$

$$\updownarrow \quad L = vt$$

$$zeV = \frac{1}{2}m\left(\frac{L}{t}\right)^2$$

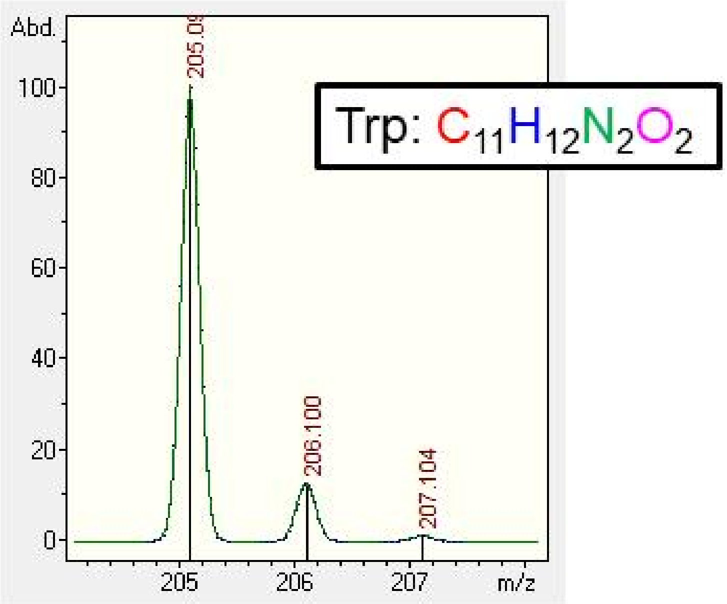
$$\updownarrow$$

$$t = L\sqrt{m/z \times \frac{1}{2eV}}$$

Average and monoisotopic mass

C, H, O, and N have isotopes

[^{13}C, ^{2}H (D), ^{15}N, ^{17}O, ^{18}O]



Trp: $C_{11}H_{12}N_2O_2$

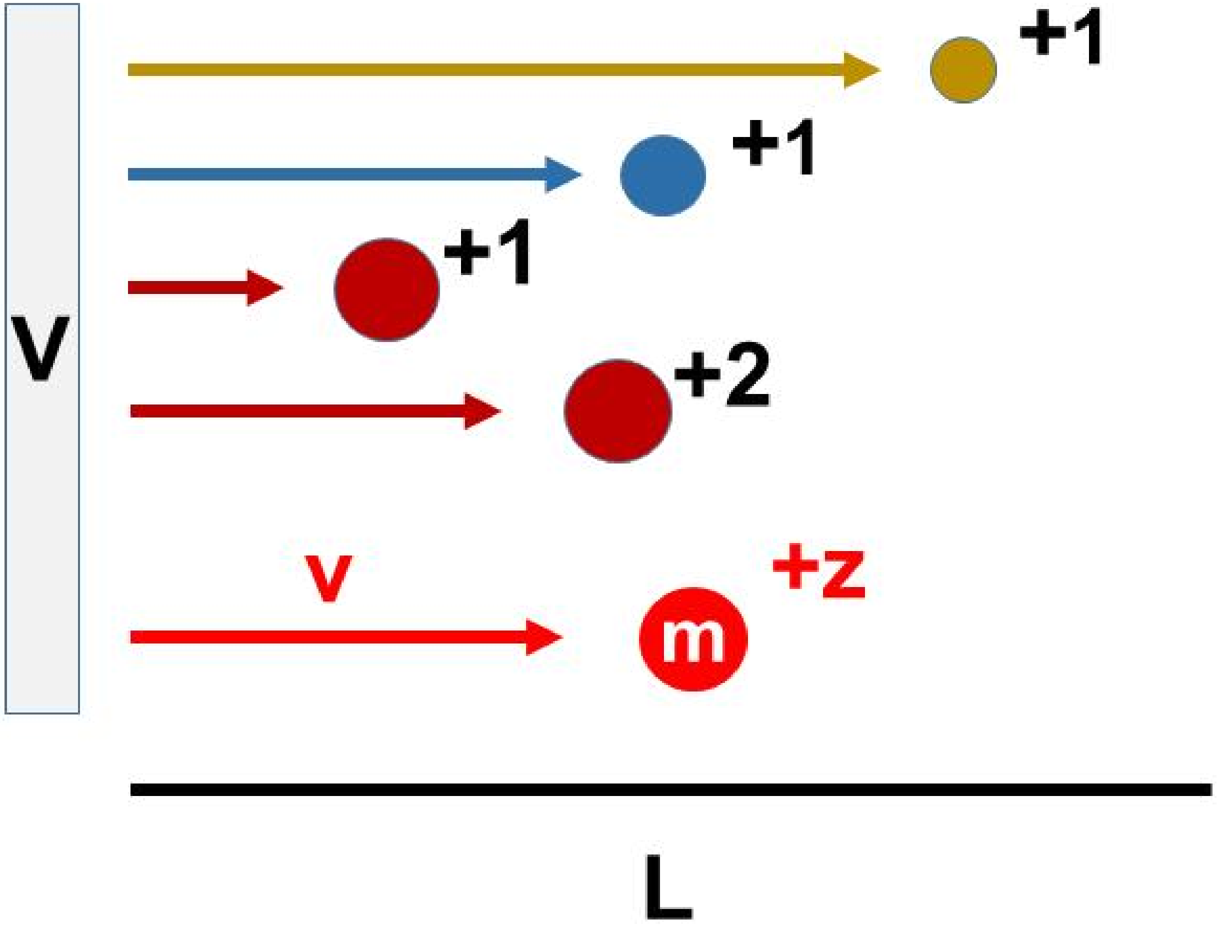
Isotopic peaks

Monoisotopic peak

	Mass of amino acid residue	
3-letter code	Average	Monoisotopic
Ala	71.079	71.037
Arg	156.188	156.101
Asn	114.104	114.043
Asp	115.089	115.027
Cys	103.139	103.009
Glu	129.116	129.043
Gln	128.131	128.059
Gly	57.052	57.021
His	137.141	137.059
Ile	113.159	113.084
Leu	113.159	113.084
Lys	128.174	128.095
Met	131.193	131.040
Phe	147.177	147.068
Pro	97.117	97.053
Ser	87.078	87.032
Thr	101.105	101.048
Trp	186.213	186.079
Tyr	163.176	163.063
Val	99.133	99.068

m/z

***m/z*: mass/charge number**



$$zeV = \frac{1}{2}mv^2$$

$$\updownarrow \quad L = vt$$

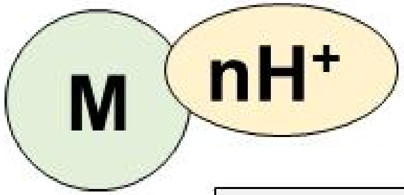
$$zeV = \frac{1}{2}m\left(\frac{L}{t}\right)^2$$

$$\updownarrow$$

$$t = L\sqrt{m/z \times \frac{1}{2eV}}$$

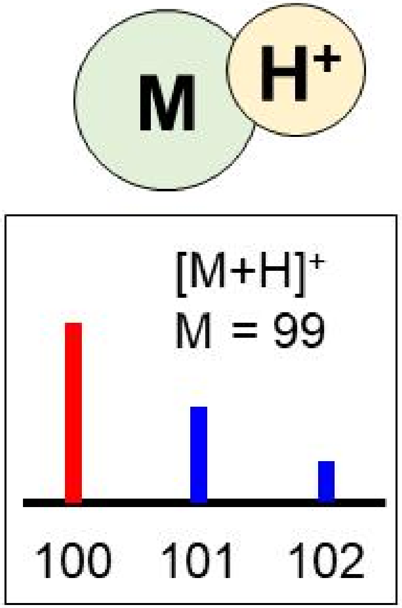
The mass can be calculated by *m/z* and isotopic peak pattern

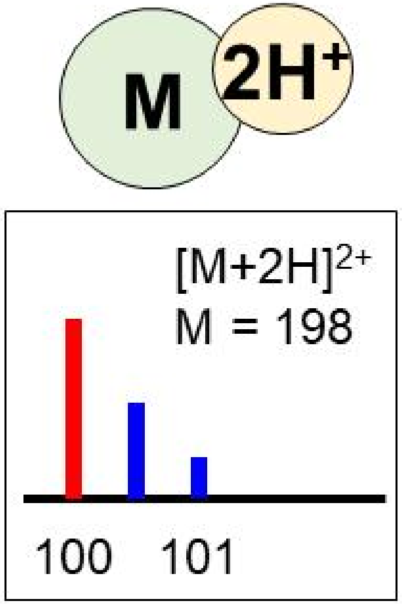
Molecules ionized by proton



m = M + n
z = n

$$m/z = \frac{M+n}{n}$$





Monoisotopic peak
→ m/z
Isotopic peaks
→ z

Type of mass spectrometer

Construction of mass spectrometer

Ion source → Analyzer → Detector → Computer

Ion source

- MALDI (Matrix Assisted Laser desorption/Ionization)
- ESI (Electrospray ionization)
- Electron ionization
- FAB (Fast atom bombardment)
- Chemical ionization

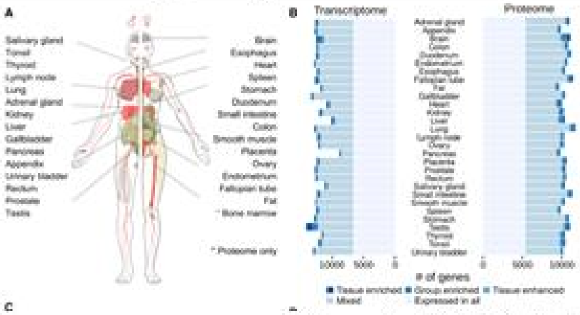
Analyzer

- TOF (Time-of-flight)
- Quadrupole
- Ion trap
- FT-ICR (Fourier-transform ion cyclotron resonance)
- Orbitrap
- Magnetic sector

Mass spectrometry-based protein analysis

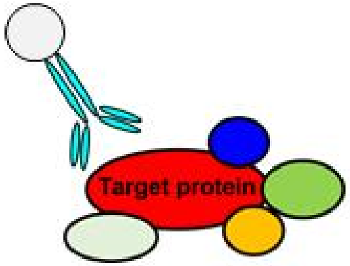
(1) Identification of unknown protein

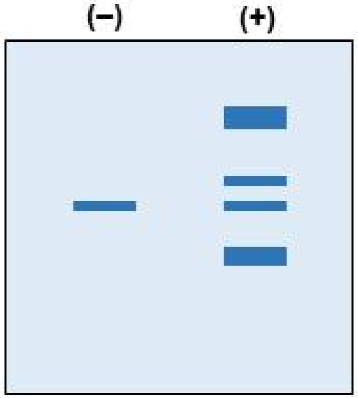
(2) Profiling of proteome in cells or tissues



Wang *et al.* (2019) *Mol. Syst. Biol.*

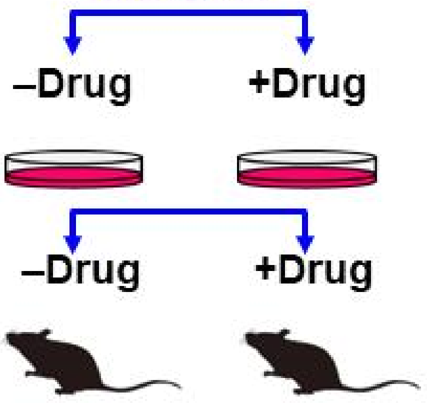
(3) Identification of proteins interacted with target protein





SDS-PAGE gel

(4) Comparative quantification of protein expression

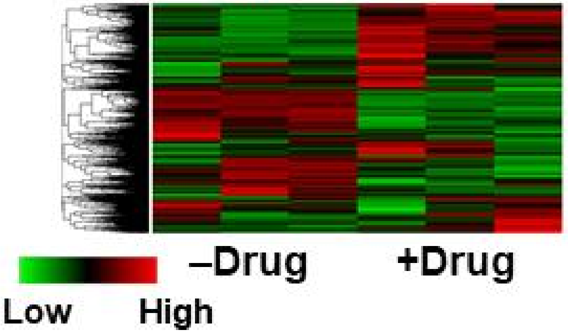


Compare

–Drug +Drug

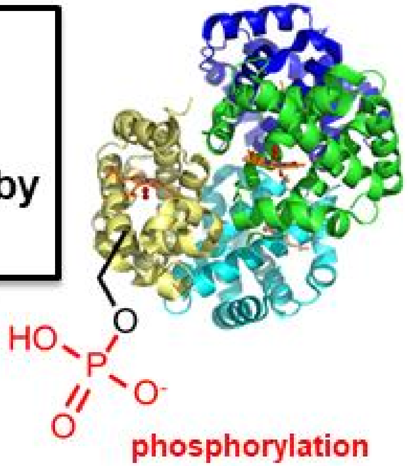
–Drug +Drug

Thousands of proteins are quantified

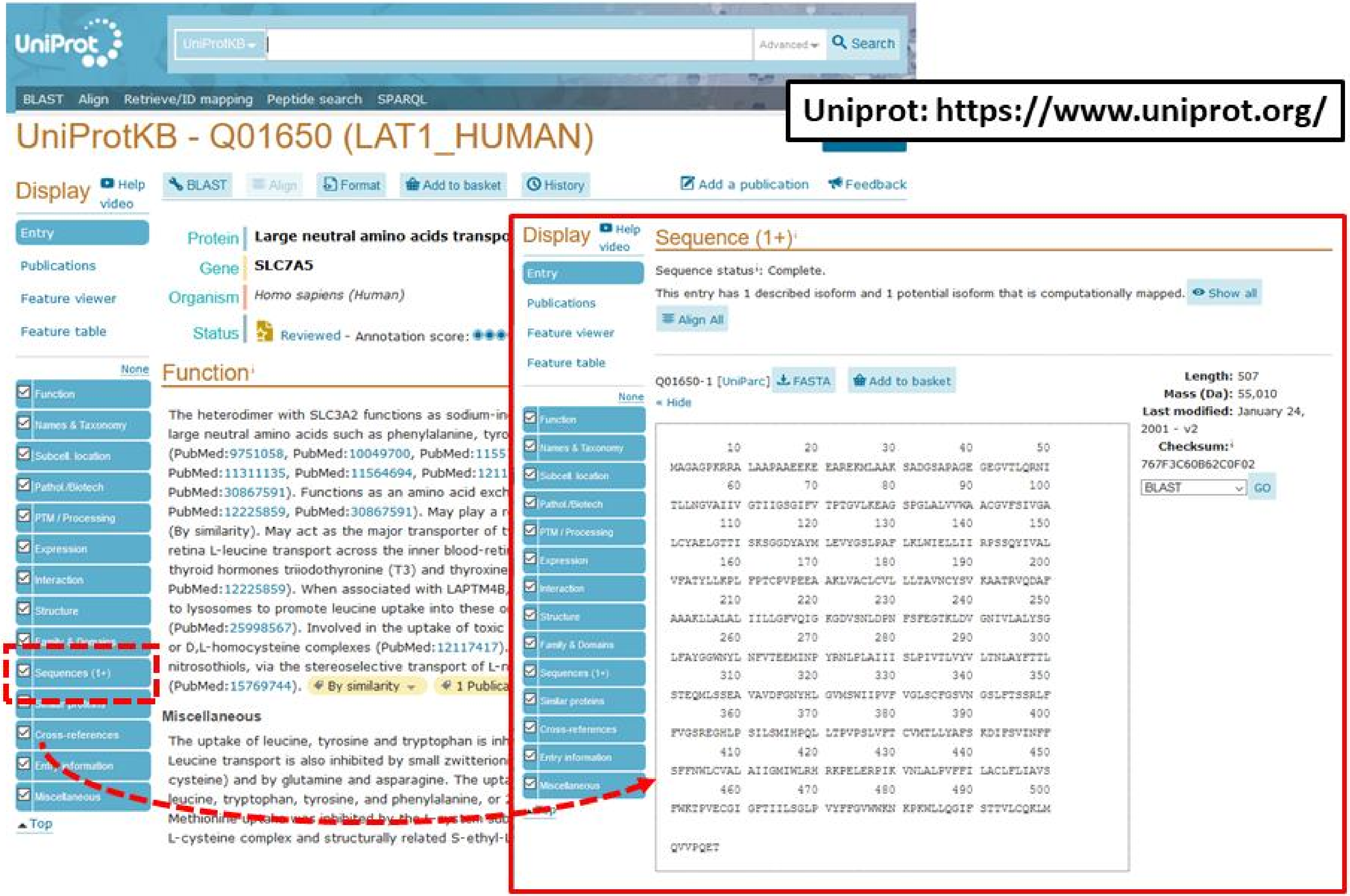


(5) Identification of phosphorylation sites (& PTM sites)

What type PTM?
Which sites?
When?
Up/down-regulated by drug?



Protein sequence database is available



Uniprot: https://www.uniprot.org/

UniProtKB - Q01650 (LAT1_HUMAN)

Protein Large neutral amino acids transpo
Gene SLC7A5
Organism *Homo sapiens (Human)*
Status Reviewed - Annotation score:

Function

The heterodimer with SLC3A2 functions as sodium-in
large neutral amino acids such as phenylalanine, tyro
(PubMed:9751058, PubMed:10049700, PubMed:1155
PubMed:11311135, PubMed:11564694, PubMed:1211
PubMed:30867591). Functions as an amino acid exch
PubMed:12225859, PubMed:30867591). May play a r
(By similarity). May act as the major transporter of t
retina L-leucine transport across the inner blood-reti
thyroid hormones triiodothyronine (T3) and thyroxine
PubMed:12225859). When associated with LAPTM4B,
to lysosomes to promote leucine uptake into these o
(PubMed:25998567). Involved in the uptake of toxic
or D,L-homocysteine complexes (PubMed:12117417).
nitrosothiols, via the stereoselective transport of L-n
(PubMed:15769744).

Miscellaneous

The uptake of leucine, tyrosine and tryptophan is inh
Leucine transport is also inhibited by small zwitterion
cysteine) and by glutamine and asparagine. The upta
leucine, tryptophan, tyrosine, and phenylalanine, or
Methionine uptake was inhibited by the L-system sub
L-cysteine complex and structurally related S-ethyl-L

Sequence (1+)

Sequence status: Complete.

This entry has 1 described isoform and 1 potential isoform that is computationally mapped.

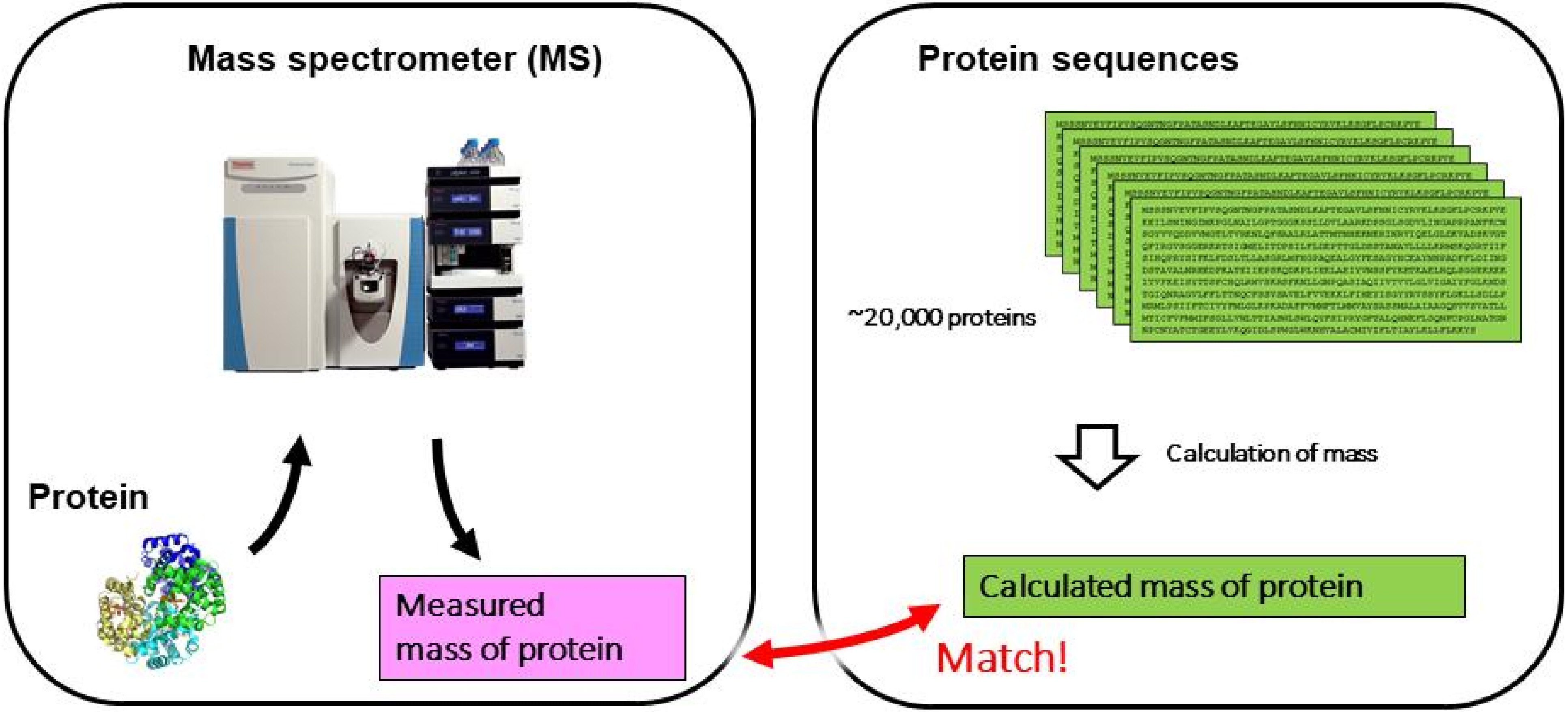
Q01650-1 [UniParc]

```
        10         20         30         40         50
MAGAGPKRRA LAAPAAEEKE EAREKMLAAK SADGSAPAGE GEGVTLQRNI
        60         70         80         90        100
TLLNGVAIIV GTIIGSGIFV TPTGVLKEAG SPGLALVVWA ACGVFSIVGA
       110        120        130        140        150
LCYAELGTTI SKSGGDYAYM LEVYGSLPAF LKLWIELLII RPSSQYIVAL
       160        170        180        190        200
VFATYLLKPL FPTCPVPEEA AKLVACLCVL LLTAVNCYSV KAATRVQDAF
       210        220        230        240        250
AAAKLLALAL IILLGFVQIG KGDVSNLDPN FSFEGTKLDV GNIVLALYSG
       260        270        280        290        300
LFAYGGWNYL NFVTEEMINP YRNLPLAIII SLPIVTLVYV LTNLAYFTTL
       310        320        330        340        350
STEQMLSSEA VAVDFGNYHL GVMSWIIPVF VGLSCFGSVN GSLFTSSRLF
       360        370        380        390        400
FVGSREGHLP SILSMIHPQL LTPVPSLVFT CVMTLLYAFS KDIFSVINFF
       410        420        430        440        450
SFFNWLCVAL AIIGMIWLRH RKPELERPIK VNLALPVFFI LACLFLIAVS
       460        470        480        490        500
FWKTPVECGI GFTIILSGLP VYFFGVWWKN KPKWLLQGIF STTVLCQKLM

QVVPQET
```

Length: 507
Mass (Da): 55,010
Last modified: January 24, 2001 - v2
Checksum: 767F3C60B62C0F02

How does mass spectrometry identify protein? (1)



Mass spectrometer (MS)

Protein

Measured mass of protein

Protein sequences

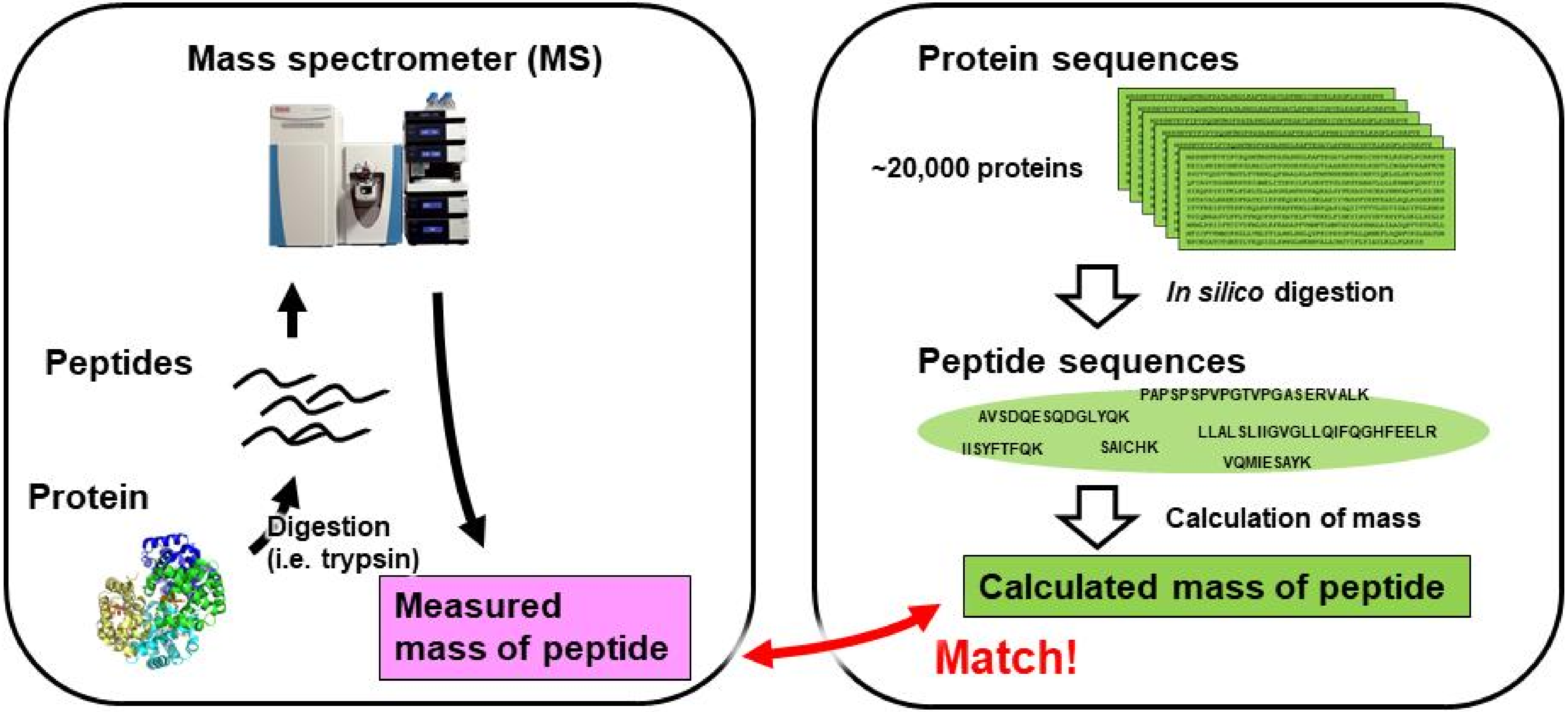
~20,000 proteins

Calculation of mass

Calculated mass of protein

Match!

How does mass spectrometry identify protein? (2)



Mass spectrometer (MS)

Peptides

Protein

Digestion (i.e. trypsin)

Measured mass of peptide

Protein sequences

~20,000 proteins

In silico digestion

Peptide sequences

PAPSPSPVPGTVPGASERVALK

AVSDQESQDGLYQK

LLALSLIIGVGLLQIFQGHFEELR

IISYFTFQK

SAICHK

VQMIESAYK

Calculation of mass

Calculated mass of peptide

Match!

Peptide mass fingerprinting (PMF) & MS/MS

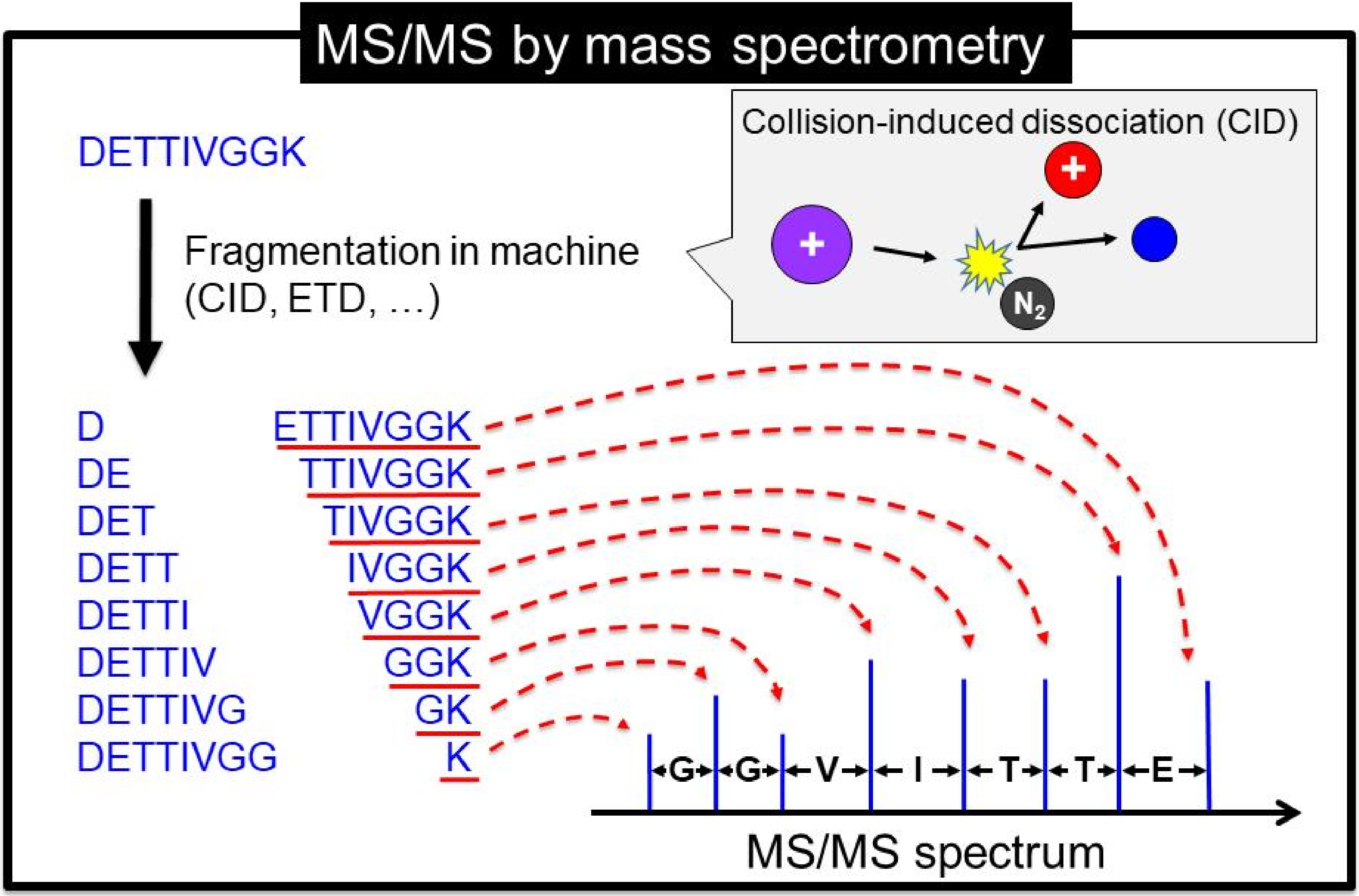
Problem of MS level identification (PMF) regarding peptide sequence

Peptide sequence	Monoisotopic mass
DETTIVGGK	918.465826
DIVGGETTK	918.465826

These different peptides (different sequence) have same mass

In order to distinguish these two peptides, peptide sequence information is needed.

Identification of peptides by Tandem MS (MS/MS)



MS/MS by mass spectrometry

DETTIVGGK

Fragmentation in machine
(CID, ETD, …)

Collision-induced dissociation (CID)

D	ETTIVGGK
DE	TTIVGGK
DET	TIVGGK
DETT	IVGGK
DETTI	VGGK
DETTIV	GGK
DETTIVG	GK
DETTIVGG	K

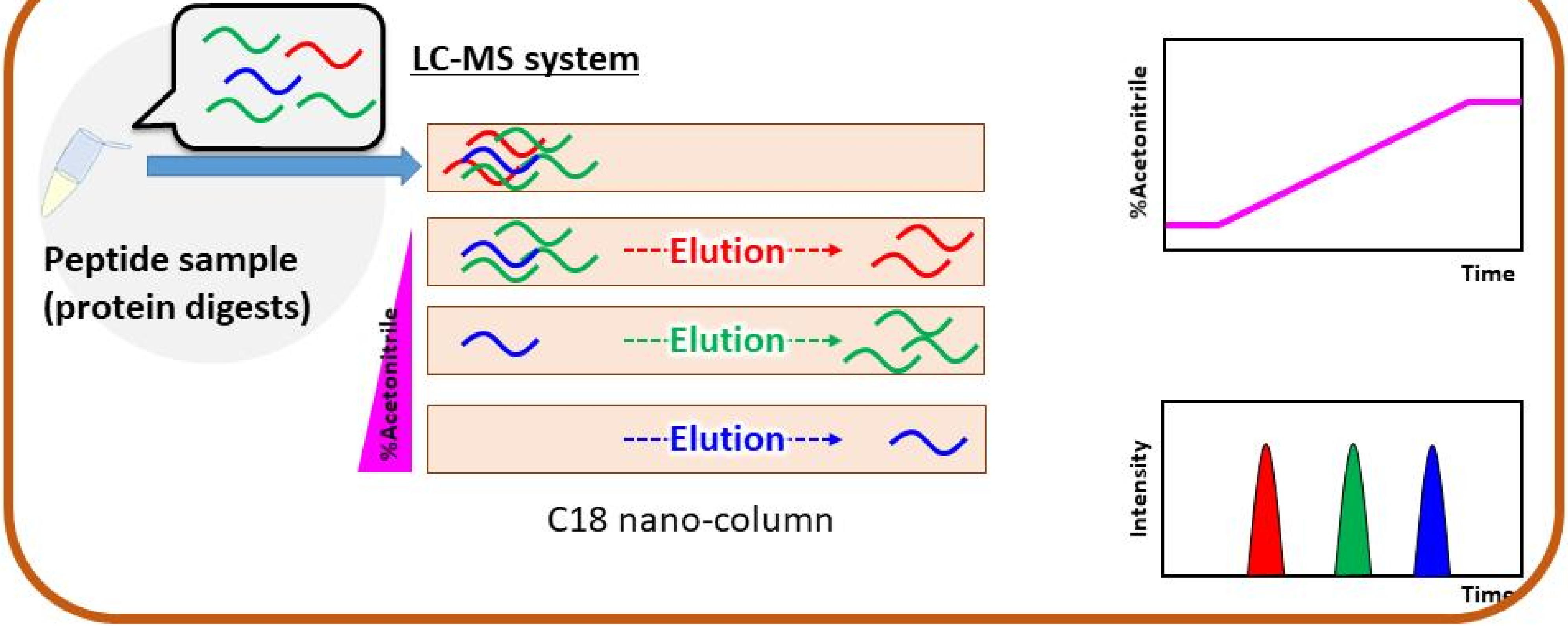
MS/MS spectrum

Liquid chromatography-mass spectrometry system (LC-MS system)

Construction of LC-MS

LC → Ion source → Analyzer → Detector → Computer

Ionize molecules



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Mass spectrometry-based protein analysis

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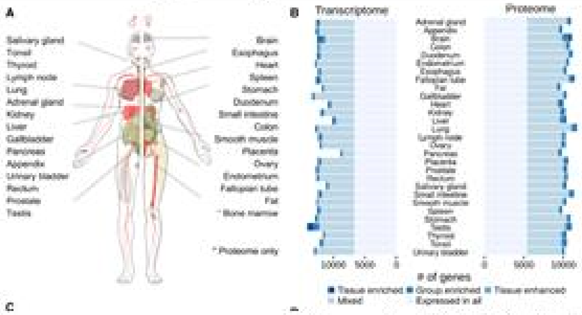
(2) Profiling of proteome in cells or tissues



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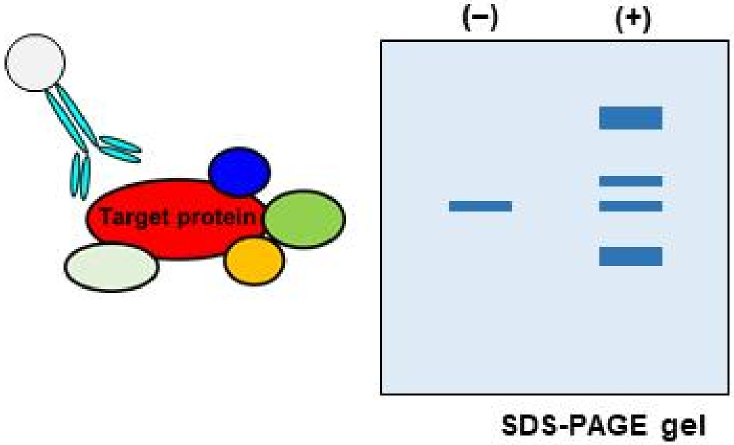

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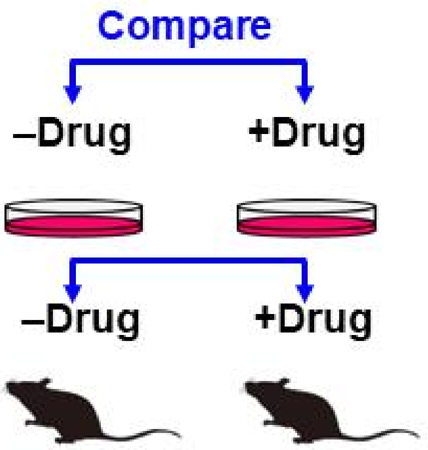
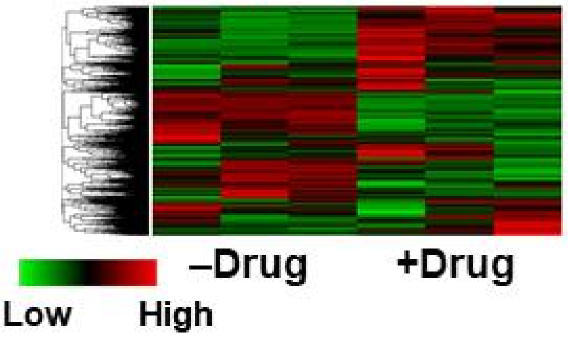


Thousands of proteins are quantified



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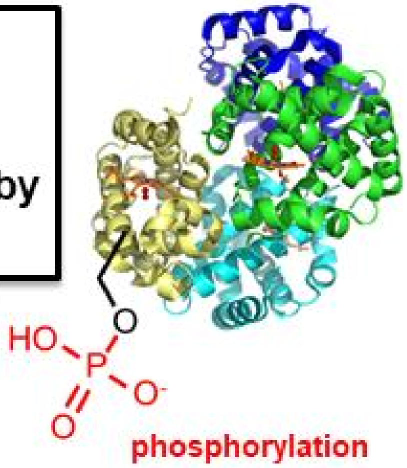
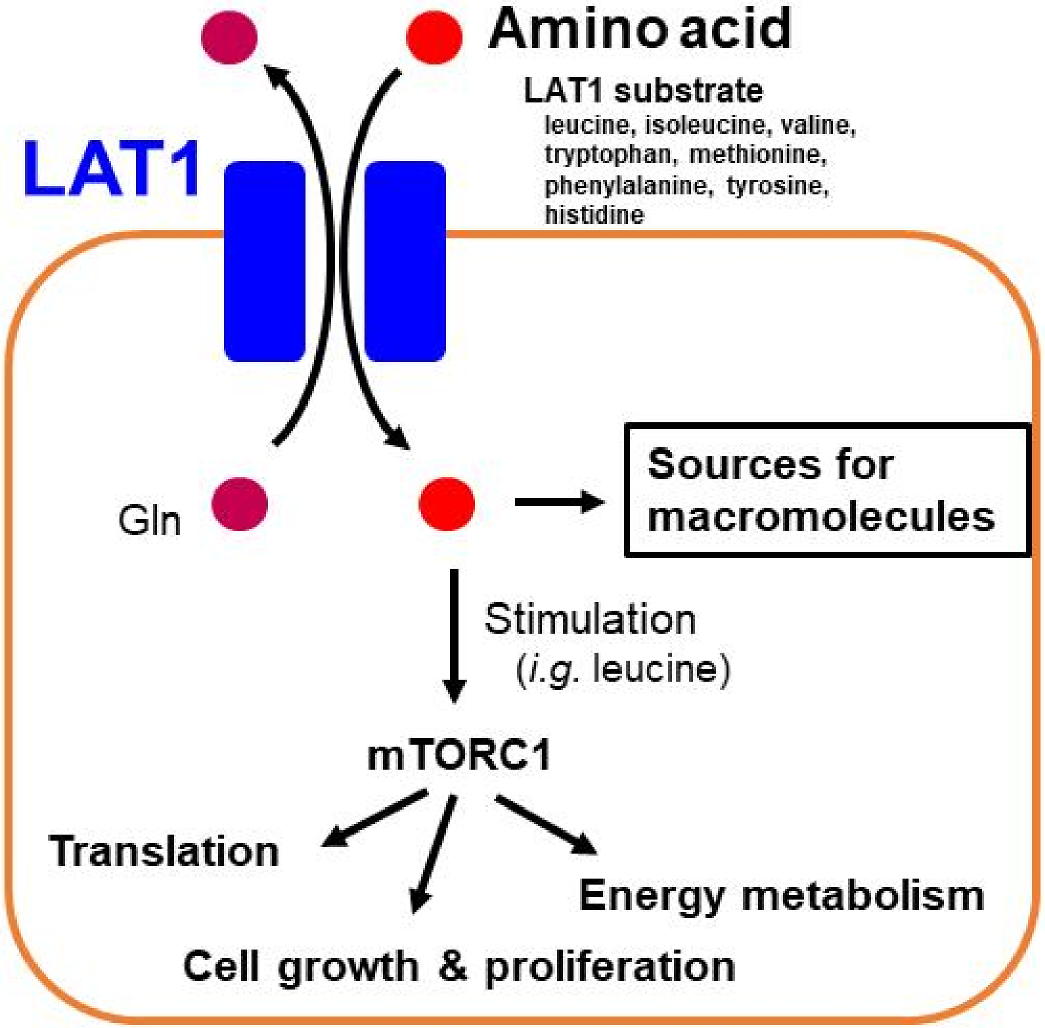
What type PTM?
Which sites?
When?
Up/down-regulated by drug?



LAT1: Amino acid transporter highly expressed in cancer cells



Amino acid

LAT1 substrate
leucine, isoleucine, valine,
tryptophan, methionine,
phenylalanine, tyrosine,
histidine

LAT1

Gln

Sources for macromolecules

Stimulation
(*i.g.* leucine)

mTORC1

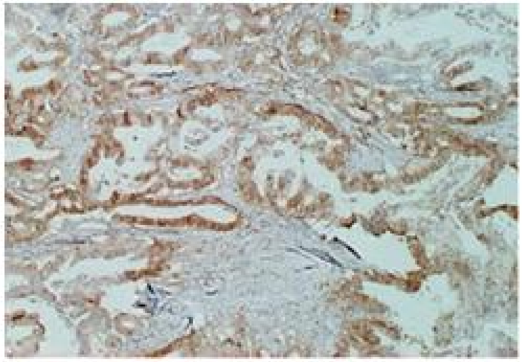
Translation

Energy metabolism

Cell growth & proliferation

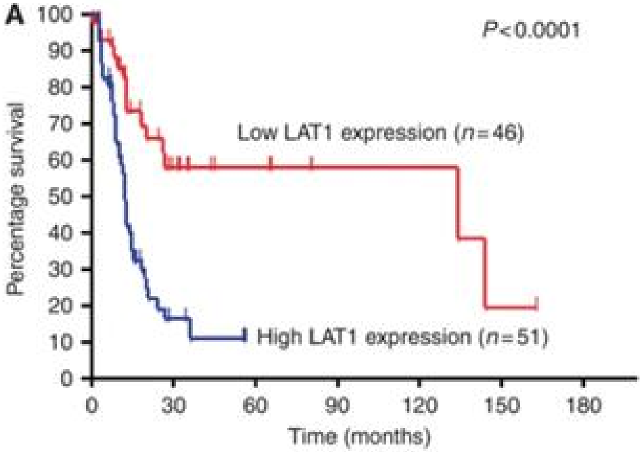
LAT1 substrates function (1) as sources of macromolecules needed for rapid growth, and (2) as signaling molecules

LAT1 is highly expressed in tumor



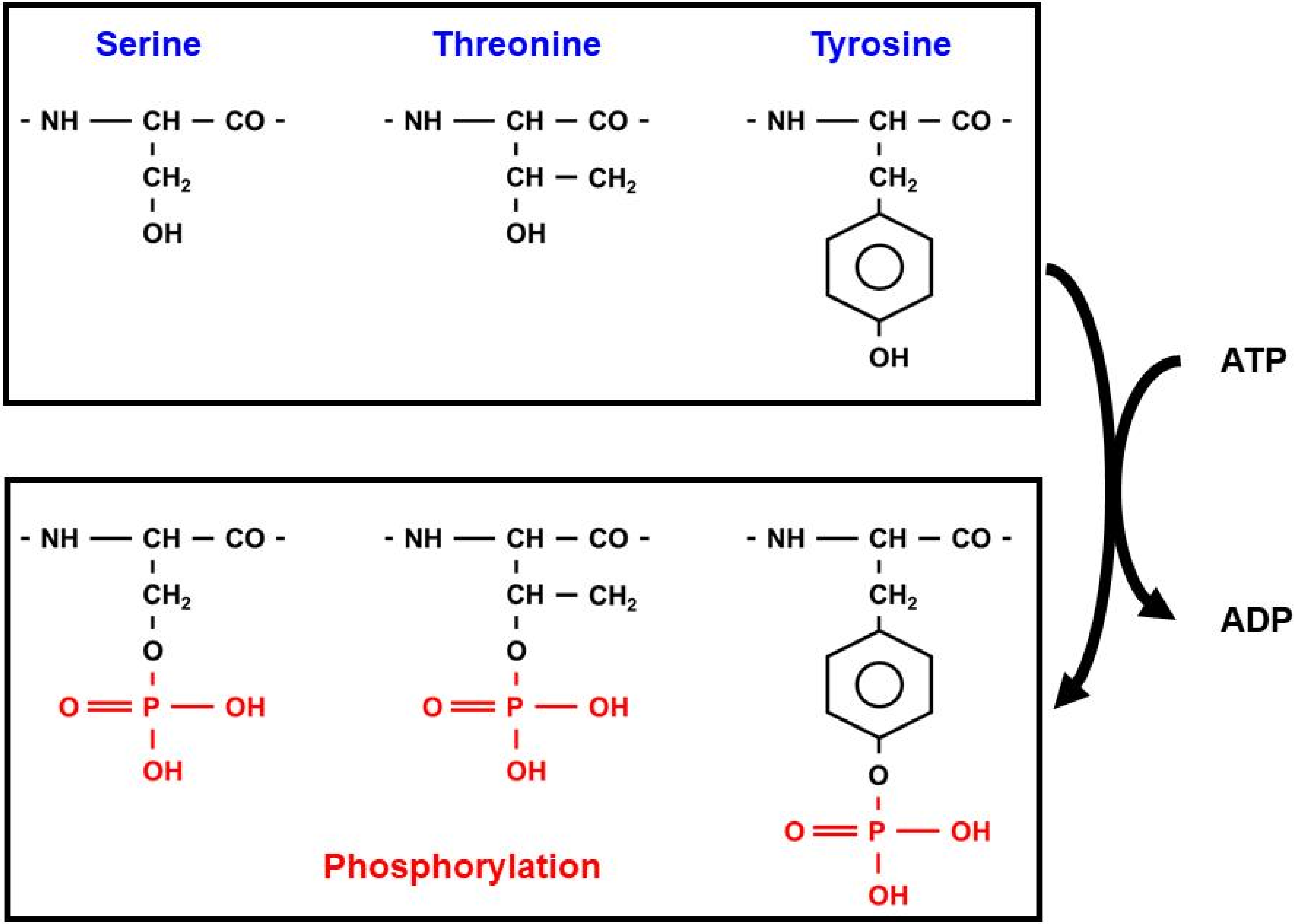
Kaira, K., et al. (2012). *British journal of cancer, 107,* 632–638.

Poor prognosis of patient with highly expressed LAT1



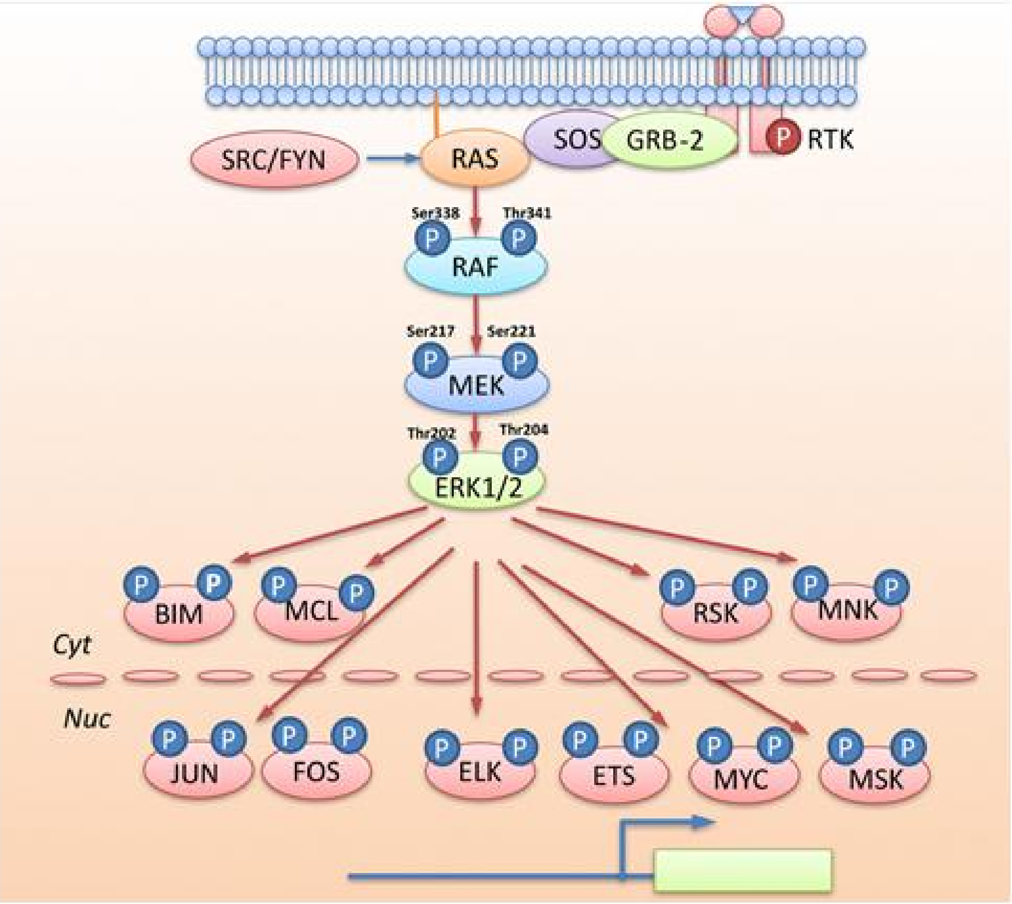
Kaira, K., et al. (2012). *British journal of cancer, 107,* 632–638.

Ser, Thr, Tyr phosphorylation



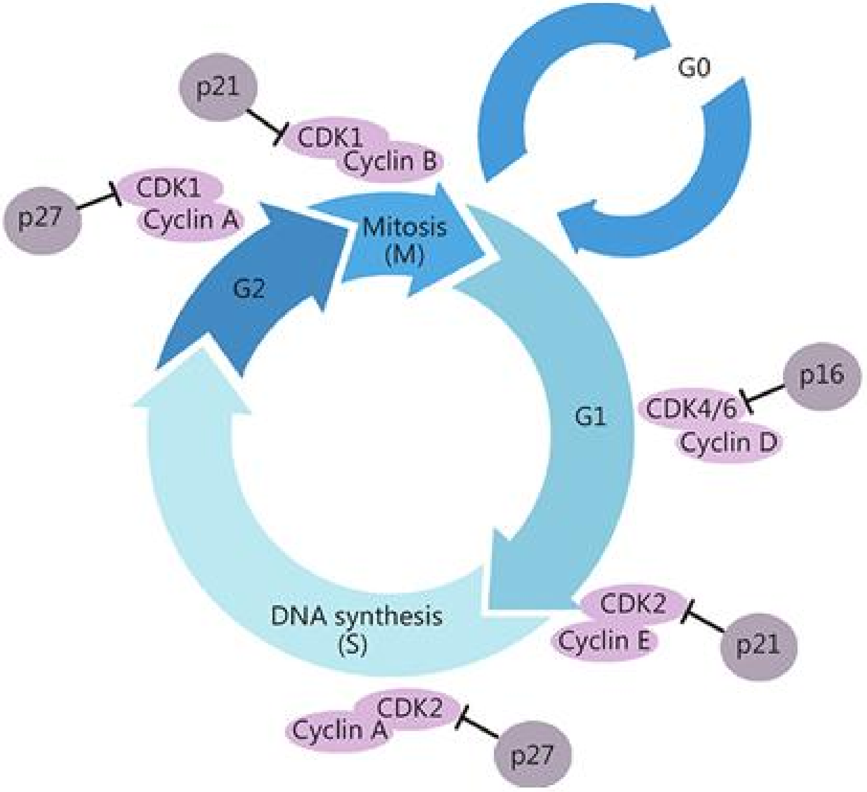
Phosphorylation signaling pathways

MAPK pathway



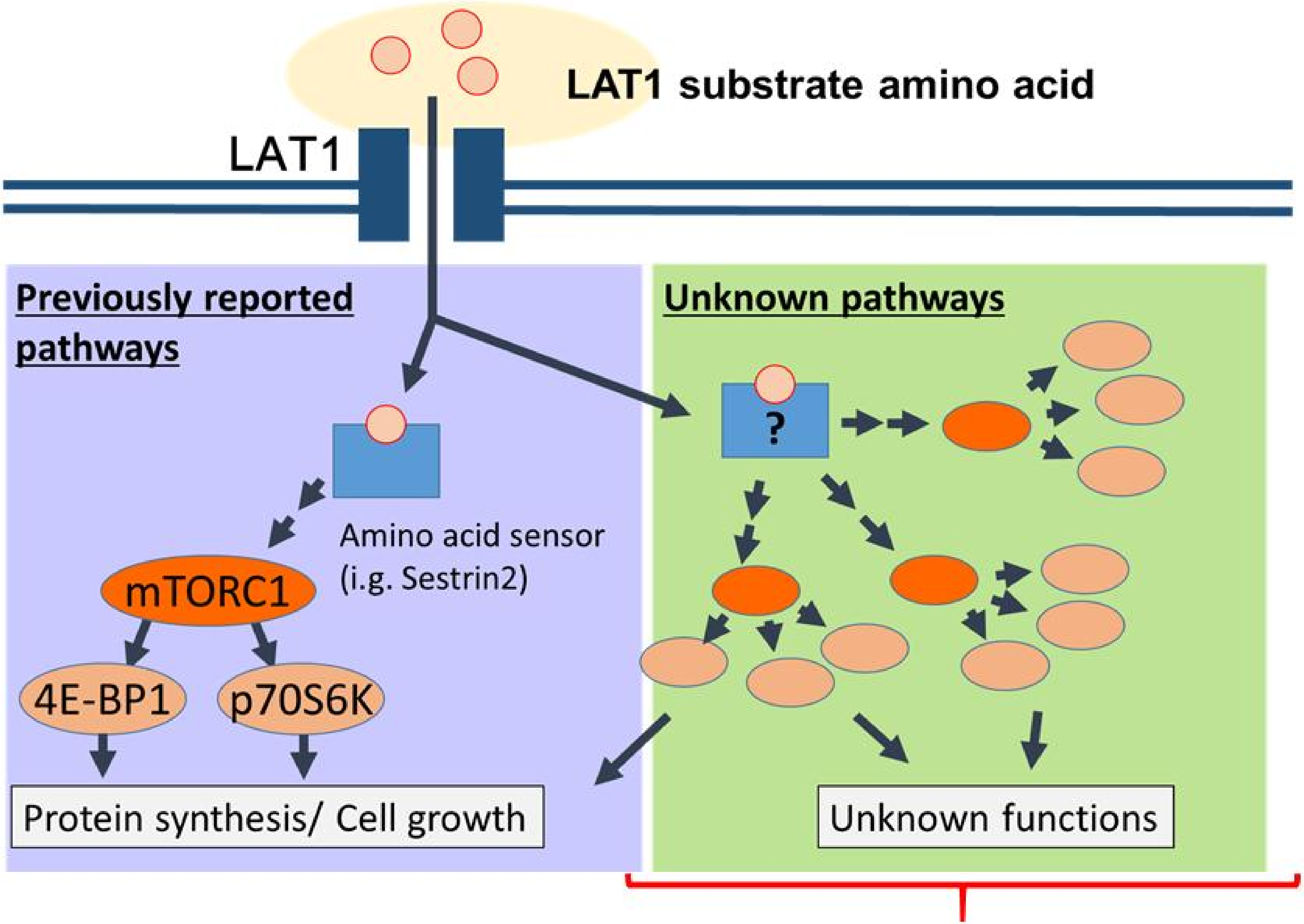
Liu, F. et al. (2018). *Acta pharmaceutica Sinica. B*, *8*(4), 552–562.

Cell cycle



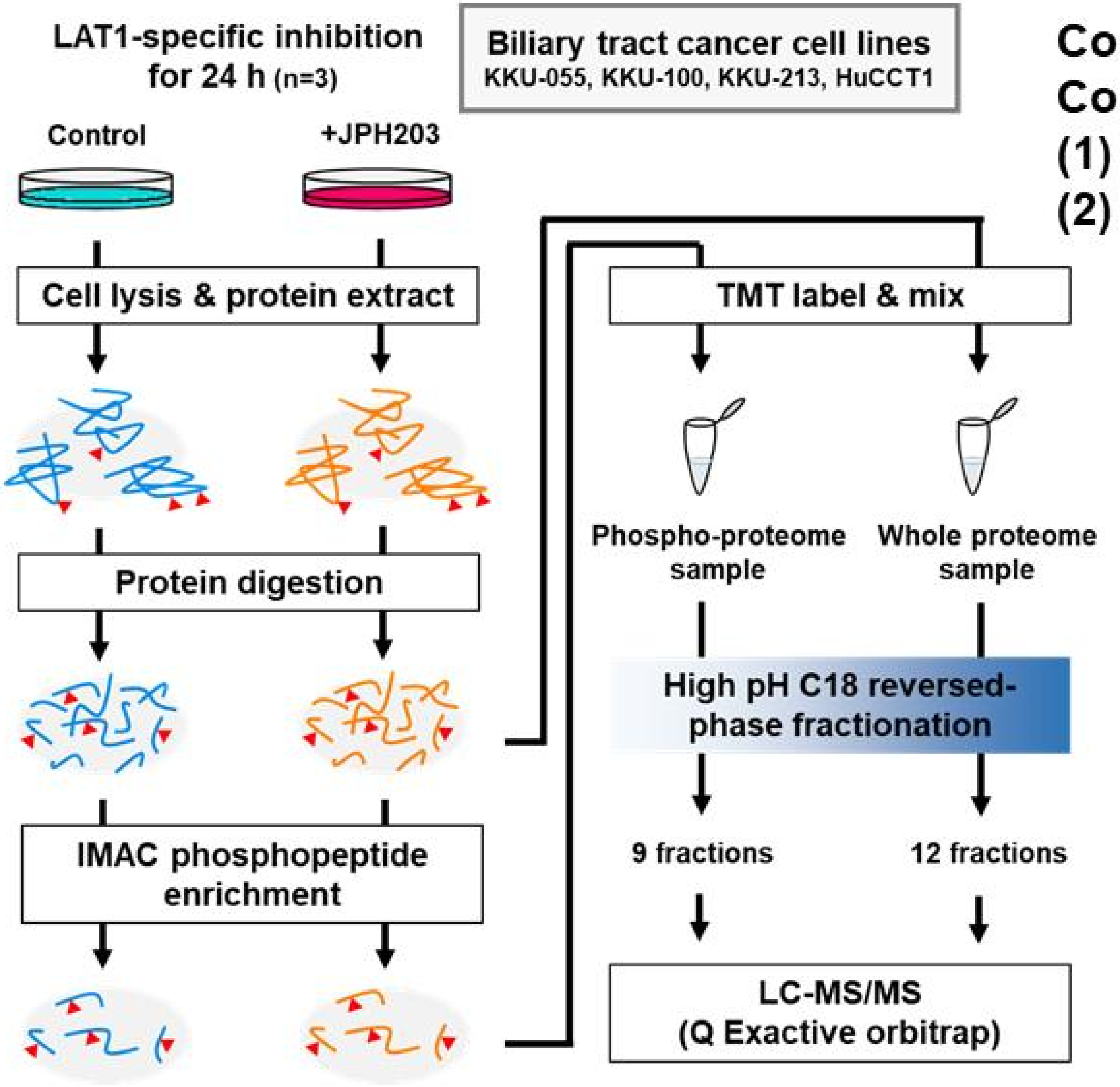
Bai, J., Li, Y., & Zhang, G. (2017). *Cancer biology & medicine*, 14(4), 348–362.

LAT1 and phosphorylation signaling



Proteomics and phosphoproteomics study

Phosphoproteomics workflow



Comparative quantification
Control vs. Drug-treatment
(1) Protein expression
(2) Phosphorylation

Okanishi, H., *et al.* (2021). Proteomics and phosphoproteomics reveal key regulators associated with cytostatic effect of amino acid transporter LAT1 inhibitor. *Cancer science*, *112*, 871–883.

Quantitative proteomics methods

Labeling quantification

Reporter ion-based

- iTRAQ (Isobaric Tag for Relative and Absolute Quantitation)
- TMT (Tandem Mass Tag)

Precursor ion-based

- SILAC (Stable Isotope Labeling)
- Dimethyl labeling
- ^{18}O labeling

Label-free quantification

Precursor ion-based

- Chromatogram peak area-based

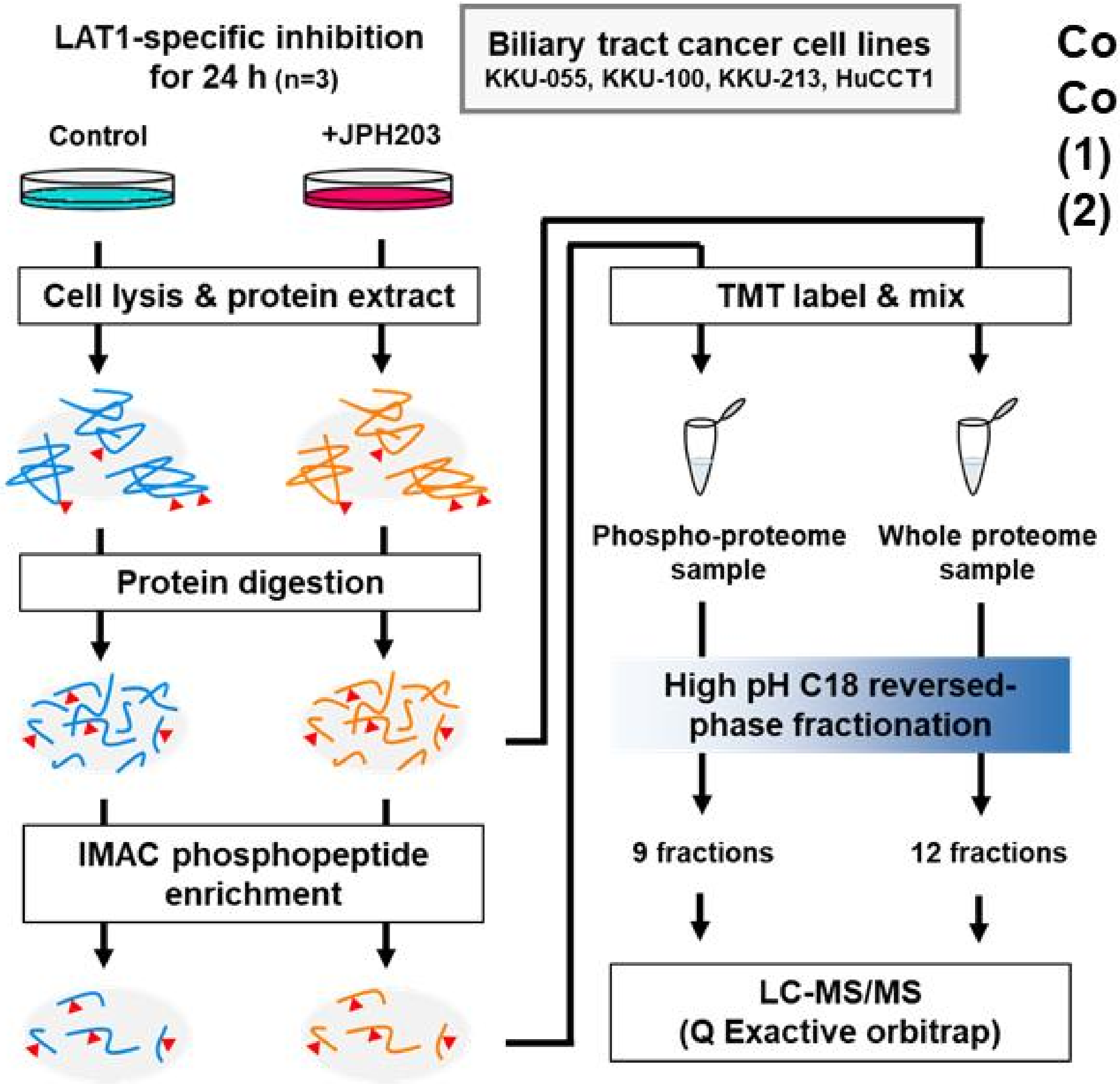
Data-independent

- SWATH-MS

Others

- Spectral counts
- emPAI

Phosphoproteomics workflow



LAT1-specific inhibition
for 24 h (n=3)

Biliary tract cancer cell lines
KKU-055, KKU-100, KKU-213, HuCCT1

Control

+JPH203

Cell lysis & protein extract

Protein digestion

IMAC phosphopeptide enrichment

TMT label & mix

Phospho-proteome sample

Whole proteome sample

High pH C18 reversed-phase fractionation

9 fractions

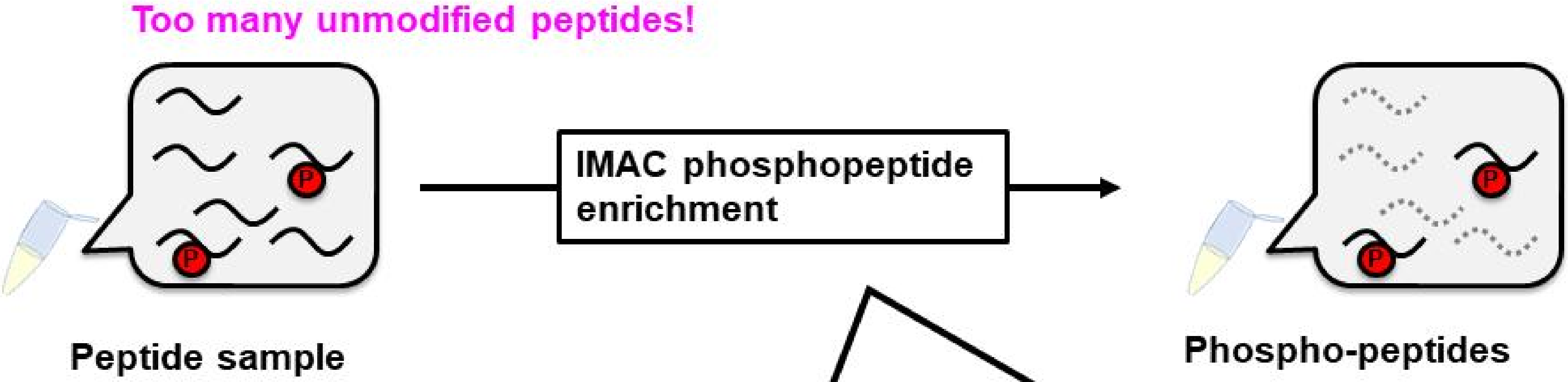
12 fractions

LC-MS/MS
(Q Exactive orbitrap)

Comparative quantification
Control vs. Drug-treatment
(1) Protein expression
(2) Phosphorylation

Okanishi, H., *et al.* (2021). Proteomics and phosphoproteomics reveal key regulators associated with cytostatic effect of amino acid transporter LAT1 inhibitor. *Cancer science*, *112*, 871–883.

Phosphopeptide enrichment technique: Immobilized metal affinity chromatography (IMAC)



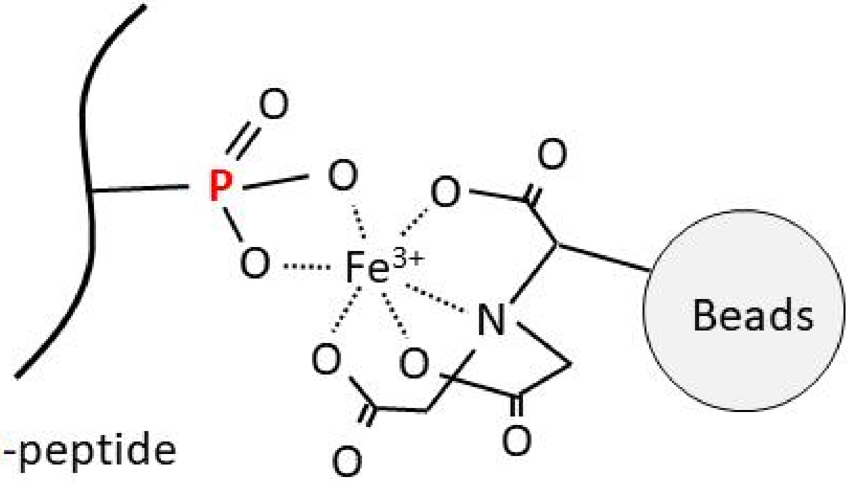
Too many unmodified peptides!

IMAC phosphopeptide enrichment

Peptide sample

Phospho-peptides

Immobilized metal affinity chromatography (IMAC)



Phospho-peptide

Identification and quantification

Identification summary

Average identified peptides:

54106 peptides (q-value < 0.01) from 6431 proteins

Average identified phosphopeptides:

21340 phosphopeptides (q-value < 0.01)

Quantification summary

Average quantifiable proteins:

4983 proteins (#unique ≥ 2 with q-value < 0.01)

Average quantifiable phosphorylation sites:

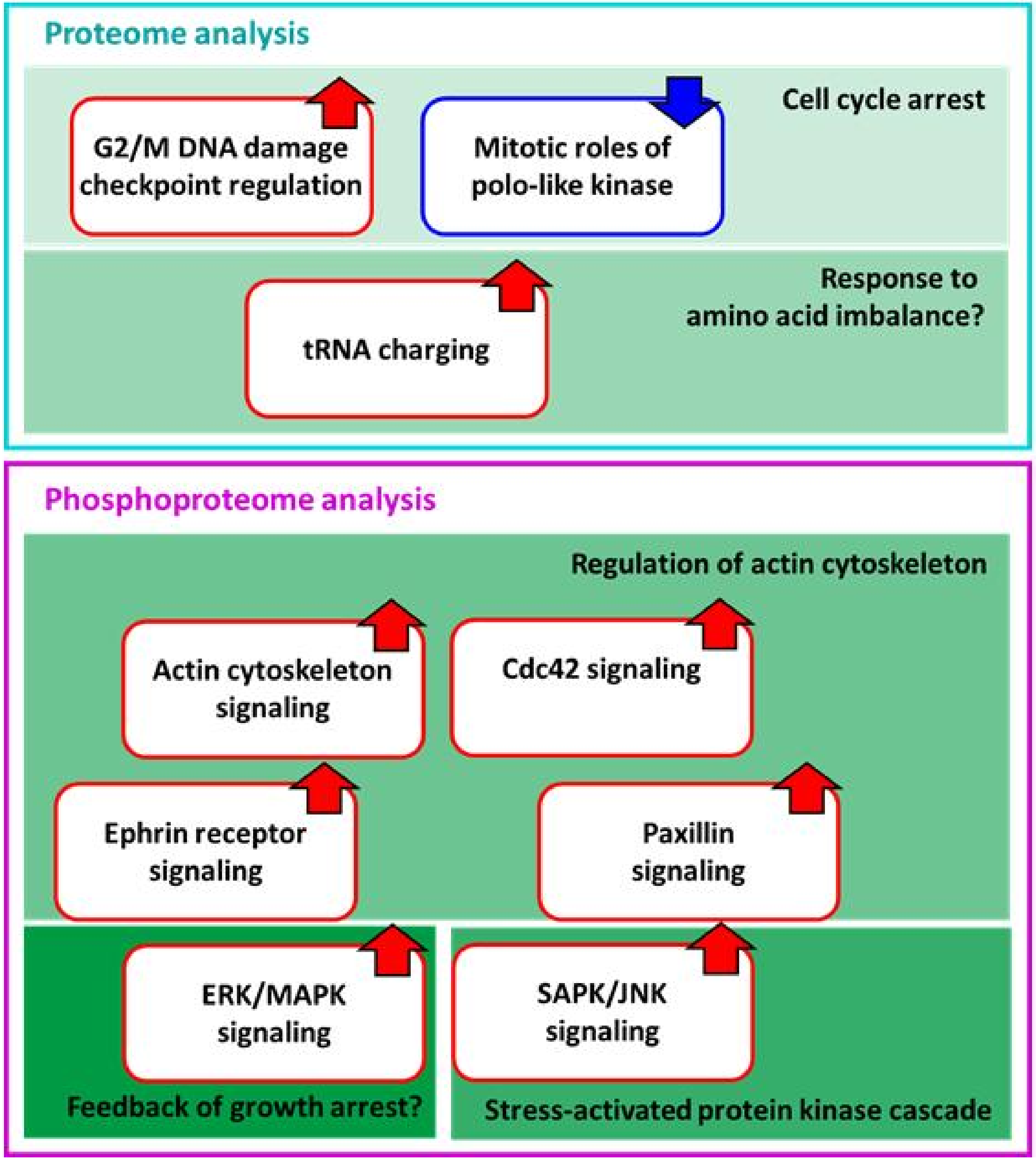
15019 phosphorylation sites (q-value < 0.01, Site probability > 0.75)

Differentially expressed proteins and phosphorylated sites

(p-value < 0.05 and fold change ≥1.2)

Proteomics	**Phosphoproteomics**
348 proteins in KKU-055	4777 sites in KKU-055
342 proteins in KKU-100	3943 sites in KKU-100
252 proteins in KKU-213	3990 sites in KKU-213
1315 proteins in HuCCT-1	5574 sites in HuCCT1

Commonly activate/inactivated pathways



Proteome analysis

Cell cycle arrest

G2/M DNA damage checkpoint regulation

Mitotic roles of polo-like kinase

Response to amino acid imbalance?

tRNA charging

Phosphoproteome analysis

Regulation of actin cytoskeleton

Actin cytoskeleton signaling

Cdc42 signaling

Ephrin receptor signaling

Paxillin signaling

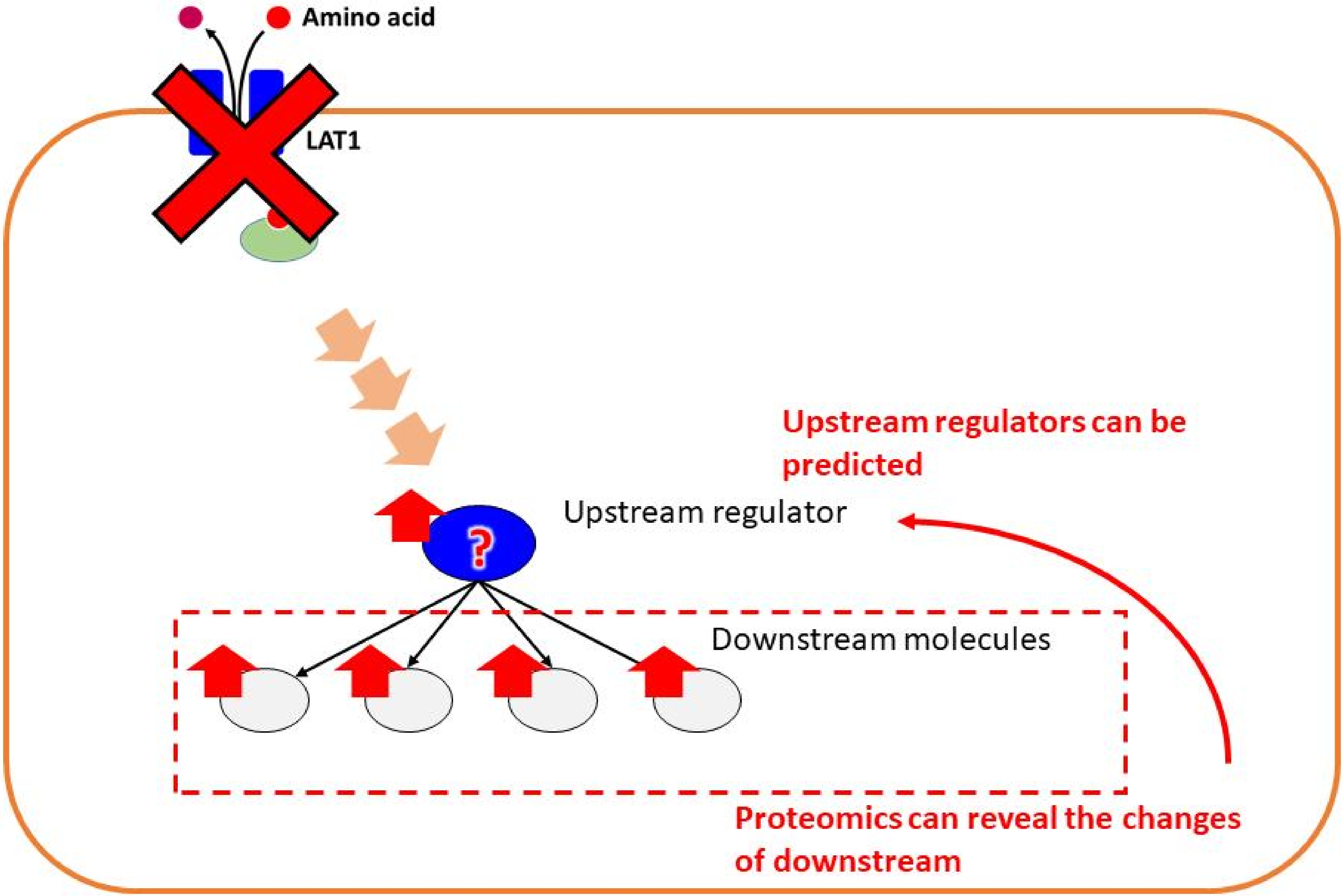
ERK/MAPK signaling

Feedback of growth arrest?

SAPK/JNK signaling

Stress-activated protein kinase cascade

Upstream regulator analysis

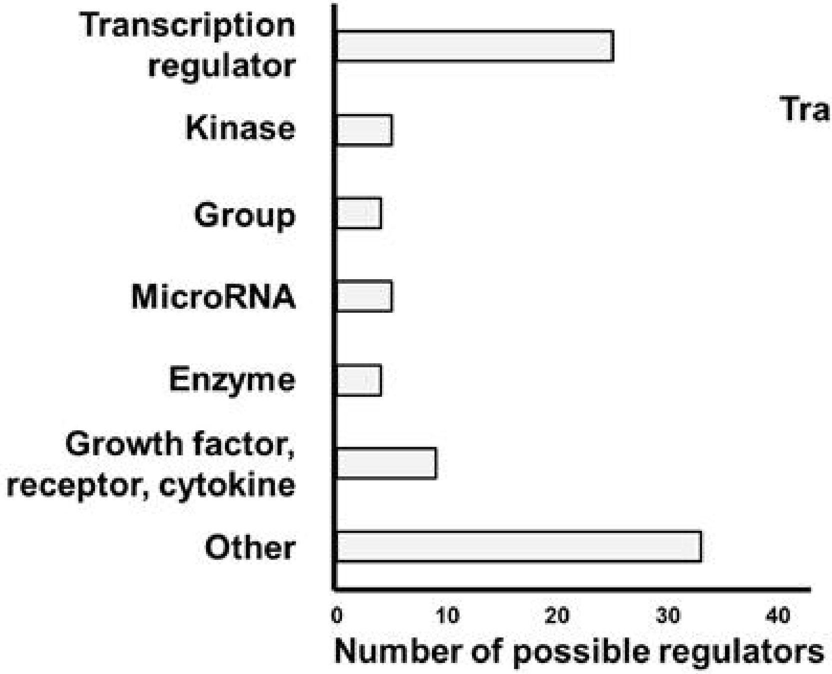


Upstream regulators can be predicted

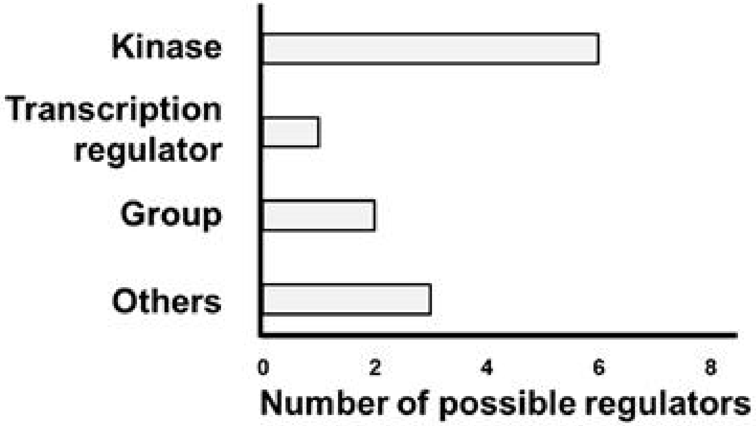
Proteomics can reveal the changes of downstream

Upstream regulator analysis

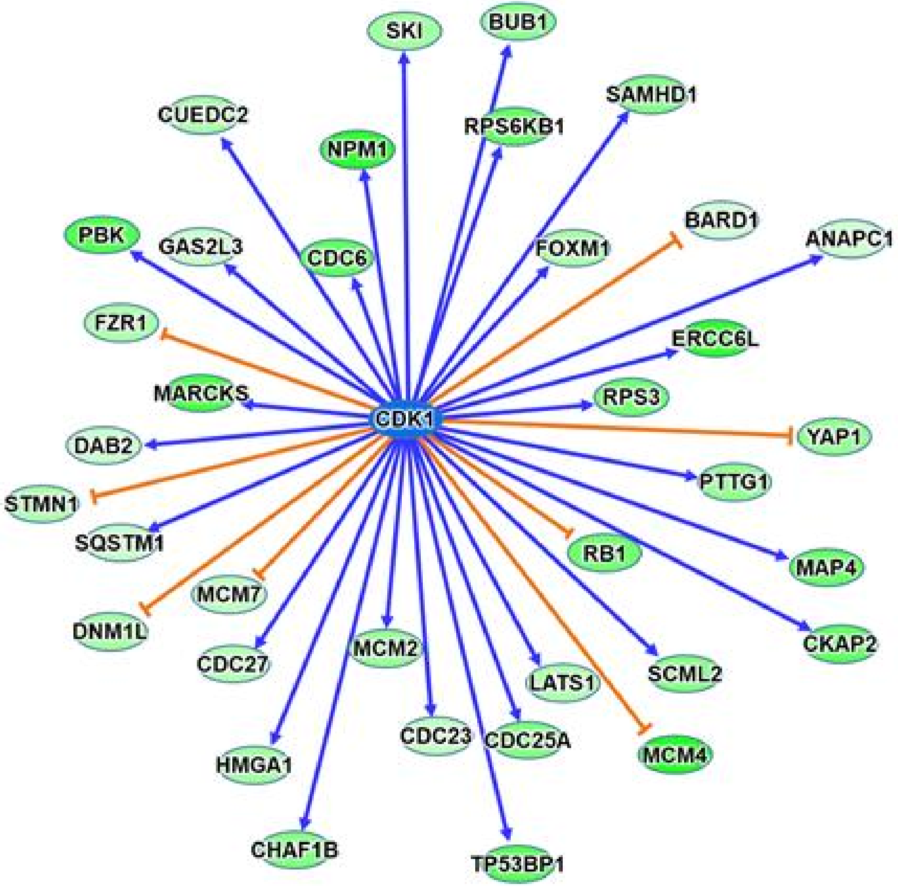
Proteomics

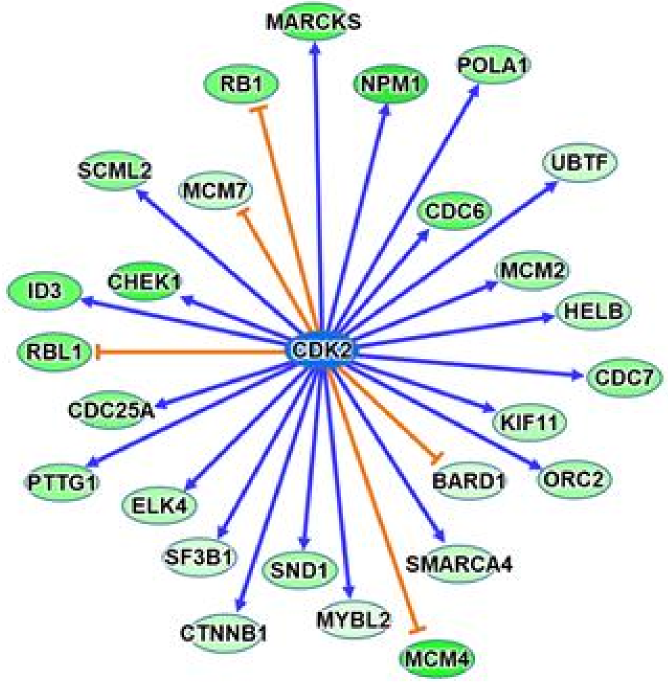


Phospho-proteomics



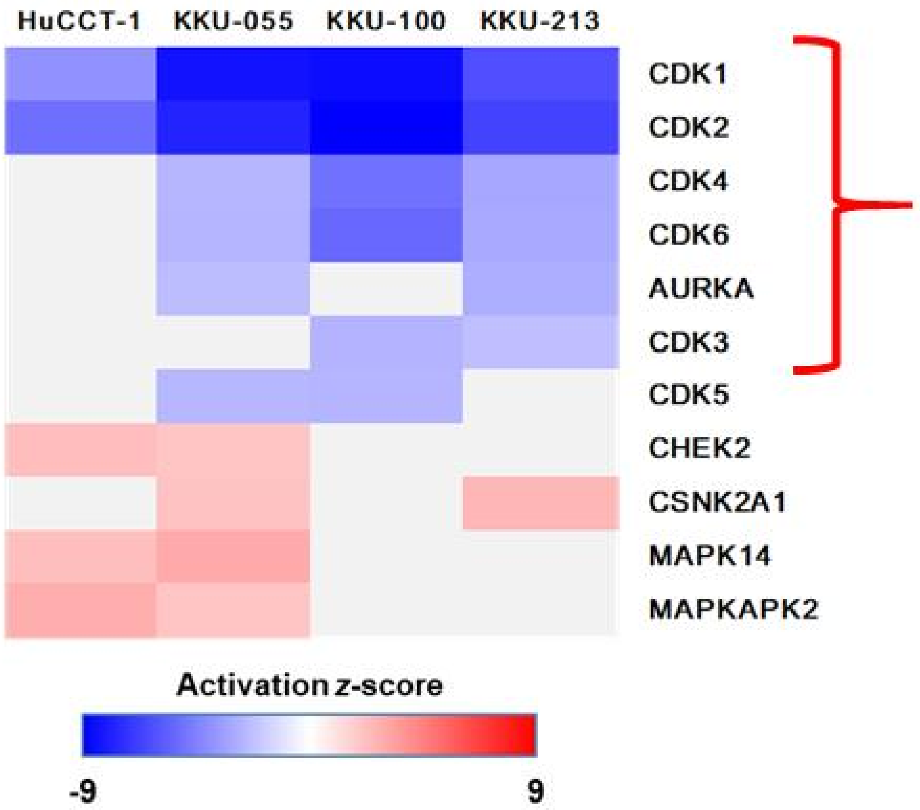
Upstream regulator analysis





Upstream regulator:
Inactivation of cell cycle proteins (CDK1 and CDK2)

Kinase substrate enrichment analysis (KSEA)

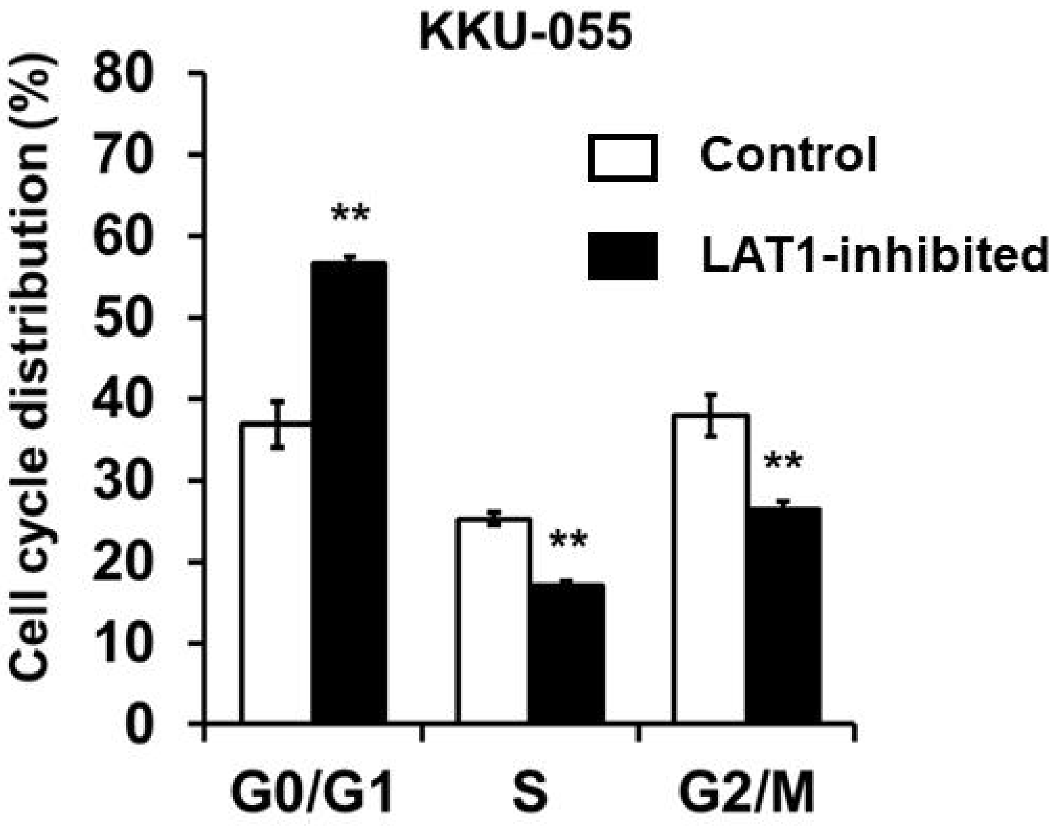


Inactivation of cell cycle-related kinases

CDK1, CDK2, CDK3, CDK4, CDK6
AURKA (aurora kinase A)

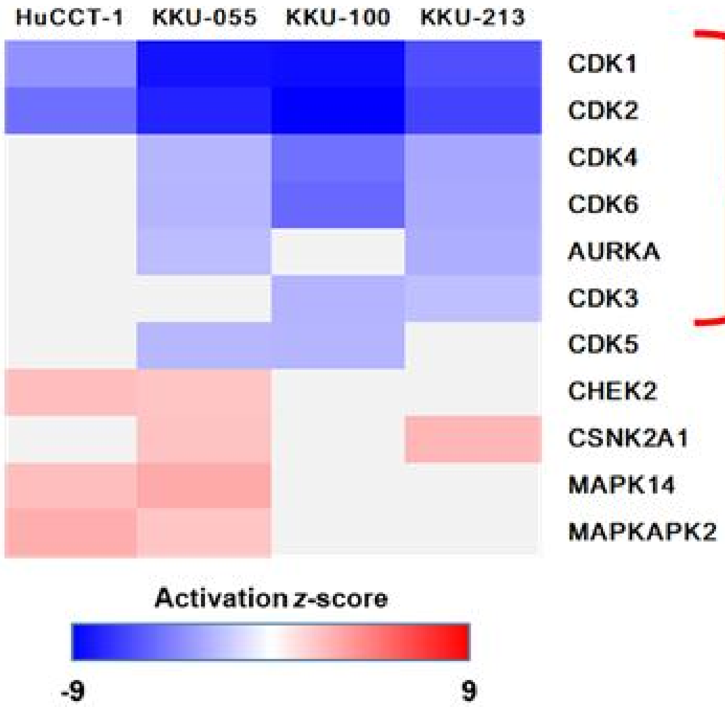
Especially, CDK1 and CDK2.

Cell cycle assay



Increase of G0/G1 phase cells by LAT1 inhibition

Combination of LAT1 inhibitor and CDKs inhibitors



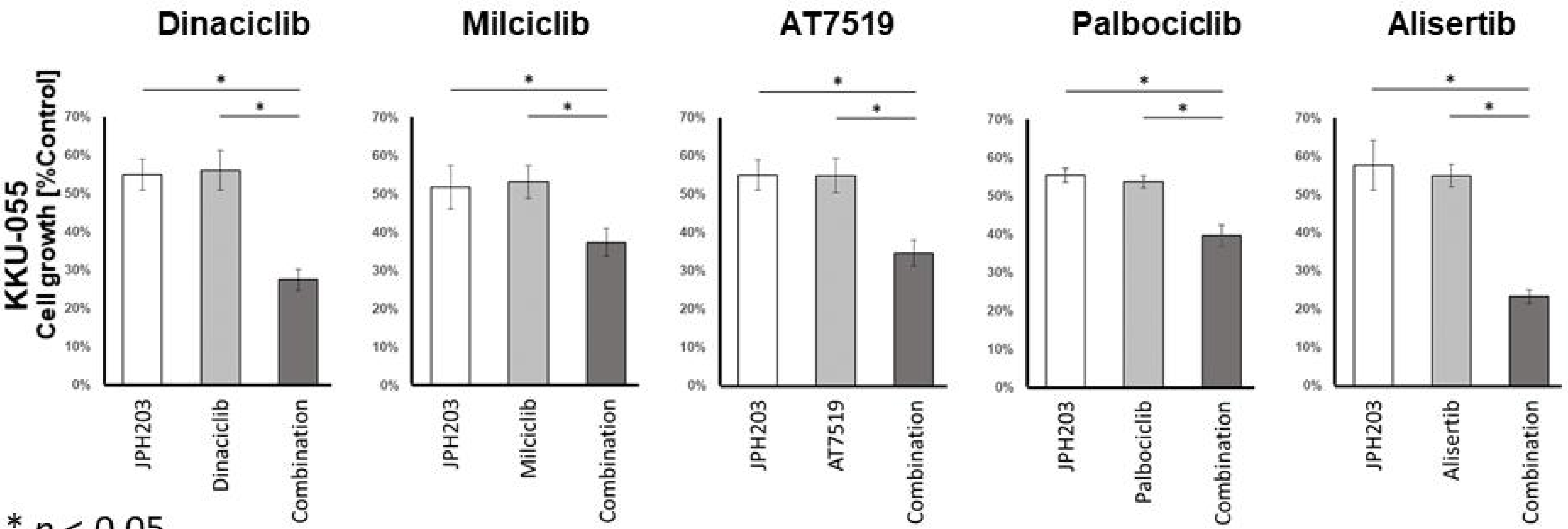
Inactivation of cell cycle-related kinases

CDK1, CDK2, CDK3, CDK4, CDK6
AURKA (aurora kinase A)

Especially, CDK1 and CDK2.

Inhibitors of these CDKs promote anti-cancer effect of LAT1 inhibitor?
(Dinaciclib, Milciclib, AT7519, Palbociclib, …)

Evaluation of drug combinations



* $p < 0.05$

☐ **JPH203 (LAT1 inhibitor)**

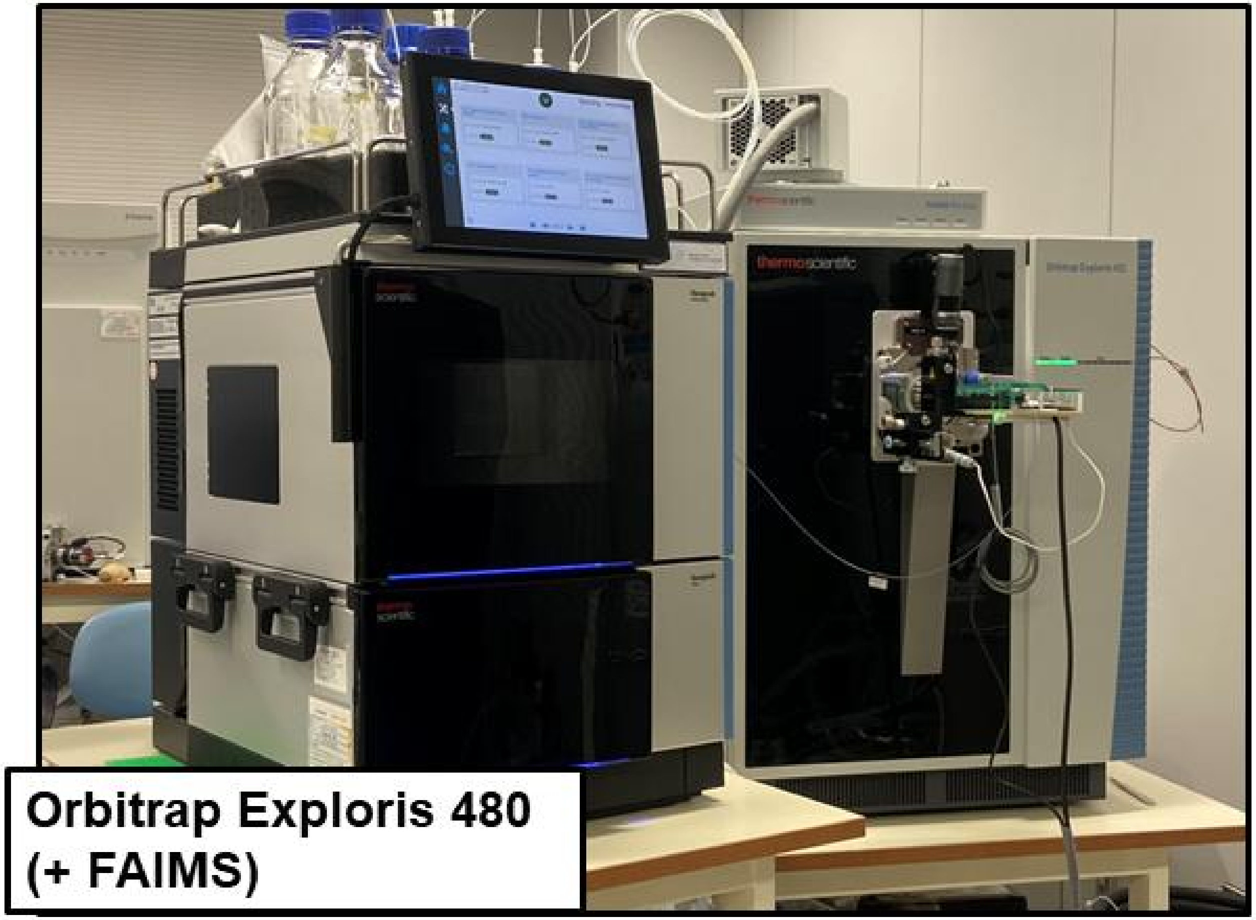
▒ **CDK inhibitor**

▓ **Combination**

Today's topics

1. **Mass spectrometry-based proteomics**
2. **Phosphoproteomics study on cancer cells treated with molecular targeted drug**
3. **LC-MS in CoMIT Omics Center (COC)**

Mass spectrometry-based protein analysis

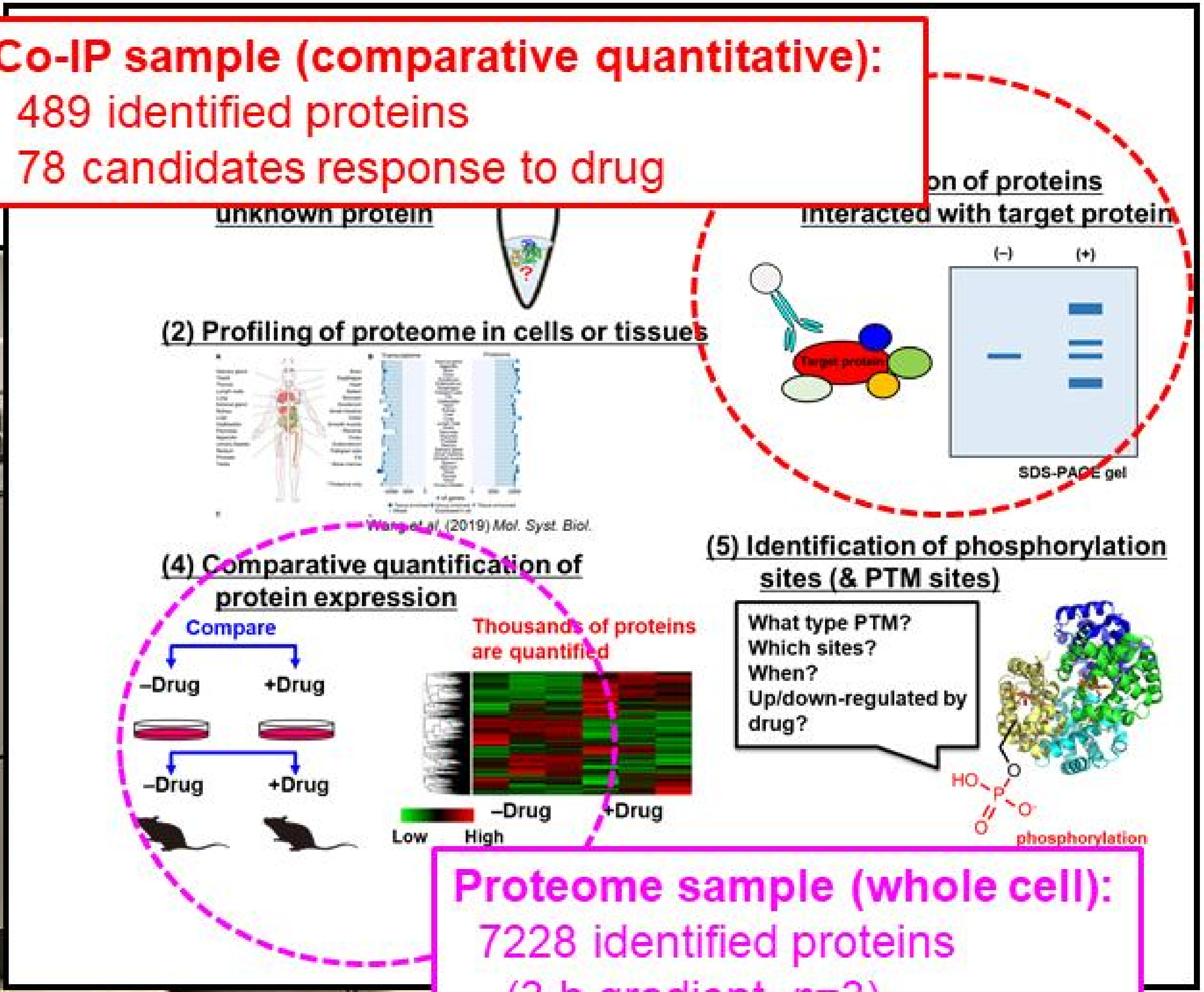


Orbitrap Exploris 480
(+ FAIMS)

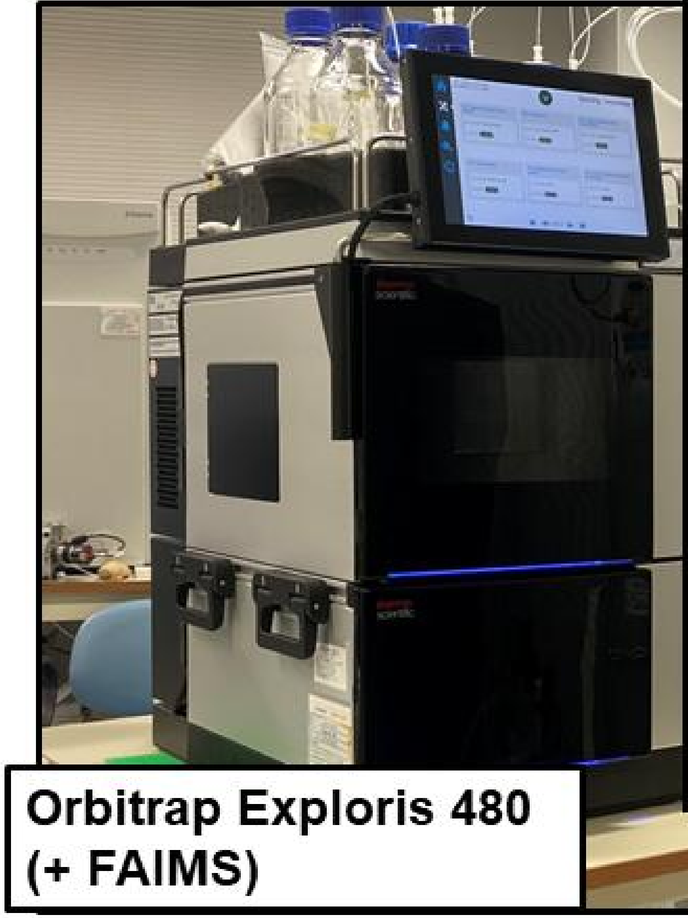
Maximum resolution:
48,000
Max scan speed:
>40 Hz
Turbo TMT available
FAIMS Pro available

Mass spectrometry-based protein analysis

Co-IP sample (comparative quantitative):
489 identified proteins
78 candidates response to drug



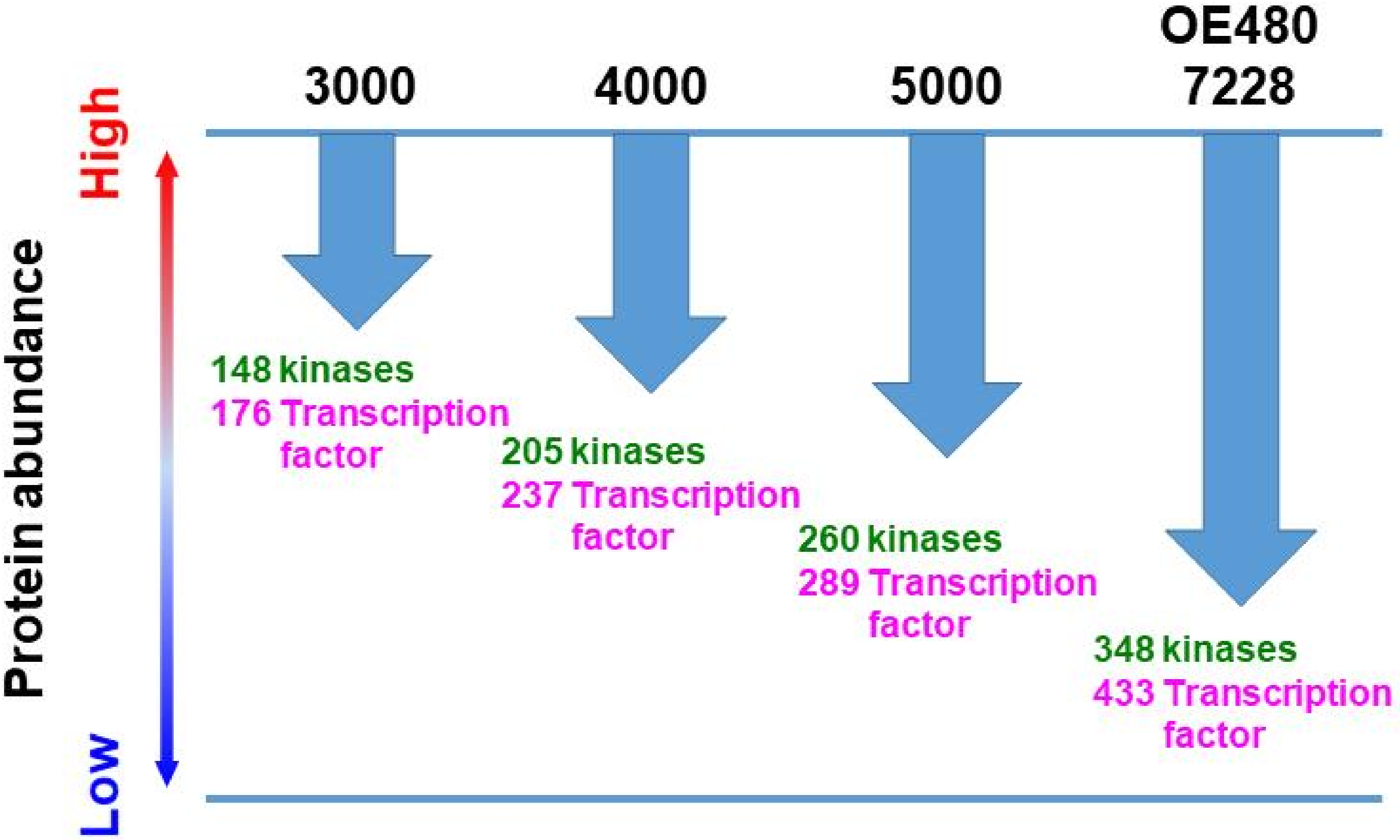
Proteome sample (whole cell):
7228 identified proteins
(3 h gradient, n=3)



Orbitrap Exploris 480
(+ FAIMS)

Mass spectrometry-based protein analysis

No. of identified proteins



High

Protein abundance

Low

3000

148 kinases
176 Transcription factor

4000

205 kinases
237 Transcription factor

5000

260 kinases
289 Transcription factor

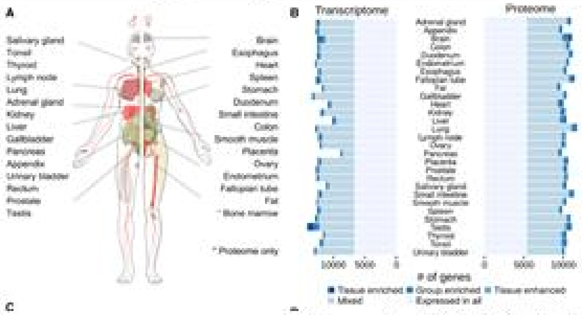
OE480
7228

348 kinases
433 Transcription factor

Mass spectrometry-based protein analysis

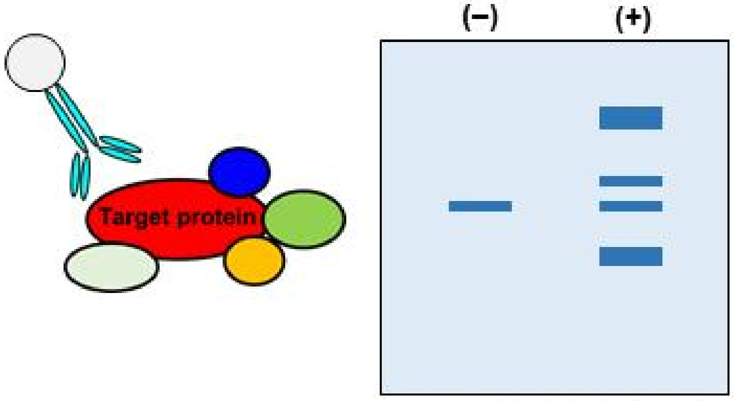
(1) Identification of unknown protein

(2) Profiling of proteome in cells or tissues



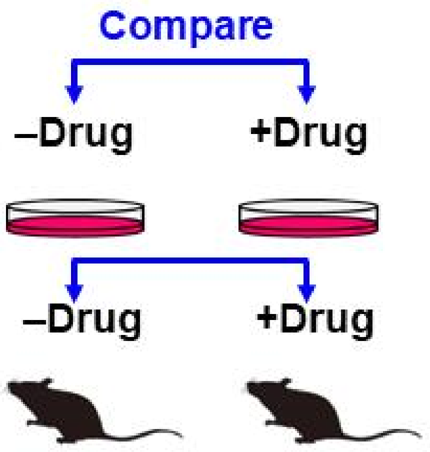
Wang *et al.* (2019) *Mol. Syst. Biol.*

(3) Identification of proteins interacted with target protein

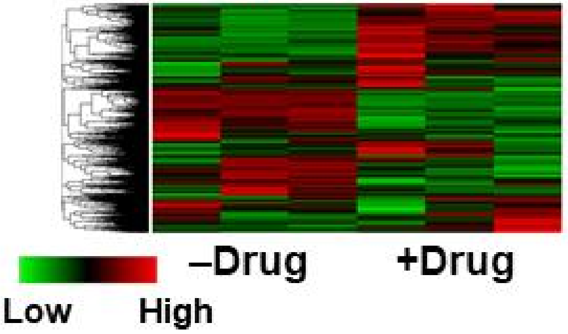


SDS-PAGE gel

(4) Comparative quantification of protein expression



Thousands of proteins are quantified



(5) Identification of phosphorylation sites (& PTM sites)

What type PTM?
Which sites?
When?
Up/down-regulated by drug?