メタボロームデータベースを用いて代謝を理解する

津川裕司（Tokyo University of Agriculture and Technology）

メタボロームデータを出す側と使う側

出す側

- 分析化学
- 質量分析
- イオン
- マススペクトル
- 質量分析インフォマティクス
- アノテーション
- データ標準化

使う側

- データの特徴理解
- 化合物IDの取得
- データの正規化
- 統計・多変量解析
- データベース検索
- 代謝マップ投影
- 適切な数理モデルの選択
- オミクスモジュールへ統合

メタボロームデータを出す側と使う側

メタボロミクスのデータ解析プロトコール

メタボロームデータを「出す側」
（4-2～4-5）

メタボロームデータを「使う側」
（4-6～4-8）

質量分析インフォマティクス

ケムインフォマティクス

バイオインフォマティクス

データ処理（ノンターゲット解析）

XCMS
MS-DIAL　MZmine 2
OpenMS

データ処理（ターゲット解析）

MRMPROBS　Skyline

未知代謝物アノテーション

MS-FINDER
GNPS　MetFrag
SIRIUS

代謝データベース

KEGG　HMDB
ID変換ツール（CTSなど）

パスウェイ解析

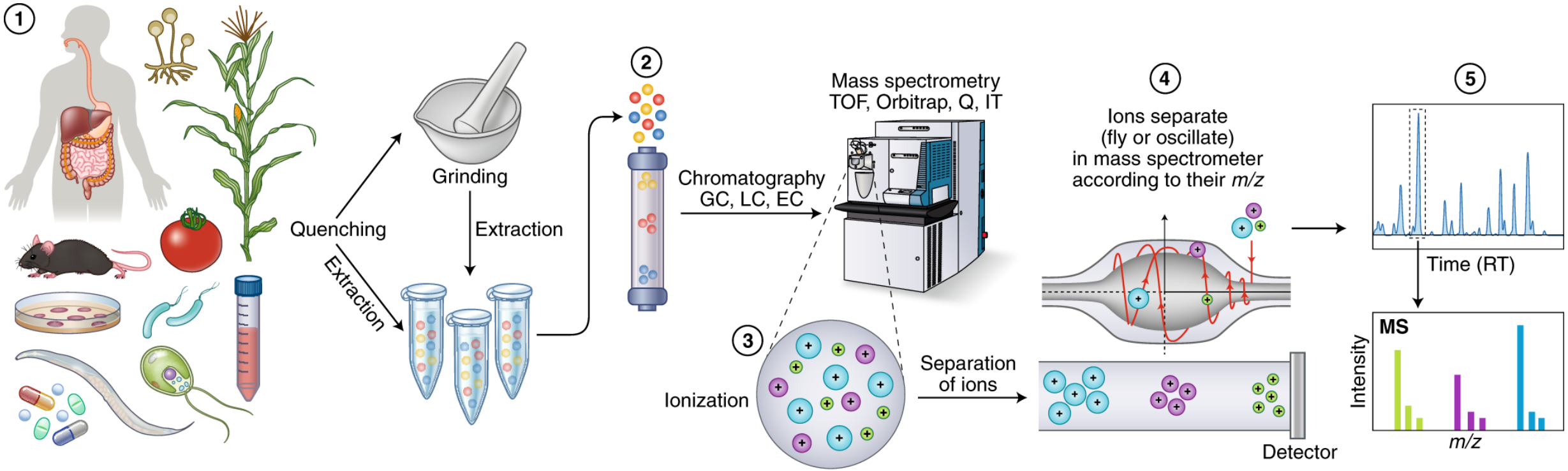
VANTED　MSEA

多変量解析及び統合解析

MetaboAnalyst
transomics2cytoscape
Garudaプラットホーム

その他
データ標準化・レポジトリ
（4-9, 4-10）

Metabolomics workflow



Sample preparation and extraction

- Avoid environmental perturbation during harvesting
- Control environment: harvesting at the same time and under the same conditions
- Snap-freezing in liquid nitrogen
- Enzyme quenching: completely terminate all enzyme activities
- Standards spiked into the quenching solvent
- Grinding, isolation of cells, fast-filtration or aspiration

Sample replication and randomization

- At least four biological replicates, preferably more
- Technical and analytic replicates are worthy of consideration
- Randomization of samples throughout workflows is essential
- In large-scale studies, quality-control samples and batch correction are essential

Chromatography–mass spectrometry

- Separation methods, composition of the mobile phase, column properties and injection volume
- Metabolites are within their range of detection
- Avoid ion suppression: dilution of extracts, sonication, filtration or centrifugation, recovery test
- Choosing ionization source and type of detection mode, MS method, scan number and speed, MS/MS and energy for fragmentation

Nature Methods **18**, 747-756, 2021

メタボロームの多様性とデータ解析の複雑さ

Chemical diversity

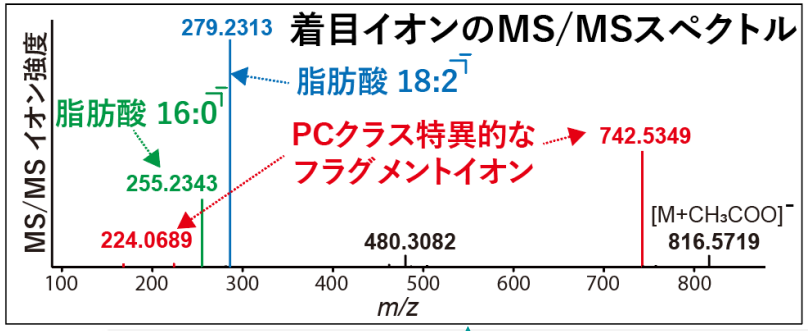
メタボローム
>10^5 chemicals

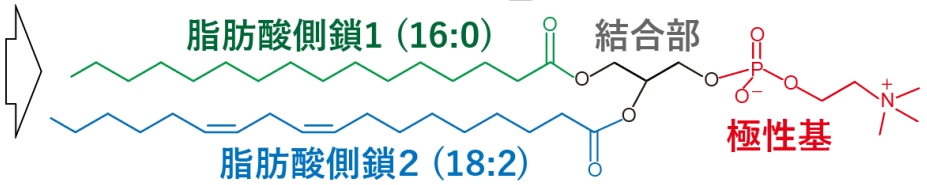
プロテオーム
~20 amion acids

ゲノム
~4 bases

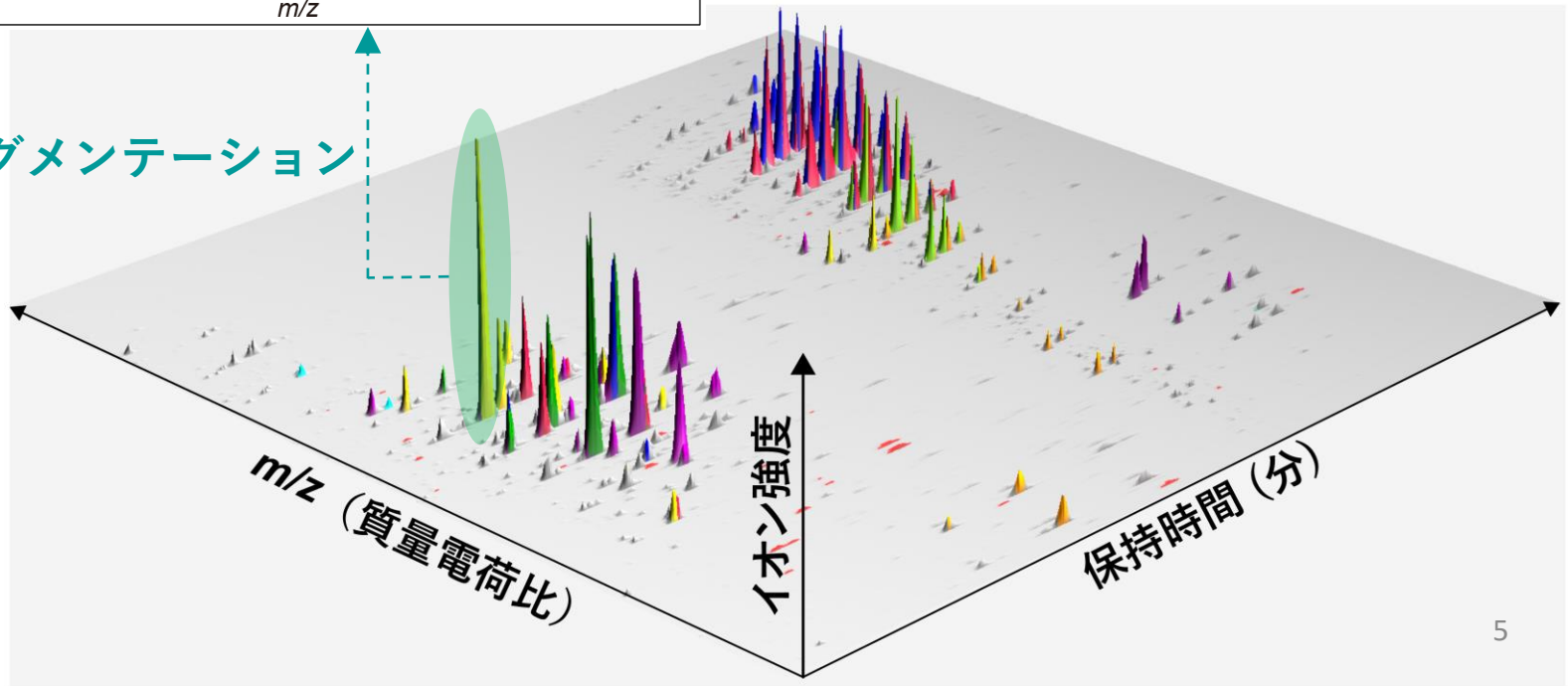
多様な代謝物混合液＋MS計測＝膨大かつ複雑なデータ

液体クロマトグラフィータンデム質量分析（LC-MS/MS）のデータ例





フラグメンテーション



データ形式：生データ（一次データ）

Vendor formats

Agilent	Bruker	LECO	SCIEX	Shimadzu	Thermo	Waters
.D	.D	.PEG	.WIFF .WIFF2	.QGD .LCD	.RAW	.RAW

Data conversion

netCDF (by vendors software), mzML (by ProteoWizard), ABF (by Reifycs), IBF (by MS-DIAL package)

mzML data structure by ProteoWizard

1st data point contents

```
<spectrum index="1" id="sample=1 period=1 cycle=2 experiment=1" defaultArrayLength="3">
  <cvParam cvRef="MS" accession="MS:1000511" name="ms level" value="1"/>
  <cvParam cvRef="MS" accession="MS:1000579" name="MS1 spectrum" value=""/>
  <cvParam cvRef="MS" accession="MS:1000129" name="negative scan" value=""/>
  <cvParam cvRef="MS" accession="MS:1000127" name="centroid spectrum" value=""/>
  <cvParam cvRef="MS" accession="MS:1000505" name="base peak intensity" value="1025.0" unitCvRef="MS" unitAccession="MS:1000131" unitN
  <cvParam cvRef="MS" accession="MS:1000504" name="base peak m/z" value="212.072150517236" unitCvRef="MS" unitAccession="MS:1000040" u
  <cvParam cvRef="MS" accession="MS:1000285" name="total ion current" value="43550.0" unitCvRef="MS" unitAccession="MS:1000131" unitNa
  <cvParam cvRef="MS" accession="MS:1000796" name="spectrum title" value="Nega_Ida_QC_1_1.2.2. File:&amp;quot;Nega_Ida_QC_1_1.wiff&amp;quot;,
  <scanList count="1">
    <cvParam cvRef="MS" accession="MS:1000795" name="no combination" value=""/>
    <scan>
      <cvParam cvRef="MS" accession="MS:1000016" name="scan start time" value="0.004416666667" unitCvRef="UO" unitAccession="UO:00000
      <cvParam cvRef="MS" accession="MS:1000616" name="preset scan configuration" value="1"/>
      <scanWindowList count="1">
        <scanWindow>
          <cvParam cvRef="MS" accession="MS:1000501" name="scan window lower limit" value="100.0" unitCvRef="MS" unitAccession="MS:10
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        </scanWindow>
      </scanWindowList>
    </scan>
  </scanList>
  <binaryDataArrayList count="2">
    <binaryDataArray encodedLength="44">
      <cvParam cvRef="MS" accession="MS:1000523" name="64-bit float" value=""/>
      <cvParam cvRef="MS" accession="MS:1000574" name="zlib compression" value=""/>
      <cvParam cvRef="MS" accession="MS:1000514" name="m/z array" value="" unitCvRef="MS" unitAccession="MS:1000040" unitName="m/z"/>
      <binary>eJxTkrg9ee/9NIcH+gm2IU1ZDgsuGWzVs6h3AACKFwqT</binary>
    </binaryDataArray>
    <binaryDataArray encodedLength="44">
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      <cvParam cvRef="MS" accession="MS:1000574" name="zlib compression" value=""/>
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      <binary>eJxj8Nh3qS/kvX3D+Tadqe4/7RmCnedtfMjpAACOwAsN</binary>
    </binaryDataArray>
  </binaryDataArrayList>
</spectrum>
<spectrum index="2" id="sample=1 period=1 cycle=3 experiment=1" defaultArrayLength="1">
  <cvParam cvRef="MS" accession="MS:1000511" name="ms level" value="1"/>
```

m/z values `binary: [44] 112.9876 174.9537 182.9914 212.0731`

Intensities `binary: [44] 4.67 1.94 14.88 10.68…`

MS-DIAL環境による質量分析データの解析

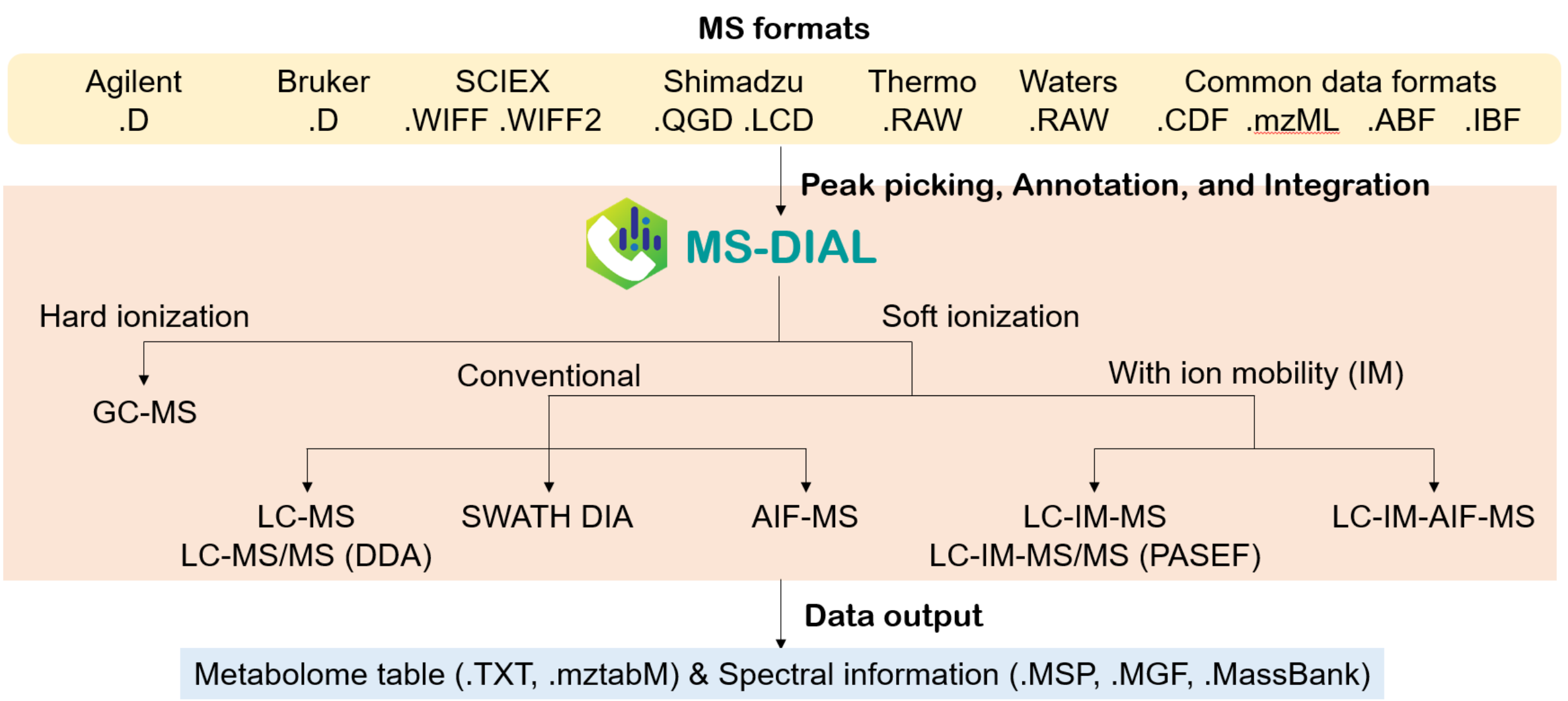


Figure credit to Hiroshi Tsugawa

メタボロームのアノテーション

1．計測方法によって方法が異なる

- GC-MS
- LC-MS/MS
- IM-MS/MS（LC-IM-MS/MS）

2．アノテーションのレベル分けをする必要がある

- Metabolomics Standards Initiativeの定義 *Metabolomics* 2007, **3**, 211–221
- Schymanski E.L. et al. の5段階レベル *Environ. Sci. Technol*. 2014, **48**, 2097–2098
- Lipidomics Standards Initiativeの定義 *Nature Metabolism* 2022, **4**, 1086–1088

アノテーション用のライブラリーファイルとフォーマット

http://prime.psc.riken.jp/compms/msdial/main.html#MSP

Last edited in Aug. 21th, 2022

ESI(+)-MS/MS from authentic standards (16,481 unique compounds)	⊕ MS/MS Positive	324,191 records	
ESI(-)-MS/MS from authentic standards (9,033 unique compounds)	⊖ MS/MS Negative	44,669 records	
ESI(+)-MS/MS from standards+bio+in silico (16,995 unique compounds)	⊕ MS/MS Positive	326,575 records	
ESI(-)-MS/MS from authentic standards (15,245 unique compounds)	⊖ MS/MS Negative	53,337 records	
All records with Kovats RI (9062 unique compounds)	ϟ EI-MS	28,220 records	
Fiehn BinBase DB (Rtx5-Sil MS, predicted Kovats RI)	ϟ EI-MS	1,021 records	
RIKEN DB (Rtx5-Sil MS, Kovats RI)	ϟ EI-MS	241 records	
Kazusa DB (Rtx5-Sil MS, Kovats RI)	ϟ EI-MS	273 records	

整理しておくべきライブラリーフォーマット（MSP形式）

GC-MS用

```
NAME: 1-NITROPYRENE; EI-B; MS
EXACTMASS: 247.0633285
FORMULA: C16H9NO2
SMILES: [O-1][N+1](=O)c(c4)c(c1)c(c3c4)
ONTOLOGY: Pyrenes
INCHIKEY: ALRLPDGCPYIVHP-UHFFFAOYSA-N
RETENTIONTIME: -1
RETENTIONINDEX: 1872.217
QUANTMASS: 201
IONMODE: Positive
COLLISIONENERGY: 70eV
LICENSE: CC BY-SA
Comment:
Num Peaks: 75
51  27
55  80
57  73
58  13
59  13
60  140
61  13
62  33
63  33
66  13
68  87
```

MS/MS用（LC-MS、IM-MS、LC-IM-MSに対応）

```
NAME: Corosolic acid; PlaSMA ID-1295
PRECURSORMZ: 471.34798
PRECURSORTYPE: [M-H]-
FORMULA: C30H48O4
Ontology: Triterpenoids
INCHIKEY: HFGSQOYIOKBQOW-UHFFFAOYNA-N
SMILES: CC1CCC2(CCC3(C)C(=CCC4C5(C)CC
RETENTIONTIME: 9.88
CCS: 222.7776231
IONMODE: Negative
Comment: Annotation level-1; PlaSMA I
Num Peaks: 5
196.13573   18
407.32126   20
471.30518   21
471.34604   3406
471.40079   20

NAME: Ginsenoside compound K; PlaSMA
PRECURSORMZ: 621.43719
PRECURSORTYPE: [M-H]-
FORMULA: C36H62O8
```

整理しておくべきライブラリーフォーマット（TXT形式）

LC-MS、IM-MS、LC-IM-MSデータに便利

	A	B	C	D	E	F	G	H	I
1	Name	MZ	RT	Adduct	InChIKey	Formula	SMILES	Ontology	CCS
2	PC 15:0_18:1(d7)	811.6199	9.5	[M+CH3COO]-	ZEWLMKXMNQOCOQ-GCHPQBSENA-N	C41H73D7NO8P	[C@](COP(=O)([O-])OCC[N+](C)	PC	284.786
3	PE 15:0_18:1(d7)	709.55191	9.64	[M-H]-	ADCNXGARWPJRBV-RGLIIYCRNA-N	C38H67D7NO8P	[C@](COP(=O)(O)OCCN)([H])(O	PE	258.184
4	PS 15:0_18:1(d7)	753.54179	8.38	[M-H]-	KVBAVKWITJZQEG-UDKXCJCZNA-N	C39H67D7NO10P	C(O)(=O)[C@@]([H])(N)COP(OC	PS	268.427
5	PG 15:0_18:1(d7)	740.54655	8.42	[M-H]-	CAKDJPLPYOYWLK-AHOXJELVNA-N	C39H68D7O10P	[H][C@](O)(CO)COP(OC[C@]([H	PG	264.974
6	PI 15:0_18:1(d7)	828.56261	8.35	[M-H]-	XCKYASHMOHAUQB-OAFUKSMZNA-N	C42H72D7O13P	[C@]([H])(OC(CCCCCCC/C=C\CC	PI	279.073
7	PA 15:0_18:1(d7)	666.50975	8	[M-H]-	NKHIVFXDPYZIBK-ZYYJJESQNA-N	C36H62D7O8P	[C@](COP(=O)(O)O)([H])(OC(CC	PA	250
8	LPC 18:1(d7)	587.40594	6.33	[M+CH3COO]-	YAMUFBLWGFFICM-HNNXNMBSNA-N	C26H45D7NO7P	C(COP(=O)([O-])OCC[N+](C)(C)C	LPC	239.829
9	LPE 18:1(d7)	485.33783	6.4	[M-H]-	PYVRVRFVLRNJLY-CCLUNVSZNA-N	C23H39D7NO7P	[C@](COP(=O)(O)OCCN)([H])(O	LPE	209.347
10	SM 18:1;2O/18:1(d9)	796.65303	9.11	[M+CH3COO]-	NBEADXWAAWCCDG-KYPZZJCONA-N	C41H72D9N2O6P	[C@](COP(=O)([O-])OCC[N+](C)	SM	287.235
11	Cer 18:1;2O/15:0(d7)	589.554235	9.34	[M+CH3COO]-	HBULQAPKKLNTLT-BXLQGFJZSA-N	C33H58D7NO3	[H][C@@](O)(\C=C\CCCCCCCC	Cer-NS	249.173
12	FA 18:0(d3)	286.283084	6.96	[M-H]-	QIQXTHQIDYTFRH-FIBGUPNXSA-N	C18H33D3O2	[2H]C([2H])([2H])CCCCCCCCCC	FA	177.728
13	FA 16:0(d3)	258.251784	6.3	[M-H]-	IPCSVZSSVZVIGE-FIBGUPNXSA-N	C16H29D3O2	[2H]C([2H])([2H])CCCCCCCCCC	FA	169.563

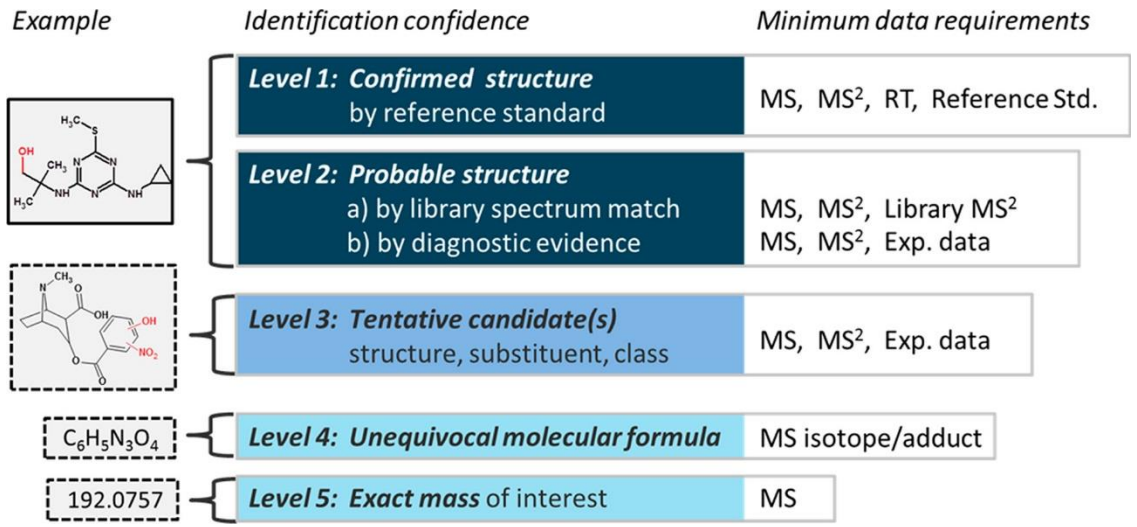
*必ずTab区切りテキストで保存すること

メタボロームのアノテーション

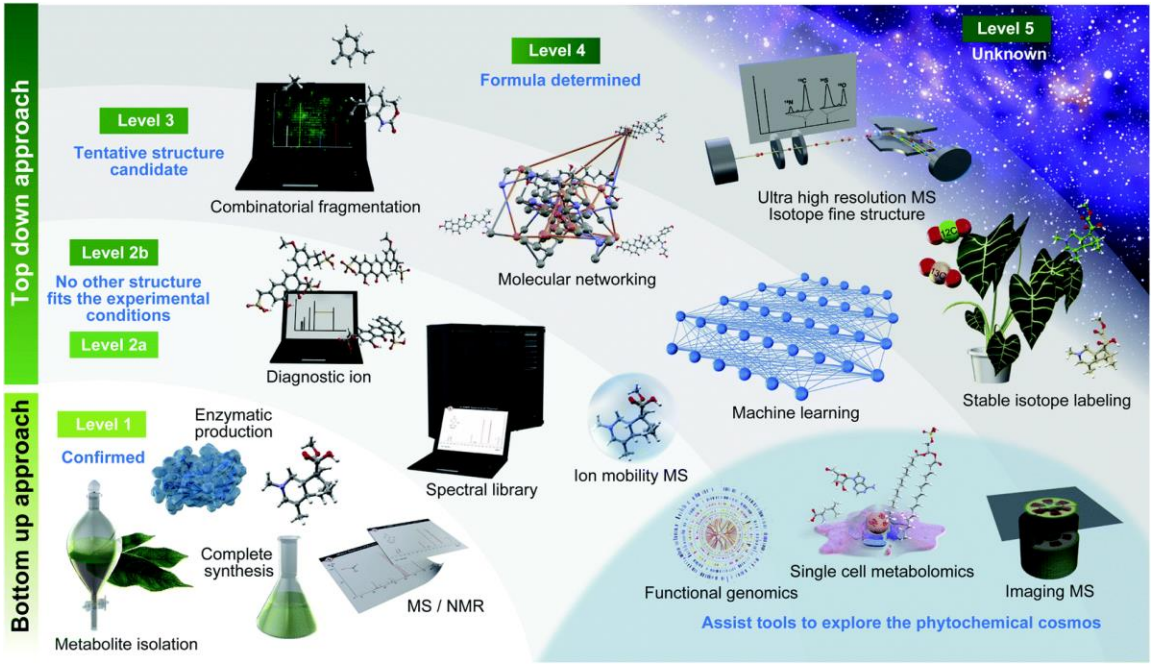
1．計測方法によって方法が異なる
・GC-MS
・LC-MS/MS
・IM-MS/MS（LC-IM-MS/MS）

2．アノテーションのレベル分けをする必要がある
・Metabolomics Standards Initiativeの定義　*Metabolomics* 2007, **3**, 211–221
・Schymanski E.L. et al. の5段階レベル　*Environ. Sci. Technol*. 2014, **48**, 2097–2098
・Lipidomics Standards Initiativeの定義　*Nature Metabolism* 2022, **4**, 1086–1088

Schymanski E.L. et al. の5段階レベル（脂質は別に定義）



Environ. Sci. Technol. 2014, **48**, 2097–2098



Nat. Prod. Rep. 2021 **38**, 1729-1759

Level 1: Confirmed structure represents the ideal situation, where the proposed structure has been confirmed via appropriate measurement of a reference standard with MS, MS/MS and retention time matching. If possible, an orthogonal method should also be used.

Level 2a: Library this involves matching literature or library spectrum data where the spectrum-structure match is unambiguous.

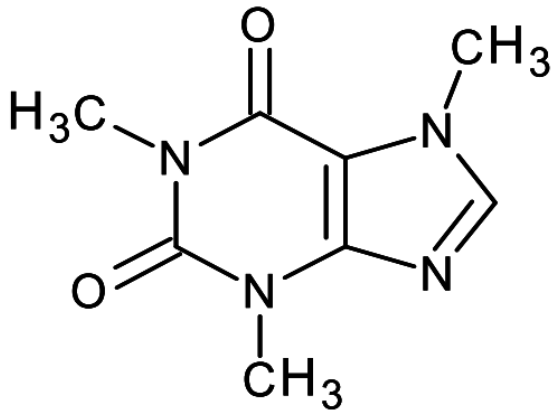
Level 2b: Diagnostic represents the case where no other structure fits the experimental information, but no standard or literature information is available for confirmation. Evidence can include diagnostic MS/MS fragments and/or ionization behavior, parent compound information and the experimental context.

Level 3: Tentative candidate(s) describes a “grey zone”, where evidence exists for possible structure(s), but insufficient information for one exact structure only (e.g., positional isomers).

Level 4: Unequivocal molecular formula is possible when a formula can be unambiguously assigned using the spectral information (e.g., adduct, isotope, and/or fragment information), but insufficient evidence exists to propose possible structures.

Level 5: Exact mass (*m/z*) can be measured in a sample and be of specific interest for the investigation, but lack information to assign even a formula.

Let's use InChIKey as a unique identifier of metabolite



InChI=1S/C8H10N4O2/c1-10-4-9-6-5(10)7(13)12(3)8(14)11(6)2/h4H,1-3H3 (caffeine)

character indicating the number of protons ('N' means neutral)

InChIKey=RYYVLZVUVIJVGH-UHFFFAOYSA-N

flag character for InChI version: 'A' for version 1

First block (14 letters)

Encodes molecular skeleton (connectivity)

Second block (8 letters)

Encodes stereochemistry and isotopes

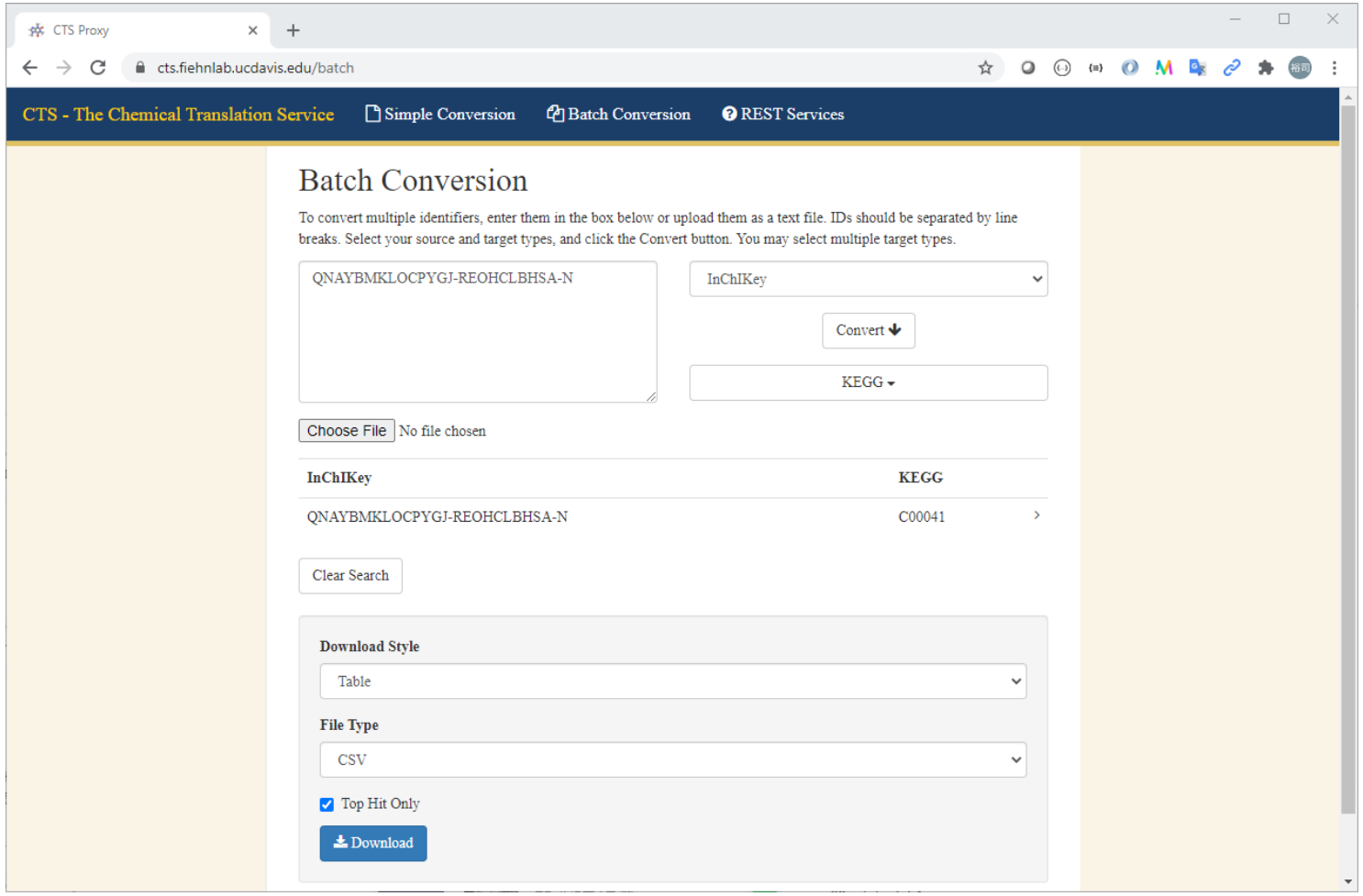
flag character ('S') indicates standard InChIKey (produced out of standard InChI)

J Cheminform **7,** 23 (2015)

InChIKeyがあれば様々なIDに変換可能

Alanine

InChIKey: QNAYBMKLOCPYGJ-REOHCLBHSA-N

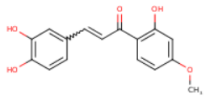


Bioinformatics **26,** 2647-2648 (2010)

ClassyFire categorizing metabolite into a chemical class

ClassyFire Browse Classify About ClassyFire Contact Downloads Help

Structure Information



Compound Identification

SMILES	
COC1=CC(O)=C(C=C1)C(=O)C=CC1=CC(O)=C(O)C=C1	
InChIKey	
InChIKey=IULVGTQOZKYHCS-UHFFFAOYSA-N	
Formula	
C16H14O5	
Mass	
286.283	

Export to:

JSON SDF CSV

Taxonomic Classification

Taxonomy Tree

Kingdom: Organic compounds
Superclass: Phenylpropanoids and polyketides
Class: Linear 1,3-diarylpropanoids
Subclass: Chalcones and dihydrochalcones
Level 5: 2'-Hydroxychalcones

J Cheminform **8,** 61 (2016)

ClassyFire Batch by Fiehn Lab

Batch Compound Classification

ClassyFire[1] is a web-based application developed by the Wishart Research Group for automated structural classifica independent tool that retrieves and formats ClassyFire results for a list of InChIKey identifiers.

If you encounter any bugs or problems, please let us know using our issue tracker.

August 2019: We are migrating to an updated server with a local database cache. Speeds are still slower than they u should be minimal.

InChIKeys (one per line):

FZWWJIXYNHHIJI-QBZLNYABNA-N
HHARWONQTCORMN-UHFFFAOYNA-N
UYALDZZEAZIEME-YWGUMEFLNA-N
YIEPZDPKKNJALX-CKPZSVDJNA-N
ZAZHPBXBNGWCDV-UHFFFAOYNA-N
NFBYZSYLZUMCFV-JJRRTKJUSA-N
RPMNUQRUHXIGHK-PYXJVEIZSA-N
JRNZEGAFLBTZDT-JTVHLFNZNA-N
WKEMJKQOLOHJLZ-UHFFFAOYSA-N
RAMPQQLLROWEJQ-JJASCTQYNA-N

Please enter one InChIKey per line

ClassyFy

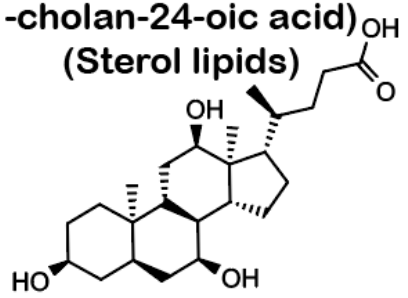
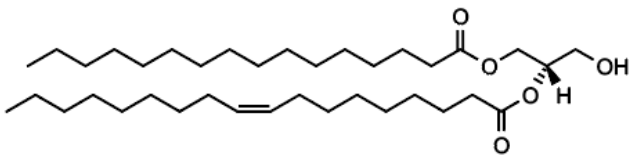
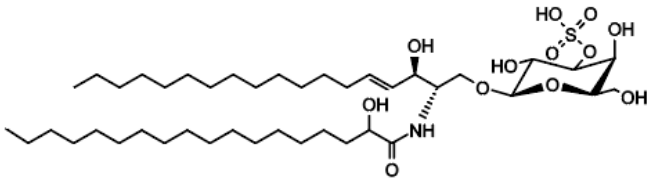
ClassyFire categorizing metabolite into a chemical class

InChIKey	Status	Kingdom	Superclass	Class	Subclass	Parent Level 1	Parent Level 2	Parent Level 3
PFRVZQKEOAYKSC-UHFFFAOYNA-N	Completed	Organic compounds	Alkaloids and derivatives	Amaryllidaceae alkaloids	Galanthamine-type amaryllidaceae alkaloids	Galanthamine-type amaryllidaceae alkaloids		
GJHTVUOIDXUACV-UHFFFAOYNA-N	Completed	Organic compounds	Phenylpropanoids and polyketides	Flavonoids	Flavonoid glycosides	Flavonoid C-glycosides	Flavonoid 8-C-glycosides	
MMJPRTHFLGOVBZ-UHFFFAOYSA-N	Completed	Organic compounds	Benzenoids	Benzene and substituted derivatives	Benzenesulfonic acids and derivatives	Benzenesulfonic acids and derivatives		
UJSYMVCGDZCLIO-DILIWIBYSA-N	Completed	Organic compounds	Lipids and lipid-like molecules	Prenol lipids	Monoterpenoids	Aromatic monoterpenoids		
ZWDZSGCQFGIYBE-UHFFFAOYSA-N	Completed	Organic compounds	Organic acids and derivatives	Carboxylic acids and derivatives	Amino acids, peptides, and analogues	Amino acids and derivatives	Beta amino acids and derivatives	
SEOZHEFAHJQWFY-USNXYBSJSA-N	Completed	Organic compounds	Phenylpropanoids and polyketides	Stilbenes	Stilbene glycosides	Stilbene glycosides		

Failed classifications occur when ClassyFire does not contain the given InChIKey in its database. If all results fail, this could be due to network issues - in this case, please try again later.

Export as CSV Reset

曖昧な脂質表記からでも、明確な定義構造のリストを出力する

	Cholic acid (3α,7α,12α-Trihydroxy-5β-cholan-24-oic acid) (Sterol lipids) 	Diacylglycerol (Glycerolipids) 	Sulfatide (Sphingolipids) 
Species level	ST 24:1;O5	DG 34:1	SHexCer 36:1;3O
Molecular species level		DG 16:0_18:1	SHexCer 18:1;O2/18:0;O
sn-Position level		DG 16:0/18:1	
Structure defined level			SHexCer 18:1;(1OH,3OH)/18:0;(2OH)
Full structure level	ST 24:0;(5bH);(3aOH, 7aOH,12aOH)(24COOH)	DG 16:0/18:1(9Z)/0:0	3'-sulfo GalβCer 18:1(4E); (1OH,3OH)/18:0;(2OH)

http://prime.psc.riken.jp/compms/msdial/lipidnomenclature.html

Liebisch G. et al. *J. Lipid Res.* 2020, **61**, 1539-1555

LipidLynxXによるIDコンバート

LipidLynxX

PLPC

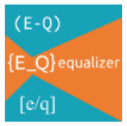
Check resources

LipidLynxX Tools | Nomenclature & Levels

Lipid ID Converter

Convert different abbreviations to unified LipidLynxX identifier.

Run Converter



Lipid ID Equalizer

Bring lipid identifiers to the same level of annotation and perform cross-level matching between different datasets.

Run Equalizer

Lipid Resource Linker

Collect available resources across databases.

Run Linker

LipidLynxXによるIDコンバート

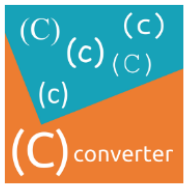
LipidLynxX Converter

Convert list | Convert file

Input lipid abbreviations

lipid_names

palmitic acid
DHA
HETE
PLPE
PC O-16:0_18:2
FaCoA 18:2;O
C18 Sphingomyelin



Lipid ID Converter

Convert different abbreviations to unified LipidLynxX identifier.

Choose the export style: LipidLynxX

他　Shorthand notation…

Choose the export Level: Bulk

他　Molecular species level

- COMP_DB and BioPAN export in **Bulk** level only.
- LipidCreator export supports **Molecular species** and **sn specific species**.
- LPPtiger export in **sn specific species** level only.

Choose the export format: .xlsx

Shorthand, Bulkを選択

TextInput	TextInput_converted
C18 Sphingomyelin	SM 36:1;2
DHA	FA 22:6
FaCoA 18:2;O	CoA 18:2;O
HETE	FA 20:4+16
palmitic acid	FA 16:0
PC O-16:0_18:2	PC O-34:2
PLPE	PE 34:2

Shorthand, Maxを選択

TextInput	TextInput_converted
C18 Sphingomyelin	SM 18:1;2/18:0
DHA	FA 22:6(4Z,7Z)
FaCoA 18:2;O	CoA 18:2;O
HETE	FA 20:4(OH)
palmitic acid	FA 16:0
PC O-16:0_18:2	PC O-16:0_18:2
PLPE	PE 16:0/18:2(9Z,12Z)

LipidLynxXによるresourceリンク

LipidLynxX Linker

Link list | Link file

Input lipid abbreviations:

lipid names (max 100 rows)

PLPC
PLPE
PC O-16:0_18:2
C18 Sphingomyelin

Choose the export format: .xlsx

Lipid Resource Linker

Collect available resources across databases.

Save output: LipidLynxX-Linker-20221119-102101-25c6.xlsx

Input Lipid	Converted Notation (LipidLynxX)	Resources
PLPC	PC(16:0/18:2<{9Z,12Z}>)	View resource details
PLPE	PE(16:0/18:2<{9Z,12Z}>)	View resource details
PC O-16:0_18:2	PC(O-16:0_18:2)	View resource details
C18 Sphingomyelin	SM(18:1;O2/18:0)	View resource details

Input Lipid:	PLPC
Shorthand Notation:	PC 16:0/18:2(9Z,12Z)
LipidLynxX Notation:	PC(16:0/18:2<{9Z,12Z}>)
BioPAN Notation:	PC 34:2

Lipid database | Metabolites database | Lipid ontology | General database | Pathways | Reactions | Related database

§ Lipid database

⇄ lipidmaps

LMGP01010594 : https://www.lipidmaps.org/data/LMSDRecord.php?LMID=LMGP01010594

⇄ swisslipids

SLM:000000792 : https://www.swisslipids.org/#/entity/SLM:000000792/

§ Metabolites database

⇄ hmdb

HMDB0007973 : https://hmdb.ca/metabolites/HMDB0007973

§ Lipid ontology

⇄ lion

0003021 : http://bioportal.bioontology.org/ontologies/LION/?p=classes&conceptid=http%3A%2F%2Fpurl.obolibrary.org%2Fobo%2FLION_0003021

§ General database

⇄ chebi

73002 : https://www.ebi.ac.uk/chebi/searchId.do?chebiId=CHEBI:73002

⇄ pubchem

5287971 : https://pubchem.ncbi.nlm.nih.gov/compound/5287971

§ Pathways

⇄ kegg

C00157 : https://www.kegg.jp/dbget-bin/www_bget?cpd:C00157

メタボロームデータを出す側と使う側

メタボロミクスのデータ解析プロトコール

メタボロームデータを「出す側」
（4-2～4-5）

メタボロームデータを「使う側」
（4-6～4-8）

質量分析インフォマティクス

ケムインフォマティクス

バイオインフォマティクス

データ処理（ノンターゲット解析）

XCMS
MS-DIAL　MZmine 2
OpenMS

データ処理（ターゲット解析）

MRMPROBS　Skyline

未知代謝物アノテーション

MS-FINDER
GNPS　MetFrag
SIRIUS

代謝データベース

KEGG　HMDB
ID変換ツール（CTSなど）

パスウェイ解析

VANTED　MSEA

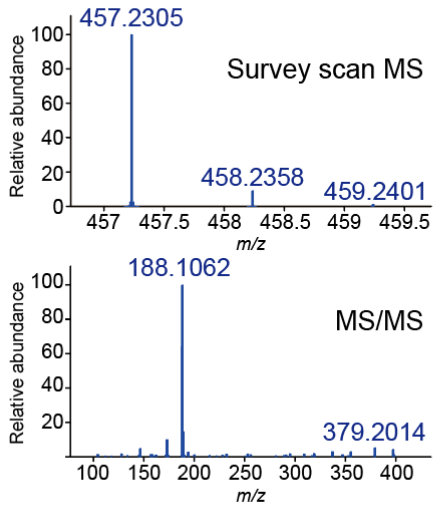
多変量解析及び統合解析

MetaboAnalyst
transomics2cytoscape
Garudaプラットホーム

その他
データ標準化・レポジトリ
（4-9, 4-10）

未知マススペクトルのアノテーション

a. Get MS & MS/MS spectrum



b. Formula generation

Input
m/z: 457.23053
Adduct: $[M+H]^+$
Tolerance: 0.003 Da

Valence- & element ratio check

$C_{25}H_{32}N_2O_6$ $C_{11}H_{37}N_8O_7SP$ $C_{21}H_{28}N_8O_4$
$C_{13}H_{34}N_{10}O_4P_2$ $C_{12}H_{38}N_6O_8P_2$

c. Formula ranking

Candidates

Scoring
Mass error
Isotopic ratio
Product ion annotation
Neutral loss annotation
Inclusion in metabolome DBs

Top: $C_{25}H_{32}N_2O_6$

Metabolome databases
HMDB
YMDB
SMPDB
UNPD
ChEBI
PlantCyc
PubChem (Biopathway)
DrugBank
BMDB
KNApSAcK
FooDB
ECMDB
T3DB

d. Structure searching

PubChem database

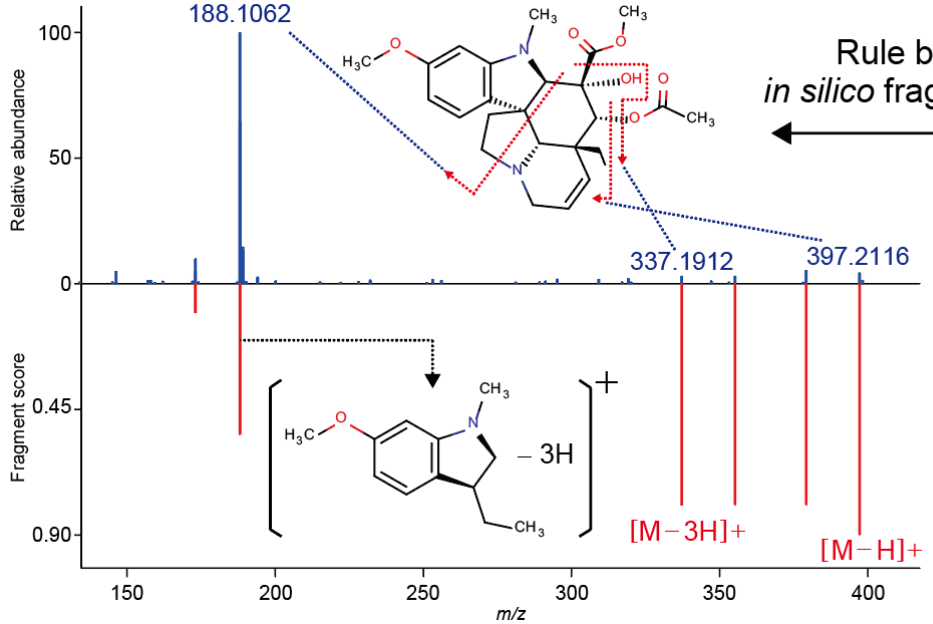
Structure candidates

Focus on first layer of InChIKey

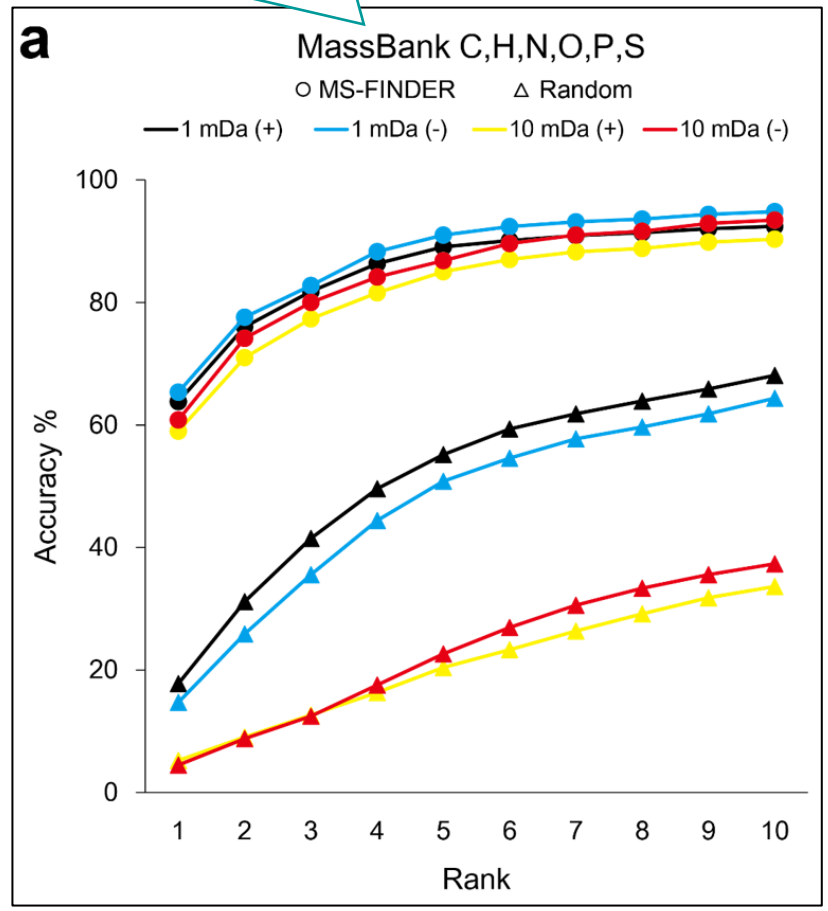
XBGOBGJHGGWIE-**********-*
ITHNZGQTXZZCTI-**********-*
HYEXIINDBCFMOM-**********-*
NVRFOCOGUIYAQL-**********-*
NQKHZSNXAUQSHC-**********-*

Rule based-
in silico fragmentation

e. Structure ranking



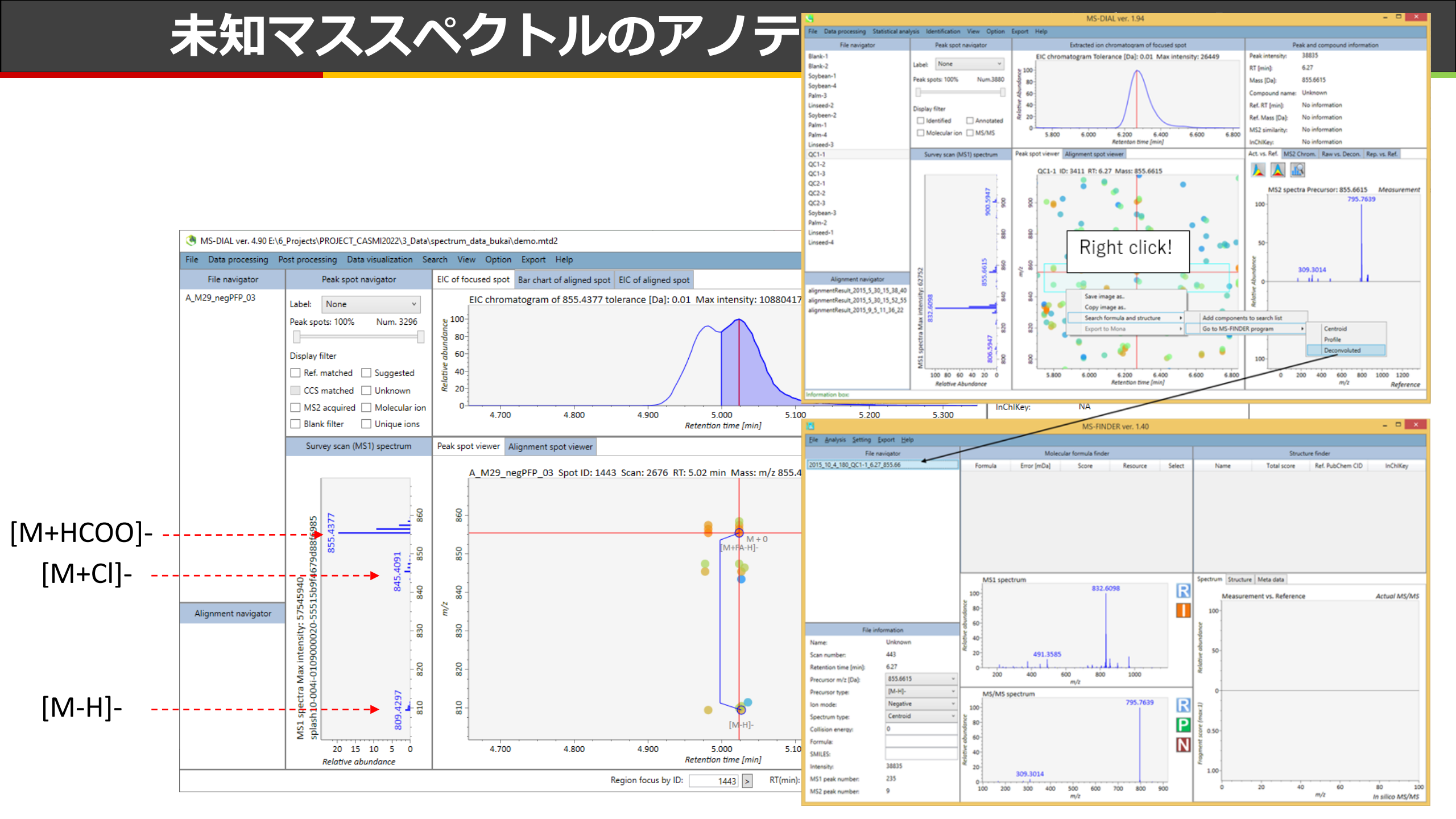
Validation using 3,000 MS/MS data



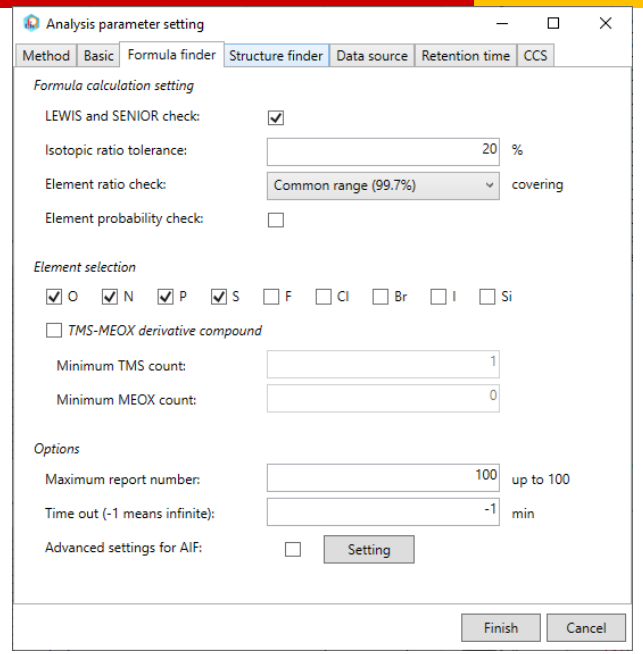
Anal. Chem. **88**, 7946-7958, 2016

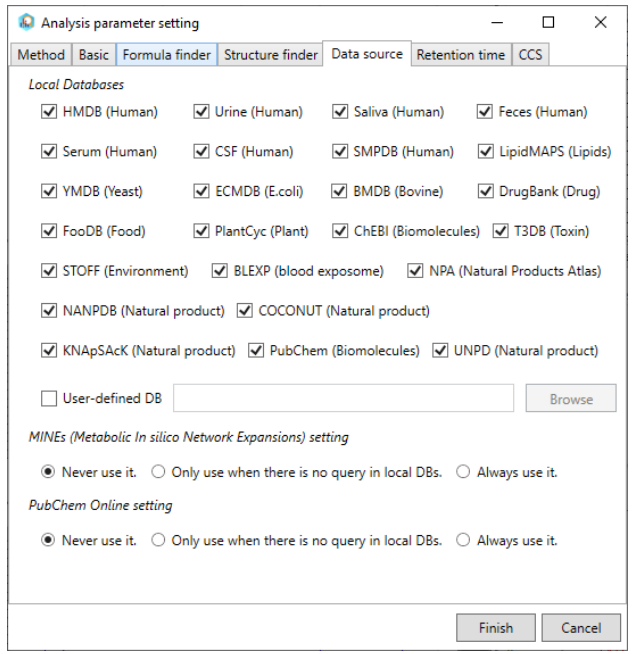
未知マススペクトルのアノテーションの簡単な流れ

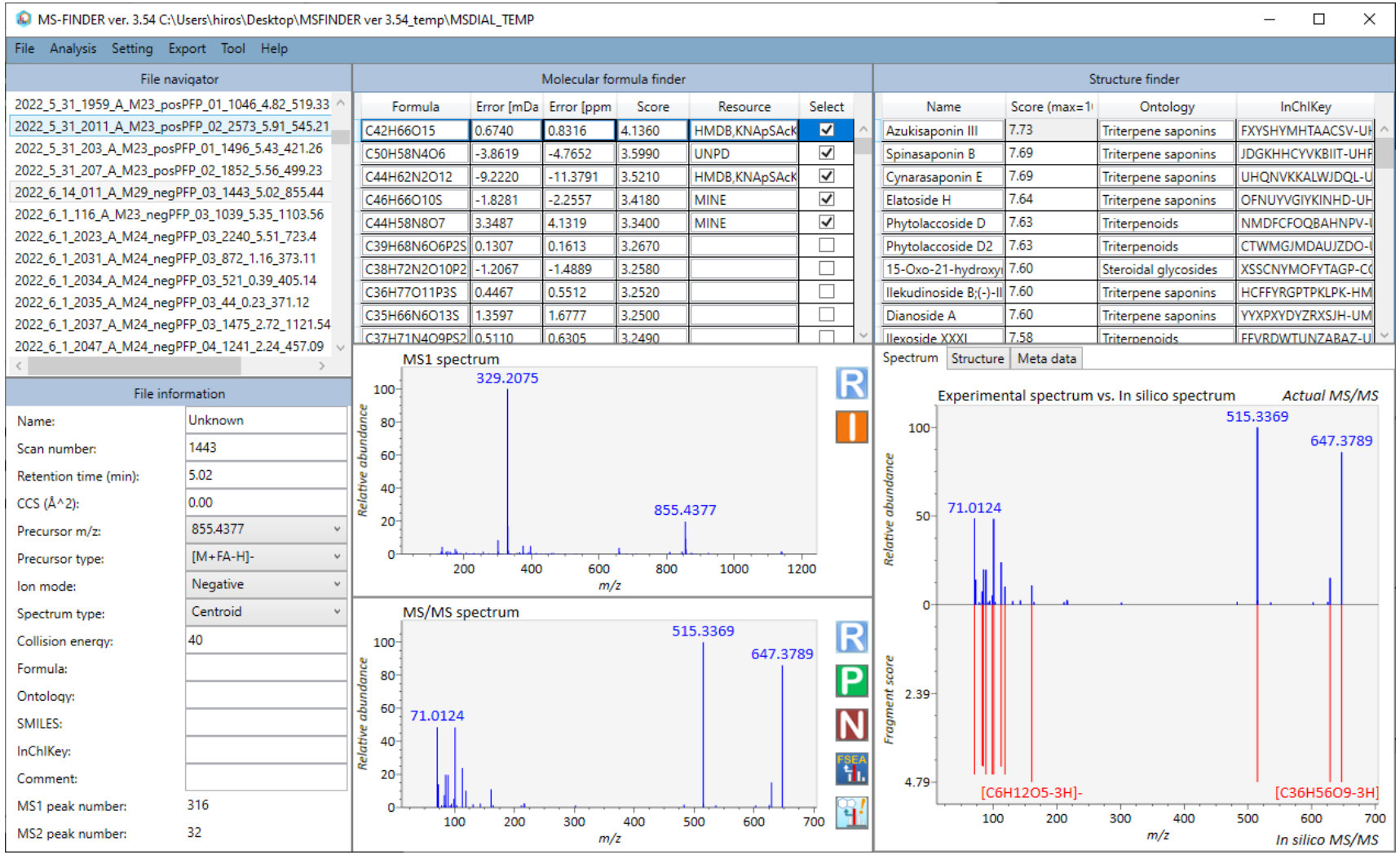
未知マススペクトルのアノテ



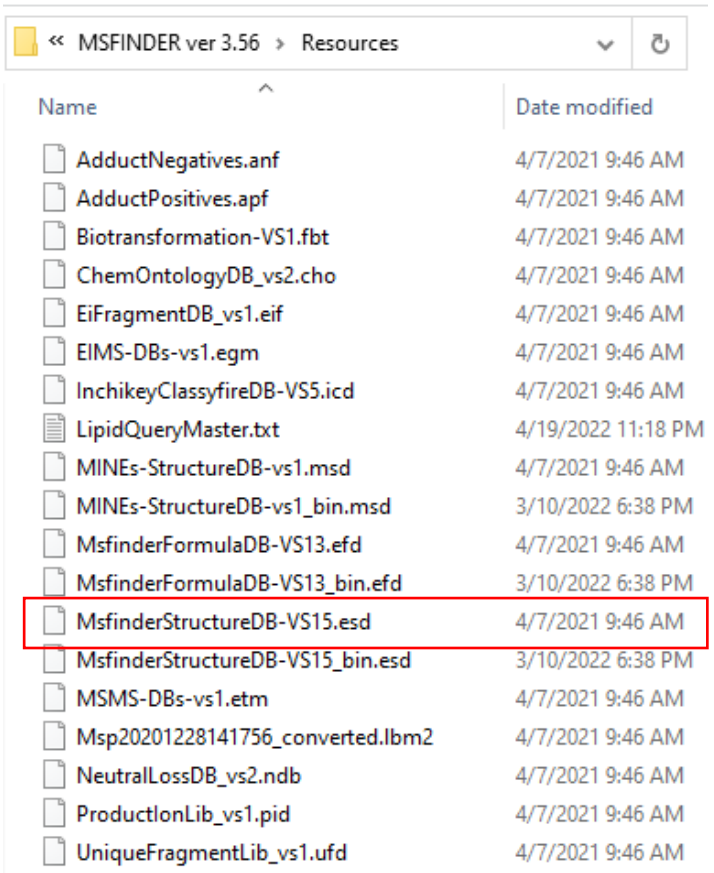
未知マススペクトルのアノテーションの簡単な流れ







MS-FINDERデータベースは化合物構造情報が豊富



	A	B	C	E	F	G	H	I	J	K	L	M	N	O	P	Q
1	Title	InChIkey	Short InCh	Exact mas	Formula	SMILES	HMDB	KNApSAck	ChEBI	DrugBank	SMPDB	YMDB	T3DB	FooDB	NANPDB	STOFF
2	buta-1,3-diyne	LLCSWKVOHI	LLCSWKV(	50.01565	C4H2	C#CC#C	N/A	N/A	CHEBI:378	N/A	N/A	N/A	N/A	N/A	N/A	N/A
3	fluoromethanol	RLWXXXHAQ	RLWXXXH.	50.01679	CH3FO	C(O)F	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
4	oxalonitrile	JMANVNJQN	JMANVNJ	52.00615	C2N2	N#CC#N	N/A	N/A	CHEBI:293	N/A	N/A	N/A	T3D0754	N/A	N/A	N/A
5	oxalonitrile(.1-)	SELGXVYREW	SELGXVYR	52.00615	C2N2	[N-]=[C]C#	N/A	N/A	CHEBI:298	N/A	N/A	N/A	N/A	N/A	N/A	N/A
6	difluoromethane	RWRIWBAIIC	RWRIWBA	52.01246	CH2F2	FCF	N/A	N/A	CHEBI:478	N/A	N/A	N/A	N/A	N/A	N/A	STOFF_52(
7	tetrahedrane	FJGIHZCEZAZ	FJGIHZCEZ	52.0313	C4H4	C12C3C1C	N/A	N/A	CHEBI:365	N/A	N/A	N/A	N/A	N/A	N/A	N/A
8	cyclobuta-1,3-diene	HWEQKSVYKI	HWEQKSV	52.0313	C4H4	C1=CC=C1	N/A	N/A	CHEBI:336	N/A	N/A	N/A	N/A	N/A	N/A	N/A
9	butenyne	WFYPICNXBK	WFYPICNX	52.0313	C4H4	C=CC#C	N/A	N/A	CHEBI:480	N/A	N/A	N/A	N/A	N/A	N/A	N/A
10	butatriene	WHVXVDDUY	WHVXVDI	52.0313	C4H4	C=C=C=C	N/A	N/A	CHEBI:376	N/A	N/A	N/A	N/A	N/A	N/A	N/A
11	prop-2-yn-1-one	NONQAKWU	NONQAKV	53.00274	C3HO	C#C[C]=O	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
12	acrylonitrile	NLHHRLWOU	NLHHRLW	53.02655	C3H3N	C=CC#N	N/A	N/A	CHEBI:282	N/A	N/A	N/A	T3D1688	N/A	N/A	STOFF_53
13	2-Propyn-1-al	IJNJLGFTSIAH	IJNJLGFTS	54.01056	C3H2O	O=CC#C	HMDB000(	N/A	CHEBI:279	N/A	N/A	N/A	N/A	FDB02408	N/A	N/A
14	propa-1,2-dien-1-one	TURAMGVWI	TURAMGV	54.01056	C3H2O	C=C=C=O	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
15	propanenitrile	VQGISNOMG	VQGISNOI	54.03437	C3H4N	C[CH]C#N	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
16	1,3-Butadiene	KAKZBPTYRLI	KAKZBPTY	54.04695	C4H6	C=CC=C	HMDB004	N/A	CHEBI:394	N/A	N/A	N/A	T3D0156	N/A	N/A	STOFF_53
17	cyclobutene	CFBGXYDUOI	CFBGXYDU	54.04695	C4H6	C1CC=C1	N/A	N/A	CHEBI:512	N/A	N/A	N/A	N/A	N/A	N/A	N/A
18	but-1-yne	KDKYADYSIP	KDKYADYS	54.04695	C4H6	CCC#C	N/A	N/A	CHEBI:480	N/A	N/A	N/A	N/A	N/A	N/A	N/A
19	buta-1,2-diene	QNRMTGGDH	QNRMTGC	54.04695	C4H6	CC=C=C	N/A	N/A	CHEBI:394	N/A	N/A	N/A	N/A	FDB00364	N/A	STOFF_56
20	1-methylcyclopropene	SHDPRTQPPV	SHDPRTQI	54.04695	C4H6	CC1=CC1	N/A	N/A	CHEBI:132	N/A	N/A	N/A	N/A	N/A	N/A	STOFF_43
21	UNPD155200	XNMQEEKYC	XNMQEEK	54.04695	C4H6	CC#CC	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
22	Cyanoformaldehyde	TUHMQDODL	TUHMQDC	55.00581	C2HNO	O=CC#N	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	STOFF_42(
23	N-Methylene-ethenamine	TUVFMMNAI	TUVFMMI	55.0422	C3H5N	C=CN=C	HMDB006	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
24	propionitrile	FVSKHRXBFJI	FVSKHRXE	55.0422	C3H5N	CCC#N	N/A	N/A	CHEBI:263	N/A	N/A	N/A	T3D1708	N/A	NANPDB_	N/A
25	prop-2-yn-1-amine	JKANAVGOD	JKANAVG(	55.0422	C3H5N	C#CCN	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
26	prop-1-en-2-ylazanide	LUWREKROQ	LUWREKR(	55.0422	C3H5N	C=C([CH2-	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
27	cyclopropanimine	QAVILNTZAV	QAVILNTZ	55.0422	C3H5N	C1CC1=N	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
28	Acrolein	HGINCPLSRVI	HGINCPLS	56.02621	C3H4O	C=CC=O	HMDB004	N/A	CHEBI:153	N/A	PW_C022(	YMDB008	T3D0037	FDB00830	N/A	STOFF_24
29	oxetene	CRYATLIDHPI	CRYATLIDI	56.02621	C3H4O	C1OC=C1	N/A	N/A	CHEBI:511	N/A	N/A	N/A	N/A	N/A	N/A	N/A
30	prop-2-yn-1-ol	TVDSBUOJIPI	TVDSBUO.	56.02621	C3H4O	OCC#C	N/A	N/A	CHEBI:289	N/A	N/A	YMDB013	N/A	N/A	N/A	STOFF_53
31	prop-1-en-1-one	UYLUJGRCKK	UYLUJGRC	56.02621	C3H4O	CC=C=O	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
32	cyclopropanone	VBBRYJMZLIY	VBBRYJMZ	56.02621	C3H4O	C1CC1=O	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
33	diazoethane	WLXALCKAK(	WLXALCK/	56.03745	C2H4N2	CC=[N+]=[	N/A	N/A	CHEBI:874	N/A	N/A	N/A	N/A	N/A	N/A	N/A
34	2-aminoacetonitrile	DFNYGALUNI	DFNYGALU	56.03745	C2H4N2	C(C#N)N	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
35	methylcyanamide	MCLITRXWHZ	MCLITRXV	56.03745	C2H4N2	CNC#N	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
36	N-(methylideneamino)me	NBHLEUNJGN	NBHLEUN.	56.03745	C2H4N2	C=NN=C	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
37	Ethyl Isocyanide	JEGVKBYNUP	JEGVKBYN	56.05002	C3H6N	CC[N+]#C	N/A	N/A	N/A	DB03399	N/A	N/A	N/A	N/A	N/A	N/A

作成すべきメタボロームテーブルの目標

代謝物アノテーションのメタデータ・定量値が整理されてるテーブル

	A	B	C	D	E	I	J	K	L	M	N	AE	AM	AN	AO	AP	AQ	AR	AS	AT
1												Public/Private		Public	Private	Private	Private	Public	Public	Public
2												Category		Blank	Mouse	Mouse	Mouse	Mouse	Mouse	Mouse
3												Tissue/Species		Blank	Adrenal gland	Adrenal gland	Adrenal gland	Adrenal gland	Adrenal gland	Adrenal gland
4												Genotype/Background		Blank	B6-*fads2*	B6-*fads2*	B6-*fads2*	C57BL/6J	C57BL/6J	C57BL/6J
5												Perturbation		Blank	No	No	No	No	No	No
6												Diet/Culture		Blank	CE2	CE2	CE2	CE2	CE2	CE2
7												Biological replicate		1	1	2	3	1	2	3
8												Technical replicate		1	1	1	1	1	1	1
9												Unit		pmol/mg tissue	pmol/mg tissue	pmol/mg tissue	pmol/mg tissue	pmol/mg tissue	pmol/mg tissue	pmol/mg tissue
10	Alignmen	Average R	Average M	Metabolite name	Adduct type	Reference RT	Reference m/z	Formula	Ontology	INCHIKEY	SMILES	MS/MS spectrum	Lipid IS	180913_Top16_7	180913_Top16_7	180913_Top16_7	180913_Top16_7	180913_Top16_7	180913_Top16_7	180913_Top16_7
11	1179	1.564	407.2805	ST 24:1;O5	[M-H]-	2.78	407.2803	C24H40O5	BileAcid	BHQCQFFYRZLCQQ-OELDTZBJSA-N	C[C@H](CCC(=O)O)[C@H]1	95.03821:9 95.0436	LPC-	0.273930167	0.371953862	52.78361615	0.051152931	28.11672998	11.91871829	1.408517337
12	1497	7.084	479.3156	ST 28:1;O;S	[M-H]-	7.18	479.32004	C28H48O4S	SSulfate	NNLNVKVMYKIRMN-UHFFFAOYNA-N	CC(C)C(C)CCC(C)C1CCC2C3	96.95593:34 247.04	LPC-	0.626126096	1.767928852	3.166793167	2.205259692	9.48315745	1.378986884	1.172087641
13	3229	13.012	742.6647	Cer 18:0;3O/24:0;(2OH)	[M+CH3COO]-	13.08	742.65662	C42H85NO5	Cer-AP	ZFUXWVVVWGWGPQ-UHFFFAOYNA-N	CCCCCCCCCCCCCCCCCCCC(	255.21466:17 279.2	Cer-NS-	0.05308538	0.268435847	0.190942692	0.115132721	0.634419853	0.176430325	0.155838743
14	3621	13.452	798.7214	Cer 22:0;3O/24:0;(2OH)	[M+CH3COO]-	13.49	798.71924	C46H93NO5	Cer-AP	UTXOYKRBIFRASG-UHFFFAOYNA-N	CCCCCCCCCCCCCCCCCCCC(	283.25528:17 309.2	Cer-NS-	0.119442106	0.172980271	0.049881097	0.038950373	0.842949194	0.105622168	0.050134169
15	3810	13.671	826.747	Cer 22:0;3O/26:0;(2OH)	[M+CH3COO]-	13.63	826.75055	C48H97NO5	Cer-AP	YFBAYAMDBBINPH-UHFFFAOYNA-N	CCCCCCCCCCCCCCCCCCCC(	259.23837:7 279.22	Cer-NS-	0.046449708	0.073833042	0.02467237	0.011455992	0.370446241	0.066677681	0.022952993
16	3062	12.766	722.6251	Cer 18:1;2O/24:1;(2OH)	[M+CH3COO]-	12.75	722.63043	C42H81NO4	Cer-AS	PYGVPCBXCGQXNA-SZHIUZGGNA-N	CCCCCCCCCCCCC\C=C\C(O	89.02348:52 250.24	Cer-NS-	0.009953509	0.573788215	0.878014571	1.19829678	0.512736849	0.320406911	0.408925694
17	3298	13.327	752.6737	Cer 20:1;2O/24:0;(2OH)	[M+CH3COO]-	13.35	752.67737	C44H87NO4	Cer-AS	ZEHOOLFQJBPFJO-BSKJHSHCNA-N	CCCCCCCCCCCCCCCCCCCC(	89.01959:94 268.27	Cer-NS-	0.408093862	0.400807944	0.126043631	0.152937495	1.014188582	0.193542296	0.124429384
18	4358	14.176	942.8302	Cer 41:3;3O(FA 16:1)	[M+CH3COO]-	13.52	942.81311	C57H105NO5	Cer-EOS	ZRVZVEHEJMFLGV-FTYSAOLSNA-N	CCCCCCCCCCCCCCCC\C=C\	88.00109:9 198.145	Cer-NS-	0.013271345	0.155576768	0.418357584	0.11685112	0.216870514	0.029503399	0.122617306
19	3297	13.104	752.6737	Cer 26:0;2O/18:1;O	[M+CH3COO]-	13.26	752.67737	C44H87NO4	Cer-HDS	YENFMISLLMYKHR-PEZBUJJGNA-N	CCCCCCCCCCCCCCCCCCCC(	245.74687:17 253.2	Cer-NS-	0.155938305	0.678736611	0.467702325	0.463394883	0.805168584	0.547583082	0.336442558
20	3505	13.305	780.7065	Cer 28:0;2O/18:1;O	[M+CH3COO]-	13.43	780.70868	C46H91NO4	Cer-HDS	ZNHQVMFCKSFDEJ-PEZBUJJGNA-N	CCCCCCCCCCCCCCCCCCCC(	267.22229:17 279.2	Cer-NS-	0.228930703	0.137118507	0.039690335	0.04353277	0.518134079	0.079659177	0.045905986
21	3193	13.218	738.6585	Cer 21:1;2O/22:0;O	[M+CH3COO]-	13.36	738.66174	C43H85NO4	Cer-HS	JJJSXOKHMQOVDQ-MHAUTQJVNA-N	CCCCCCCCCCCCCCCCCCCC(	89.02362:351 267.2	Cer-NS-	0.301923101	1.231429671	0.62324553	1.27218793	1.889521155	1.706476586	0.987582733
22	2048	9.857	598.5488	Cer 18:0;2O/16:0	[M+CH3COO]-	10.22	598.54163	C34H69NO3	Cer-NDS	GCGTXOVNNFGTPQ-UHFFFAOYNA-N	CCCCCCCCCCCCCCCC(O)C((	196.62474:15 237.2	Cer-NS-	0.009953509	1.582664002	2.450073648	1.661691663	2.277631058	1.596723943	1.253354233
23	2214	10.957	626.5753	Cer 18:0;2O/18:0	[M+CH3COO]-	11.36	626.57294	C36H73NO3	Cer-NDS	KZTJQXAANJHSCE-UHFFFAOYNA-N	CCCCCCCCCCCCCCCCCC(=C	113.38002:15 239.2	Cer-NS-	0.009953509	0.379185411	0.595355024	0.339097368	0.505867648	0.430159554	0.391408936
24	3032	12.869	718.6396	Cer 43:3;2O	[M+CH3COO]-	12.86	718.6355	C43H81NO3	Cer-NDS	FYQPEFKNMQVMGV-BYBPBHJYNA-N	CCCCCCCC(O)C(CO)NC(=C	223.1974:15 251.21	Cer-NS-	0	0.274237015	0.357213014	0.367164549	0.435703658	0.248418618	0.163087057
25	3598	14.01	794.7579	Cer 24:0;2O/24:0	[M+CH3COO]-	14.21	794.76068	C48H97NO3	Cer-NDS	FYXOQZCSSKQEMX-UHFFFAOYNA-N	CCCCCCCCCCCCCCCCCCCC(	295.2905:7 319.226	Cer-NS-	0.069674562	0.138700644	0.013408897	0.01431999	0.4317784	0.095000944	0.032617411
26	2867	12.604	698.6224	Cer 18:0;3O/22:0	[M+CH3COO]-	12.83	698.63043	C40H81NO4	Cer-NP	CIMNZQFRNXDRER-UHFFFAOYNA-N	CCCCCCCCCCCCCCCCCCCC(	222.90825:3 232.50	Cer-NS-	0.033178363	0.895489328	0.514365287	1.061970474	0.409698822	0.604229607	0.48624104
27	2869	12.569	698.6434	Cer 18:0;3O/22:0	[M+CH3COO]-	12.83	698.63043	C40H81NO4	Cer-NP	CIMNZQFRNXDRER-UHFFFAOYNA-N	CCCCCCCCCCCCCCCCCCCC(	253.2002:6 255.225	Cer-NS-	0.013271345	0.637601059	0.431230126	0.679913135	0.294394363	0.441960914	0.322549957
28	2988	12.953	712.6422	Cer 18:0;3O/23:0	[M+CH3COO]-	13.1	712.64606	C41H83NO4	Cer-NP	MBPABCUJJLJOFM-UHFFFAOYNA-N	CCCCCCCCCCCCCCCCCCCC(	89.01154:17 89.018	Cer-NS-	0.049767544	4.822879805	3.159672474	4.038237238	1.569121957	4.134016239	1.947984289
29	2989	12.964	712.6581	Cer 18:0;3O/23:0	[M+CH3COO]-	13.1	712.64606	C41H83NO4	Cer-NP	MBPABCUJJLJOFM-UHFFFAOYNA-N	CCCCCCCCCCCCCCCCCCCC(	89.0156:17 89.0169	Cer-NS-	0	3.299282237	2.107342243	2.271723246	1.173161538	2.747356495	1.204428116
30	3102	13.096	726.6601	Cer 18:0;3O/24:0	[M+CH3COO]-	13.23	726.66174	C42H85NO4	Cer-NP	ZESJDNWGTANZCC-UHFFFAOYNA-N	CCCCCCCCCCCCCCCCCCCC(	72.98572:15 89.022	Cer-NS-	0.119442106	13.15177437	8.143491288	11.15928197	3.642639589	11.61784838	6.548851369
31	3083	12.623	724.6453	Cer 18:0;3O/24:1	[M+CH3COO]-	12.82	724.64606	C42H83NO4	Cer-NP	DNXQPFZSRNGGHL-DQRAZIAONA-N	CCCCCCCCCCCCCCCC(O)C(O	225.20282:17 237.2	Cer-NS-	0.049767544	4.971600648	3.767363683	5.360831533	1.439588437	3.582302681	1.999326511
32	3063	11.423	722.627	Cer 18:0;3O/24:2	[M+CH3COO]-	12.57	722.63043	C42H81NO4	Cer-NP	VMYKQFBIKRNRBI-DPTWWRMPNA-N	CCCCCCCCCCCCCCCC(O)C(O	255.22197:13 267.2	Cer-NS-	0.009953509	0.357035498	0.298750224	0.354562957	0.123645633	0.300934668	0.175771606
33	3217	13.202	740.6649	Cer 18:0;3O/25:0	[M+CH3COO]-	13.26	740.67737	C43H87NO4	Cer-NP	PMJABXIZLCOFDV-UHFFFAOYNA-N	CCCCCCCCCCCCCCCCCCCC(	89.02377:69 91.004	Cer-NS-	0.185798831	1.365383905	0.704235267	1.029893696	0.852271682	1.379578927	0.743556174
34	3314	13.305	754.6916	Cer 18:0;3O/26:0	[M+CH3COO]-	13.38	754.69299	C44H89NO4	Cer-NP	GKRXVCWVXYHWOD-UHFFFAOYNA-N	CCCCCCCCCCCCCCCCCCCC(	255.21931:17 267.2	Cer-NS-	0.209023685	0.434560192	0.242432857	0.251459028	0.899865437	0.344599698	0.155838743
35	3407	13.427	768.7103	Cer 45:0;3O	[M+CH3COO]-	13.59	768.70868	C45H91NO4	Cer-NP	IMVRXMWBRZAXKE-UHFFFAOYNA-N	CCCCCCCCCCCCCCCCCCCC(	309.26501:34 403.4	Cer-NS-	0.172527486	0.168233861	0.039153979	0.039523173	0.393507132	0.072578361	0.044697934
36	3521	13.525	782.7246	Cer 20:0;3O/26:0	[M+CH3COO]-	13.62	782.7243	C46H93NO4	Cer-NP	XXCJZFVZHPNILU-UHFFFAOYNA-N	CCCCCCCCCCCCCCCCCCCC(	115.02112:17 295.2	Cer-NS-	0.228930703	0.186692121	0.050953808	0.032076778	1.070614168	0.113293051	0.059798587
37	3506	13.549	780.7102	Cer 26:1;3O/20:0	[M+CH3COO]-	13.58	780.70868	C46H91NO4	Cer-NP	UTXJJCHIDYEUQD-NWBJSICCNA-N	CCCCCCCCCCCCCCCCCCCC(	108.57462:15 310.2	Cer-NS-	0.252155557	0.165069588	0.031108641	0.018329587	0.587316755	0.053696186	0.028993255
38	3612	13.647	796.7332	Cer 22:0;3O/25:0	[M+CH3COO]-	13.73	796.73999	C47H95NO4	Cer-NP	KMKZFVYLHRBJLC-UHFFFAOYNA-N	CCCCCCCCCCCCCCCCCCCC(	89.01967:9 107.102	Cer-NS-	0.152620469	0.122351899	0.032181353	0.020620786	0.439628916	0.076708837	0.033221437
39	3715	13.768	810.7481	Cer 22:0;3O/26:0	[M+CH3COO]-	13.84	810.75562	C48H97NO4	Cer-NP	JNLJJOPFYFEMKL-UHFFFAOYNA-N	CCCCCCCCCCCCCCCCCCCC(	152.98378:6 259.09	Cer-NS-	0.182480995	0.141337538	0.047199317	0.022339185	0.697714641	0.095591012	0.044697934
40	3879	14.01	838.7832	Cer 22:0;3O/28:0	[M+CH3COO]-	13.88	838.78693	C50H101NO4	Cer-NP	YAVNDLUAWGYTPL-UHFFFAOYNA-N	CCCCCCCCCCCCCCCCCCCC(	307.30249:7 323.26	Cer-NS-	0.019907018	0.080161589	0.018772456	0.007446395	0.255141782	0.04661537	0.015100653
41	1692	8.102	526.4471	Cer 18:1;2O/11:0	[M+CH3COO]-	8.41	526.44769	C29H57NO3	Cer-NS	YFZDTXOZADTFGB-ZNTNEXAZNA-N	CCCCCCCCCCC\C=C\C(O	184.16429:52 210.1	Cer-NS-	0.258791229	0.490989732	0.486474781	0.480006072	0.460727179	0.496247168	0.429462583
42	1686	7.86	524.431	Cer 20:2;2O/9:0	[M+CH3COO]-	8	524.43207	C29H55NO3	Cer-NS	ABUUKXUMKCZXAH-JWQURLDWNA-N	CCCCCCCCCC\C=C\CC\C=C	147.11418:15 165.1	Cer-NS-	0.537489476	0.547419271	0.753043652	0.560198017	1.089259144	0.54817315	0.587717431
43	1902	8.837	568.5011	Cer 18:1;2O/14:0	[M+CH3COO]-	8.91	568.49469	C32H63NO3	Cer-NS	ZKRPGPZHULJLKJ-IMVLJIQENA-N	CCCCCCCCCCCCC\C=C\C(O	226.21634:17 237.2	Cer-NS-	0.019907018	0.207259898	0.223660401	0.339670168	0.310586053	0.188231684	0.13288575
44	1975	9.173	582.5118	Cer 17:1;2O/16:0	[M+CH3COO]-	9.34	582.51031	C33H65NO3	Cer-NS	KXVLPPCAUYSNGY-BYCLXTJYNA-N	CCCCCCCCCCCCCCCC(=O)N	223.19334:34 237.2	Cer-NS-	0.009953509	0.434560192	0.488083849	0.851753017	0.584372811	0.687429192	0.386576727
45	2041	9.576	596.5234	Cer 18:1;2O/16:0	[M+CH3COO]-	9.9	596.52594	C34H67NO3	Cer-NS	YDNKGFDKKRUKPY-ORIPQNMZNA-N	CCCCCCCCCCCCCCCC(=O)N	235.19879:34 237.2	Cer-NS-	0.082945907	14.89317941	21.81305718	36.26680719	43.87506394	16.97330532	10.73837665
46	2031	8.963	594.511	Cer 18:2;2O/16:0	[M+CH3COO]-	9.23	594.51031	C34H65NO3	Cer-NS	GMWIWVUTMCBDSP-ZNPGVSGMNA-N	CCCCCCCCCCCCCCC(=O)N	235.20248:110 237.	Cer-NS-	0.009953509	0.685065158	1.256145465	2.780369298	5.453164923	0.834356118	0.890334525
47	2114	10.026	610.5399	Cer 18:1;2O/17:0	[M+CH3COO]-	10.15	610.54163	C35H69NO3	Cer-NS	ICWGMOFDULMCFL-SJCQXOIGNA-N	CCCCCCCCCCCCCCCC(=O)	237.22255:86 251.2	Cer-NS-	0.043131872	0.408191249	0.406557755	0.756095483	0.435703658	0.542862538	0.355771394
48	2203	10.565	624.5556	Cer 18:1;2O/18:0	[M+CH3COO]-	10.65	624.55725	C36H71NO3	Cer-NS	VODZWWMEJITOND-OWWNRXNENA-N	CCCCCCCCCCCCCCCCCC(=C	235.21579:17 237.2	Cer-NS-	0.02654269	8.1606607	12.32492171	18.31297627	5.30449577	9.111829683	8.228044027
49	2189	9.728	622.5427	Cer 18:2;2O/18:0	[M+CH3COO]-	9.84	622.54163	C36H69NO3	Cer-NS	WNPWDGNHTKGEDS-LLRUVXLENA-N	CCCCCCCCCCCCCCCCCC(=C	235.18997:17 280.2	Cer-NS-	0.009953509	0.590664339	0.868360166	1.686322047	1.513187028	0.5859375	0.738723965

メタボロームデータを出す側と使う側

メタボロミクスのデータ解析プロトコール

メタボロームデータを「出す側」
（4-2～4-5）

メタボロームデータを「使う側」
（4-6～4-8）

質量分析インフォマティクス

ケムインフォマティクス

バイオインフォマティクス

データ処理（ノンターゲット解析）

XCMS
MS-DIAL　MZmine 2
OpenMS

データ処理（ターゲット解析）

MRMPROBS　Skyline

未知代謝物アノテーション

MS-FINDER
GNPS　MetFrag
SIRIUS

代謝データベース

KEGG　HMDB
ID変換ツール（CTSなど）

パスウェイ解析

VANTED　MSEA

多変量解析及び統合解析

MetaboAnalyst
transomics2cytoscape
Garudaプラットホーム

その他
データ標準化・レポジトリ
（4-9, 4-10）

パスウェイ解析に使えるリソース

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Technology Feature | Open Access | Published: 13 December 2018

ComPath: an ecosystem for exploring, analyzing, and curating mappings across pathway databases

Daniel Domingo-Fernández, Charles Tapley Hoyt, Carlos Bobis-Álvarez, Josep Marín-Llaó & Martin Hofmann-Apitius

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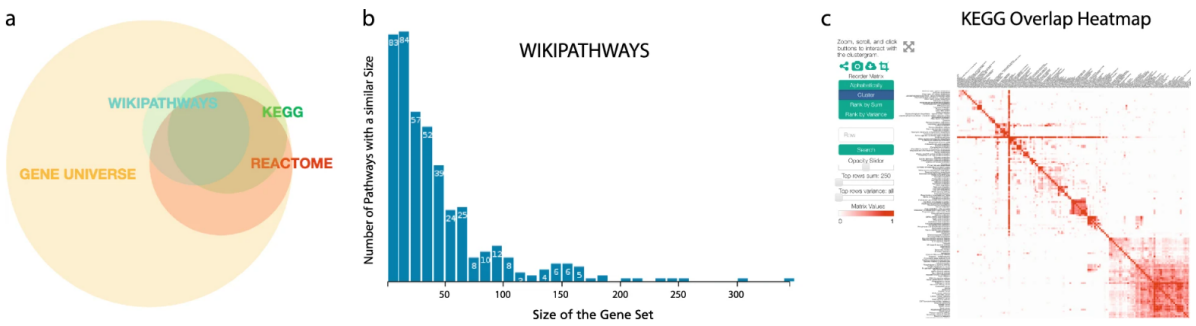
Fig. 2

From: ComPath: an ecosystem for exploring, analyzing, and curating mappings across pathway databases



a An Euler diagram summarizing the human gene-centric coverage of KEGG, Reactome, and WikiPathways compared to the universe of all genes from HGNC (more details in Supplementary Table 1). **b** Histogram views present gene promiscuity or pathway size distributions. **c** The pathway similarity landscape of KEGG visualized as a heatmap

Cytoscape is an open source software platform for visualizing complex networks and integrating these with any type of attribute data. A lot of *Apps* are available for various kinds of problem domains, including bioinformatics, social network analysis, and semantic web. Learn more...

Release Notes

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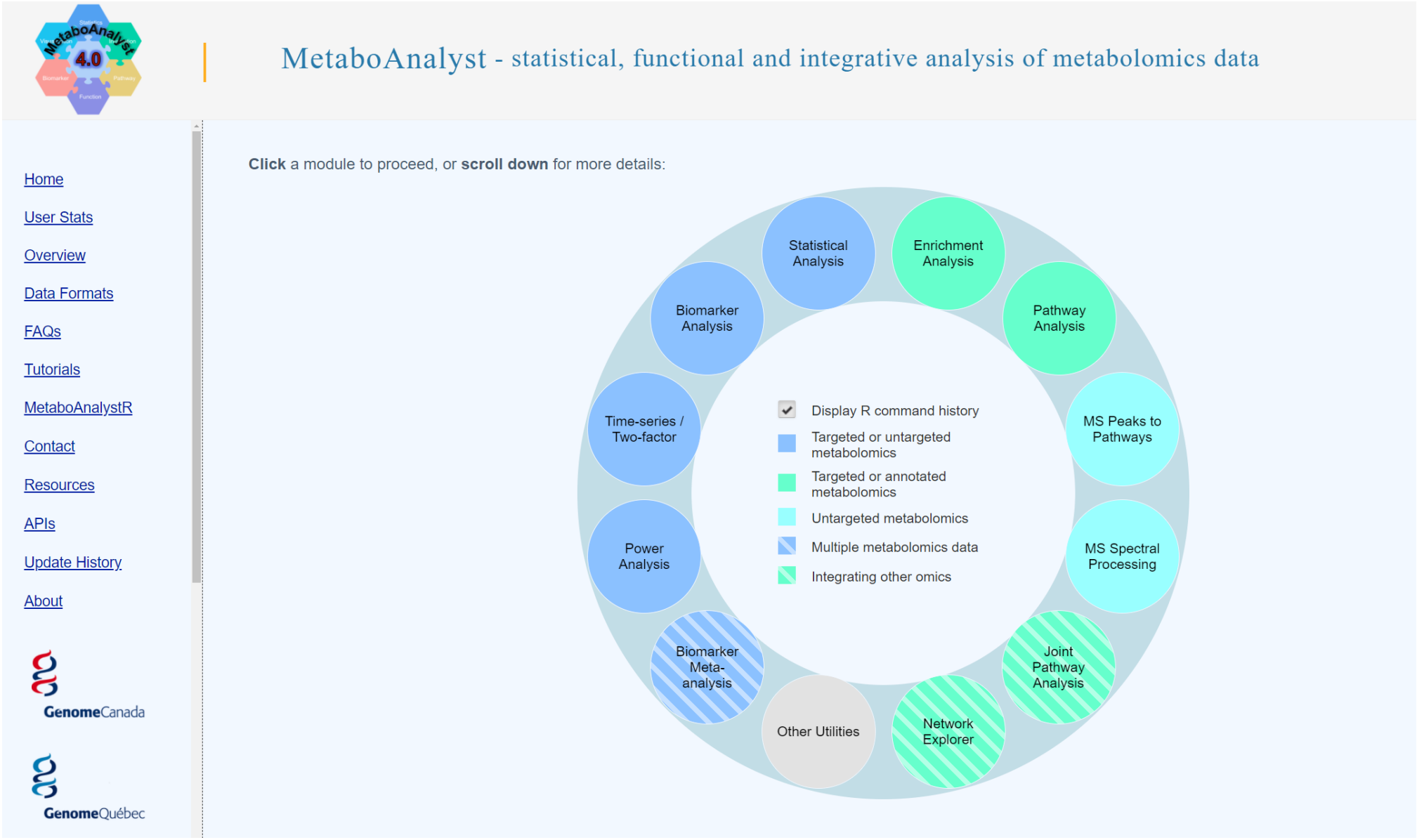
App Developers Docs

MetaboAnalyst is a great (really top) tool for analyses.



Current Protocols in Bioinformatics **68,** e86 (2019)

MetaboAnalyst is a great (really top) tool for analyses.

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC	AD	AE	AF	AG	AH
1	Patient ID	Muscle loss	1,6-Anhyd	1-Methylr	2-Aminob	2-Hydroxy	2-Oxoglut	3-Aminois	3-Hydroxy	3-Hydroxy	3-Indoxyls	4-Hydroxy	Acetate	Acetone	Adipate	Alanine	Asparagin	Betaine	Carnitine	Citrate	Creatine	Creatinine	Dimethyla	Ethanolan	Formate	Fucose	Fumarate	Glucose	Glutamine	Glycine	Glycolate	Guanidoa	Hippurate	Histidine	Hyp
2	PIF_178	cachexic	40.85	65.37	18.73	26.05	71.52	1480.3	56.83	10.07	566.8	120.3	126.47	9.49	38.09	314.19	159.17	109.95	265.07	3714.5	196.37	16481.6	632.7	645.48	441.42	336.97	7.69	395.44	871.31	2038.56	685.4	154.47	4582.5	925.19	
3	PIF_087	cachexic	62.18	340.36	24.29	41.68	67.36	116.75	43.82	79.84	368.71	432.68	212.72	11.82	327.01	871.31	157.59	244.69	120.3	2617.57	212.72	15835.35	607.89	487.85	252.14	198.34	18.92	8690.62	601.85	1107.65	651.97	109.95	1737.15	845.56	
4	PIF_090	cachexic	270.43	64.72	12.18	65.37	23.81	14.3	5.64	23.34	665.14	292.95	314.19	4.44	131.63	464.05	89.12	116.75	25.03	862.64	221.41	24587.66	735.1	407.48	249.64	186.79	7.1	1352.89	301.87	620.17	141.17	183.09	4315.64	284.29	1
5	NETL_005_V1	cachexic	154.47	52.98	172.43	74.44	1199.91	555.57	175.91	25.03	411.58	214.86	37.34	206.44	144.03	589.93	273.14	278.66	200.34	13629.61	85.63	20952.22	1064.22	820.57	468.72	407.48	96.54	862.64	1685.81	5064.45	70.81	102.51	757.48	1043.15	2
6	PIF_115	cachexic	22.2	73.7	15.64	83.93	33.12	29.67	76.71	69.41	165.67	97.51	407.48	44.26	15.03	1118.79	42.52	391.51	84.77	854.06	105.64	6768.26	242.26	365.04	114.43	26.05	19.69	6836.29	432.68	395.44	26.58	52.98	1152.86	327.01	
7	PIF_110	cachexic	212.72	31.82	18.36	80.64	47.94	17.46	31.82	35.16	183.09	132.95	81.45	14.44	25.28	237.46	157.59	66.69	40.04	1958.63	200.34	15677.78	614	459.44	314.19	123.97	5.05	512.86	298.87	482.99	428.38	57.97	3568.85	459.44	
8	NETL_019_V1	cachexic	151.41	36.6	8.67	42.52	223.63	56.26	11.59	25.79	223.63	59.15	51.42	3.25	8.41	336.97	71.52	149.9	127.74	3944.19	383.75	8022.46	333.62	217.02	67.36	55.7	4.71	237.46	561.16	3428.92	290.03	101.49	2368.47	327.01	
9	NETCR_014_V1	cachexic	31.5	6.82	4.18	12.94	25.03	8.67	1.73	8.76	111.05	33.78	7.46	2.8	3.53	69.41	13.87	15.33	9.87	788.4	5.81	2208.35	73.7	55.7	49.9	18.17	1.86	80.64	71.52	196.37	70.11	42.52	254.68	130.32	
10	NETCR_014_V2	cachexic	51.42	30.27	7.54	34.81	80.64	17.99	9.03	3.25	391.51	145.47	9.97	8.67	8.25	102.51	32.79	31.19	7.32	1669.03	35.16	6634.24	214.86	183.09	68.03	72.97	3.56	177.68	145.47	292.95	33.12	56.26	365.04	183.09	
11	PIF_154	cachexic	117.92	52.46	19.49	72.24	73.7	57.97	26.84	28.5	116.75	50.4	100.48	9.12	14.59	962.95	221.41	149.9	487.85	4675.07	126.47	8690.62	350.72	437.03	320.54	57.4	12.06	972.63	1022.49	3294.47	589.93	188.67	632.7	706.27	
12	NETL_022_V1	cachexic	20.7	221.41	15.18	28.79	357.81	93.69	13.07	4.26	361.41	59.74	27.94	6.49	18.54	164.02	32.14	219.2	230.44	3533.34	1450.99	8433.78	361.41	184.93	83.93	138.38	10.91	170.72	179.47	492.75	132.95	137	2697.28	247.15	
13	NETL_022_V2	cachexic	127.74	177.68	12.68	15.03	68.03	105.64	29.08	53.52	376.15	160.77	30.88	7.92	259.82	502.7	64.72	137	35.87	854.06	1863.11	6904.99	273.14	175.91	165.67	94.63	11.47	473.43	445.86	607.89	149.9	154.47	19341.34	497.7	
14	NETL_008_V1	cachexic	59.74	50.91	6.82	46.06	111.05	8.08	17.12	16.78	379.93	174.16	55.15	9.21	11.02	217.02	32.14	167.34	14.88	1772.24	125.21	15677.78	678.58	354.25	46.06	210.61	6.05	419.89	237.46	880.07	228.15	83.93	4272.69	154.47	1
15	PIF_146	cachexic	89.12	32.79	10.38	32.14	32.46	43.38	8.08	20.49	317.35	86.49	95.58	8.67	9.03	167.34	47.94	56.83	16.95	323.76	102.51	12209.87	437.03	144.03	91.84	101.49	3.49	183.09	121.51	330.3	249.64	99.48	2643.87	190.57	
16	PIF_119	cachexic	23.57	6.89	2.12	7.85	8.33	2.97	1.7	5.58	82.27	17.64	69.41	6.23	3.16	34.47	13.33	41.68	24.53	265.07	11.7	1480.3	46.99	37.34	79.84	24.05	1.48	43.82	36.6	104.58	12.06	18.17	113.3	24.05	
17	PIF_099	cachexic	41.26	8.67	2.56	7.85	6.89	6.36	3.42	6.23	90.02	25.03	79.84	3.16	4.81	26.84	14.3	4.06	18.36	80.64	18.54	1635.98	56.26	29.96	57.4	31.19	2.23	57.97	26.84	74.44	36.23	25.28	92.76	22.87	
18	PIF_162	cachexic	589.93	21.98	15.18	46.06	32.79	31.82	25.03	7.69	109.95	148.41	91.84	17.64	22.87	441.42	79.04	157.59	62.8	897.85	419.89	9701.15	395.44	200.34	53.52	64.07	10.49	105.64	512.86	160.77	181.27	112.17	934.49	160.77	
19	PIF_160	cachexic	112.17	25.28	15.49	47.94	28.79	16.12	30.27	21.33	347.23	73.7	70.81	4.22	15.8	188.67	54.05	78.26	24.05	2489.91	170.72	10198.54	1422.26	244.69	89.12	26.84	3.39	387.61	214.86	1141.39	190.57	51.42	4023.87	190.57	
20	PIF_113	cachexic	167.34	19.89	13.46	31.19	47.94	79.04	11.7	12.55	184.93	74.44	42.52	9.39	12.43	237.46	35.87	60.34	12.06	4447.07	97.51	6974.39	275.89	290.03	160.77	61.56	5.21	221.41	225.88	2298.47	141.17	18.54	2807.36	343.78	
21	PIF_143	cachexic	183.09	90.92	8.94	64.07	20.49	18.73	26.05	51.42	204.38	115.58	82.27	3.82	20.49	333.62	61.56	68.72	15.18	2643.87	55.7	11158.98	379.93	407.48	314.19	117.92	3.1	473.43	399.41	1096.63	595.86	132.95	4230.18	419.89	
22	NETCR_007_V1	cachexic	208.51	53.52	5.26	47.94	212.72	50.4	30.27	6.82	200.34	46.53	25.03	5.05	18.54	254.68	96.54	131.63	29.37	2835.57	44.26	9798.65	361.41	450.34	130.32	82.27	4.85	267.74	487.85	992.27	437.03	57.4	4675.07	347.23	
23	NETCR_007_V2	cachexic	34.81	95.58	23.57	68.03	287.15	104.58	60.34	42.95	333.62	117.92	82.27	5.26	28.79	555.57	94.63	170.72	19.3	5377.61	48.91	14328.42	665.14	713.37	198.34	156.02	7.85	528.48	888.91	1261.43	478.19	98.49	6438.17	437.03	1
24	PIF_137	cachexic	333.62	35.87	7.92	54.6	20.49	63.43	29.96	47.47	247.15	237.46	50.4	4.35	23.1	399.41	102.51	66.02	20.91	1958.63	71.52	13359.73	539.15	350.72	154.47	93.69	19.11	845.56	445.86	1958.63	23.81	49.4	6568.23	720.54	
25	PIF_100	cachexic	32.46	9.68	3.9	11.02	170.72	2.97	6.36	2.46	34.81	70.11	77.48	2.29	3.6	78.26	16.61	50.91	4.44	223.63	9.58	1261.43	102.51	16.12	58.56	13.6	17.46	5943.18	38.09	52.46	10.91	19.69	217.02	14.15	
26	NETL_004_V1	cachexic	4.71	11.13	43.38	30.88	104.58	54.05	7.61	7.92	210.61	31.19	13.07	7.61	6.11	170.72	27.66	94.63	28.79	1422.26	38.86	4865.87	214.86	86.49	36.23	24.29	8.17	109.95	116.75	518.01	107.77	108.85	645.48	146.94	
27	PIF_094	cachexic	68.72	13.87	12.18	25.03	28.22	72.97	11.47	25.03	119.1	134.29	103.54	12.06	32.14	454.86	98.49	88.23	42.52	3677.54	43.82	8349.86	350.72	252.14	202.35	86.49	7.17	403.43	415.72	1422.26	204.38	95.58	1919.85	383.75	
28	PIF_132	cachexic	214.86	127.74	31.5	33.78	88.23	64.07	54.05	164.02	692.29	278.66	411.58	14.73	68.72	1312.91	132.95	156.02	33.78	9045.29	105.64	33860.35	1556.2	1436.55	1480.3	181.27	7.54	1032.77	539.15	2751.77	428.38	265.07	8022.46	1863.11	2
29	PIF_163	cachexic	304.9	25.79	27.11	40.45	70.81	126.47	16.95	51.42	144.03	89.12	108.85	8.67	14.15	357.81	37.34	107.77	117.92	2230.54	62.18	11271.13	336.97	468.72	368.71	109.95	5.7	632.7	772.78	3428.92	90.02	145.47	1339.43	1164.45	
30	NETCR_003_V1	cachexic	37.71	10.8	5	8.25	11.7	8.41	6.75	5.26	44.26	29.37	22.2	4.9	5.81	29.08	15.64	4.53	2.18	415.72	4.26	1737.15	71.52	32.79	21.98	12.55	0.9	69.41	32.14	68.72	42.95	15.18	533.79	53.52	
31	NETL_028_V1	cachexic	45.6	473.43	16.28	63.43	221.41	15.49	41.68	52.46	1043.15	149.9	31.82	14.01	21.33	473.43	125.21	114.43	91.84	3714.5	424.11	21590.31	665.14	212.72	115.58	167.34	10.07	333.62	333.62	720.54	148.41	62.8	9045.29	473.43	
32	NETL_028_V2	cachexic	34.12	92.76	8.25	16.61	55.15	3.39	9.03	16.61	278.66	30.57	10.38	6.05	8.94	212.72	35.52	56.26	54.6	915.99	270.43	4188.09	142.59	208.51	102.51	38.09	1.82	62.8	114.43	415.72	172.43	62.8	2864.07	148.41	
33	NETCR_013_V1	cachexic	107.77	16.61	26.84	32.46	62.8	29.67	44.26	20.91	459.44	162.39	70.81	5.31	8.5	330.3	45.15	64.72	70.81	3071.74	40.85	11731.12	424.11	336.97	196.37	159.17	2.69	267.74	492.75	671.83	267.74	96.54	550.04	347.23	
34	NETL_020_V1	cachexic	13.33	50.91	2.92	40.85	46.99	22.42	10.07	4.06	97.51	75.19	29.37	8.58	11.36	95.58	19.69	127.74	61.56	2186.37	7.92	5431.66	230.44	135.64	130.32	60.95	2.32	126.47	157.59	336.97	94.63	18.92	1790.05	108.85	
35	NETL_020_V2	cachexic	27.94	80.64	15.8	64.72	88.23	11.7	19.49	5.26	125.21	183.09	42.52	28.5	11.02	145.47	66.69	208.51	151.41	2298.47	34.81	8349.86	327.01	202.35	142.59	57.4	4.14	156.02	214.86	424.11	257.24	51.42	3640.95	61.56	
36	PIF_192	cachexic	141.17	68.03	40.85	12.81	26.05	21.76	45.6	20.7	123.97	56.83	24.29	18.36	39.65	87.36	47.47	22.87	11.13	2392.27	27.66	5014.05	190.57	125.21	120.3	42.52	2.86	99.48	145.47	454.86	66.69	19.11	407.48	101.49	
37	NETCR_012_V1	cachexic	14.01	46.06	29.08	24.53	64.07	13.07	11.82	21.12	48.91	21.33	9.58	8.33	6.49	89.12	24.05	45.15	6.62	1790.05	11.47	4315.64	142.59	102.51	62.18	18.17	2.01	79.84	145.47	262.43	20.91	25.03	437.03	135.64	
38	NETCR_012_V2	cachexic	244.69	116.75	40.04	61.56	174.16	53.52	45.15	44.7	62.8	43.38	16.44	11.13	10.18	273.14	117.92	347.23	23.1	4188.09	192.48	13359.73	411.58	407.48	148.41	101.49	6.05	445.86	368.71	749.95	307.97	198.34	2724.39	507.76	1
39	PIF_089	cachexic	123.97	81.45	55.15	70.81	92.76	561.16	43.38	31.82	144.03	76.71	152.93	4.01	30.57	478.19	132.95	116.75	23.34	2951.3	232.76	16481.6	632.7	645.48	379.93	204.38	9.97	595.86	482.99	2697.28	72.97	82.27	1826.21	482.99	
40	NETCR_002_V1	cachexic	141.17	28.5	20.29	14.3	97.51	8.41	5.58	23.1	48.42	64.72	18.54	13.74	13.2	327.01	62.8	126.47	120.3	1380.22	38.09	7631.2	237.46	144.03	175.91	43.38	3.67	210.61	454.86	871.31	200.34	21.12	584.06	487.85	
41	PIF_179	cachexic	35.16	26.58	5.21	30.27	7.39	8.41	5.81	21.33	132.95	62.8	103.54	6.96	6.42	194.42	42.1	75.94	18.54	1002.25	37.71	3197.1	125.21	50.91	146.94	48.42	2.18	445.86	278.66	528.48	117.92	24.29	3533.34	142.59	
42	PIF_114	cachexic	685.4	36.23	32.46	85.63	25.03	184.93	38.09	32.79	572.49	228.15	188.67	8.41	16.78	304.9	66.02	146.94	19.69	3604.72	76.71	12332.58	1032.77	239.85	403.43	79.04	10.28	314.19	533.79	595.86	164.02	130.32	812.41	254.68	
43	NETCR_006_V1	cachexic	278.66	40.45	55.15	51.42	74.44	354.25	94.63	16.28	595.86	265.07	95.58	7.92	16.44	601.85	177.68	39.25	90.02	459.44	132.95	19930.37	1141.39	539.15	89.12	336.97	7.32	1450.99	780.55	1881.83	550.04	33.78	1326.1	148.41	
44	PIF_141	cachexic	15.8	23.57	17.99	37.34	21.33	26.84	7.1	42.52	138.38	65.37	21.98	10.91	13.87	103.54	64.07	34.12	65.37	1366.49	54.05	7115.28	204.38	237.46	165.67	37.71	2.14	117.92	181.27	487.85	244.69	561.16	2038.56	330.3	
45	NETCR_025_V1	cachexic	29.96	96.54	6.55	65.37	1053.63	14.15	45.15	41.68	117.92	51.94	29.37	4.01	27.66	403.43	41.26	130.32	60.95	4964.16	71.52	14764.78	528.48	383.75	62.18	130.32	31.19	407.48	403.43	678.58	232.76	103.54	7259.02	100.48	1
46	NETCR_025_V2	cachexic	16.95	114.43	2.53	77.48	2465.13	19.49	62.18	14.01	82.27	114.43	125.21	5	37.34	632.7	89.12	120.3	15.96	7480.09	117.92	22247.84	812.41	735.1	119.1	237.46	75.94	399.41	528.48	699.24	464.05	164.02	2321.57	145.47	1
47	NETCR_016_V1	cachexic	292.95	57.97	167.34	82.27	468.72	53.52	14.59	11.36	518.01	376.15	72.24	6.62	57.97	502.7	101.49	54.05	23.81	2697.28	90.02	14328.42	584.06	614	27.66	196.37	23.81	788.4	555.57	962.95	177.68	127.74	1366.49	492.75	1
48	PIF_116	cachexic	29.67	70.11	5.58	18.73	5.53	2.61	2.44	14.44	188.67	52.98	91.84	3.03	3.94	86.49	8	28.79	5.53	2208.35	41.26	2864.07	90.92	82.27	87.36	30.27	1.12	87.36	92.76	257.24	16.44	66.69	1380.22	35.16	
49	PIF_191	control	18.92	24.53	3.29	10.49	9.68	26.84	5.37	12.94	50.4	26.31	13.6	4.9	3.35	104.58	33.12	59.15	13.2	502.7	2.75	1702.75	44.7	48.91	34.47	17.12	1.99	34.81	46.99	237.46	32.14	17.99	478.19	132.95	
50	PIF_164	control	127.74	1032.77	8.58	66.02	38.09	66.69	21.76	43.82	376.15	149.9	116.75	7.61	19.11	432.68	121.51	109.95	59.74	4230.18	259.82	15063.05	497.7	432.68	219.2	196.37	6.89	327.01	290.03	2275.6	130.32	116.75	6634.24	265.07	
51	NETL_013_V1	control	34.81	12.3	5.87	15.18	16.78	11.25	2.23	2.46	108.85	57.4	3.49	5.58	3.9	48.91	12.43	5.37	14.44	177.68	6.36	2392.27	83.93	66.69	17.29	26.58	1.21	75.19	24.29	46.06	46.53	16.95	665.14	30.57	
52	PIF_188	control	65.37	24.05	4.71	15.8	7.24	3.13	14.59	9.12	37.71	48.42	9.49	3	6.42	41.26	13.07	11.25	18.92	87.36	9.03	2489.91	142.59	35.87	15.49	47.47	1.6	44.26	35.52	89.12	50.91	106.7	275.89	44.26	
53	PIF_195	control	15.18	94.63	11.36	8.17	5.64	5.99	6.49	3.6	62.8	41.68	86.49	6.05	4.81	78.26	19.49	8.58	5.26	214.86	18.54	3604.72	142.59	34.12	52.98	31.82	3.71	114.43	29.37	141.17	38.86	87.36	4817.45	51.42	
54	NETCR_015_V1	control	70.81	75.94	22.65	60.95	230.44	53.52	17.81	6.96	137	59.15	16.28	7.1	6.17	376.15	130.32	311.06	206.44	4105.16	46.99	9996.6	304.9	906.87	292.95	148.41	6.82	320.54	437.03	1286.91	320.54	192.48	572.49	502.7	1
55	PIF_102	control	25.28	101.49	8.33	59.15	88.23	22.65	34.12	46.99	441.42	432.68	202.35	7.1	18.54	330.3	64.07	55.15	111.05	3327.58	93.69	7480.09	340.36	320.54	235.1	64.07	9.58	336.97	284.29	871.31	34.81	34.81	1085.72	129.02	1
56	NETL_010_V1	control	34.47	12.81	3.78	8.33	14.3	24.29	3.16	5.99	42.52	52.98	9.12	10.49	3.46	28.79	14.3	7.92	16.12	259.82	84.77	1480.3	102.51	58.56	45.6	15.33	1.36	42.95	43.82	86.49	7.85	83.93	487.85	26.58	
57	NETL_010_V2	control	18.54	8.41	3.78	4.85	8.08	22.87	3.22	5.05	31.19	21.33	6.82	12.55	3.46	21.76	8.17	11.25	16.95	179.47	395.44	1064.22	41.26	51.42	21.54	5.7	0.79	38.09	23.34	78.26	5.42	51.94	632.7	26.58	

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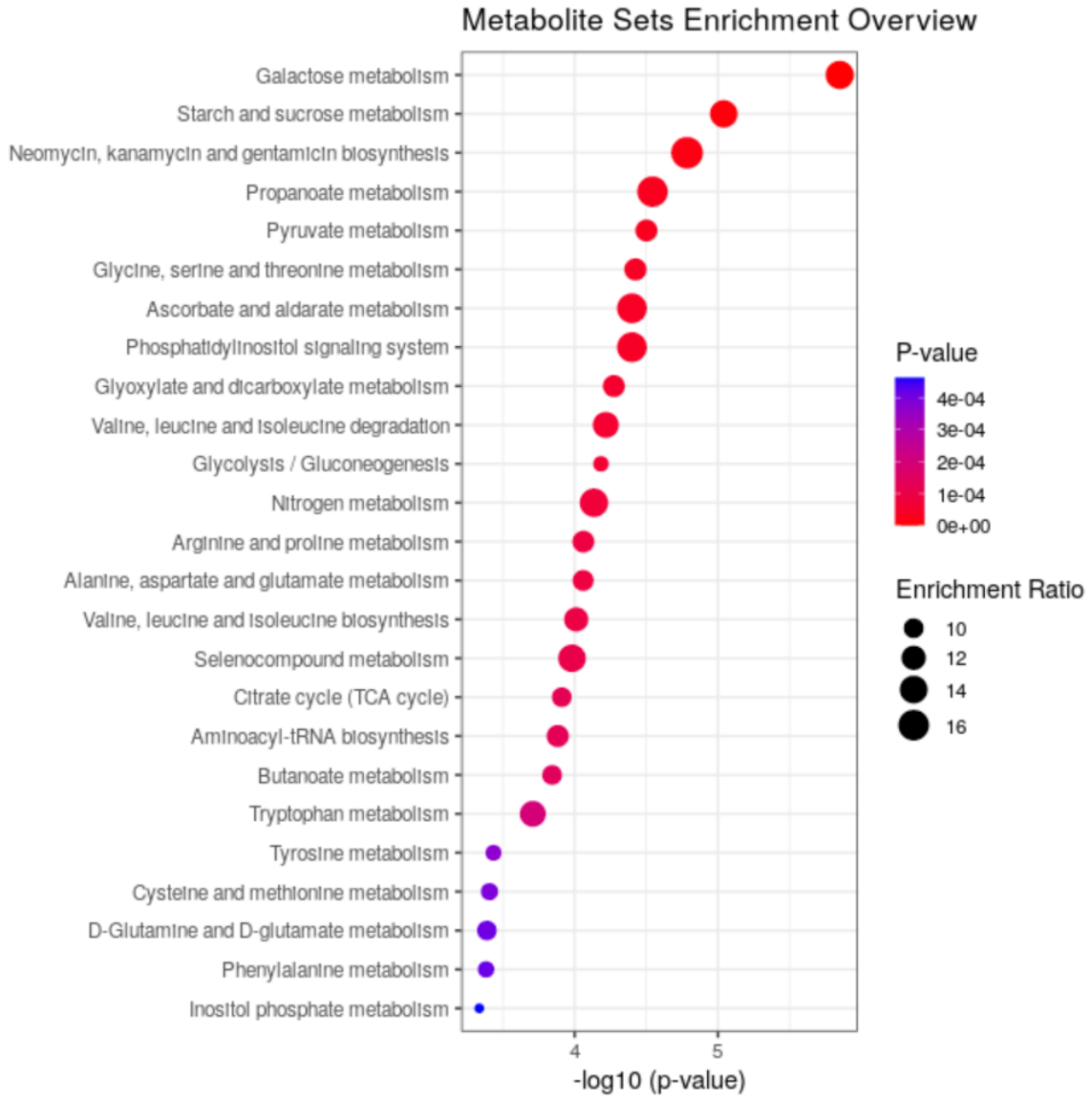
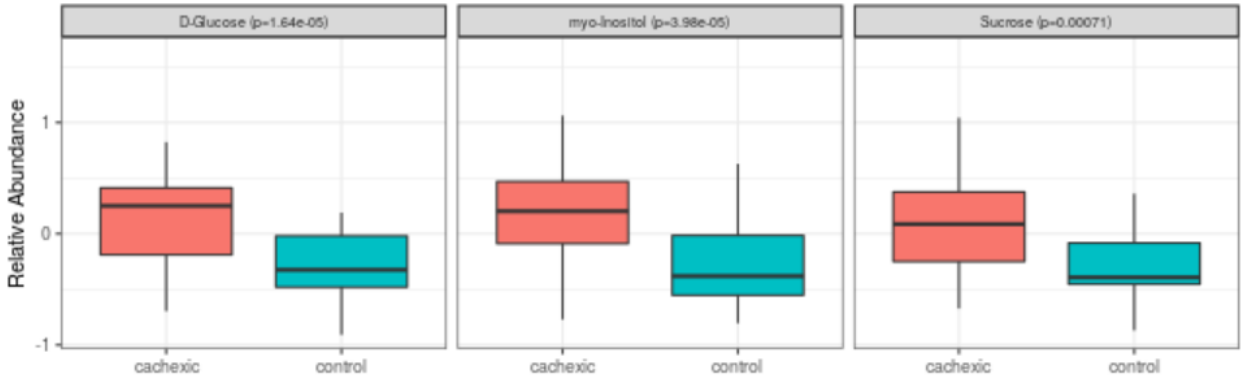
Enrichment Analysis in MetaboAnalyst





Set Name	Metabolites
Galactose metabolism	Stachyose; D-Tagatose 6-phosphate; D-Gal alpha 1->6D-Gal alpha 1->6D-Glucose; **Sucrose**; Raffinose; Melibiose; D-Galactose; Galactosylglycerol; Epimelibiose; Melibiitol; alpha-D-Galactosyl-(1->3)-1D-myo-inositol; Alpha-D-Glucose; Alpha-Lactose; Glucose 1-phosphate; Uridine diphosphategalactose; Uridine diphosphate glucose; Galactose 1-phosphate; D-Galactose; Glucose 6-phosphate; D-Tagatose 1,6-bisphosphate; **D-Glucose**; D-Fructose; Galactitol; Glycerol; D-Mannose; Sorbitol; **myo-Inositol**

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Gene List

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AASS  -0.139042168
ACAA2  1.401267672
ACADL  -2.608712824
ACADM  -0.876538515
ACADS  0.150535255
ACADSB  -1.637743607
ACHE  2.567118372
ACSM1  -2.348501729
ACTA2  -0.282176735
ACTB  1.559623747
ACTC1  -1.690352151
ADCY1  2.916857724
ADH1A  -0.87610472
AGL  -0.399133917
AGTR1  -1.078340189
AKR1A1  2.178398898
AKR1B1  -1.077265882
```

ID Type: Official Gene Symbol

Metabolite List

Compound list with optional fold changes

```
#KEGG  logFC
C00006  0.512160717
C00024  0.351757155
C00026  -2.669056963
C00029  0.379186578
C00031  1.669222153
C00047  -2.492289379
C00049  2.963835134
C00062  -2.558919927
C00064  1.77810046
C00072  0.632536475
C00077  -2.09045808
C00084  0.347392968
C00089  -1.460843412
C00097  3.046798674
C00101  -1.495004303
C00109  0.476718643
C00111  -2.672997377
```

ID Type: KEGG ID

Specify organism: Homo sapiens (human)

Try our example data

Submit

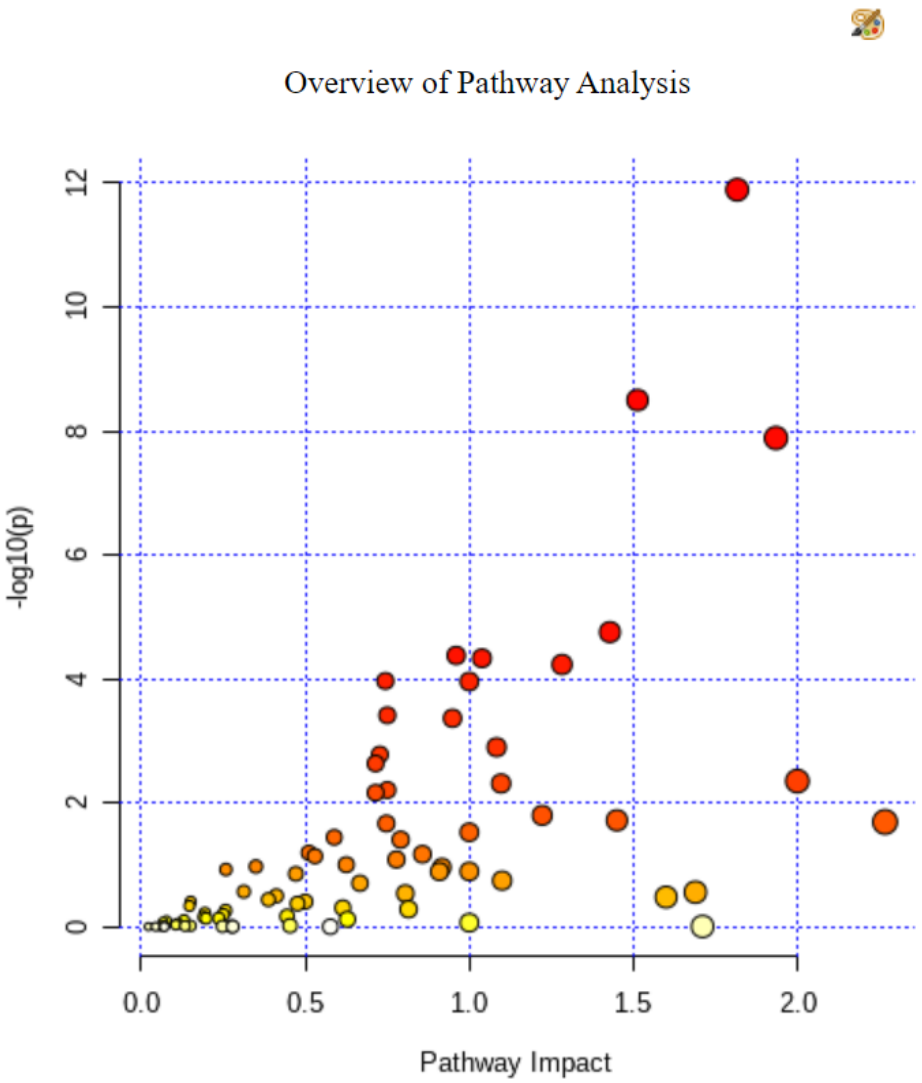
R Command History

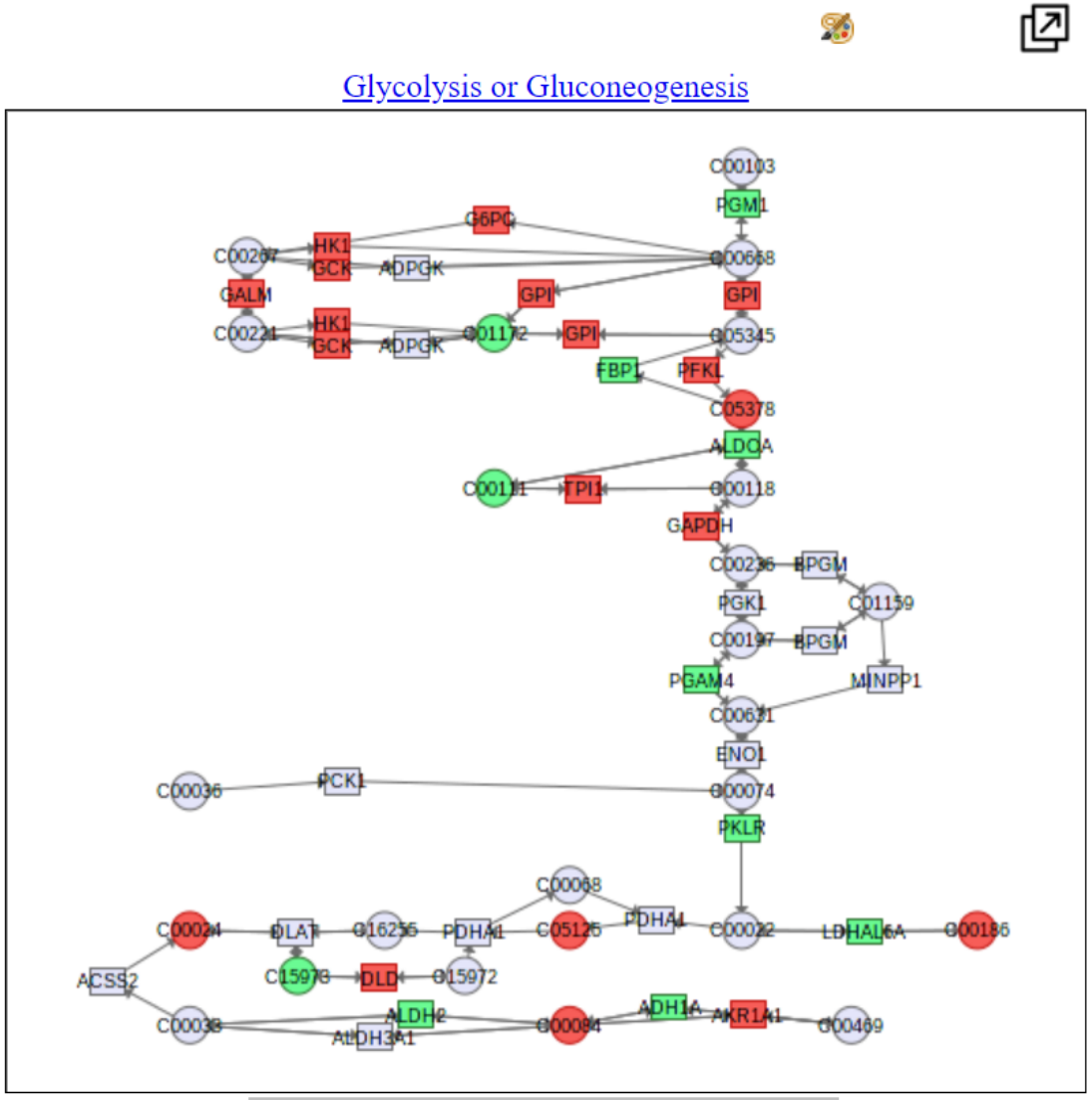
Keep collapsed Save

```
1.  mSet<-InitDataObjects("conc", "msetqea", FALSE)
2.  mSet<-Read.TextData(mSet, "Replacing_with_your_file_path", "rowu", "disc");
3.  mSet<-CrossReferencing(mSet, "name");
4.  mSet<-CreateMappingResultTable(mSet)
5.  mSet<-SanityCheckData(mSet)
6.  mSet<-ReplaceMin(mSet);
7.  mSet<-PreparePrenormData(mSet)
8.  mSet<-Normalization(mSet, "NULL", "LogNorm", "MeanCenter", ratio=FALSE, ratioNum=20)
9.  mSet<-PlotNormSummary(mSet, "norm_0_", "png", 72, width=NA)
10. mSet<-PlotSampleNormSummary(mSet, "snorm_0_", "png", 72, width=NA)
11. mSet<-SetMetabolomeFilter(mSet, F);
12. mSet<-SetCurrentMsetLib(mSet, "kegg_pathway", 2);
13. mSet<-CalculateGlobalTestScore(mSet)
14. mSet<-PlotQEA.Overview(mSet, "qea_0_", "net", "png", 72, width=NA)
15. mSet<-PlotEnrichDotPlot(mSet, "qea", "qea_dot_0_", "png", 72, width=NA)
16. mSet<-PlotQEA.MetSet(mSet, "Galactose metabolism", "png", 72, width=NA)
17. mSet<-PlotQEA.MetSet(mSet, "Galactose metabolism", "png", 72, width=NA)
18. mSet<-PlotQEA.MetSet(mSet, "Galactose metabolism", "png", 72, width=NA)
19. mSet<-PreparePrenormData(mSet)
20. mSet<-SanityCheckData(mSet)
21. mSet<-CreateMappingResultTable(mSet)
```


Current Protocols in Bioinformatics **68,** e86 (2019)

Integrated analysis in MetaboAnalyst





Current Protocols in Bioinformatics **68,** e86 (2019)

Integrated analysis in MetaboAnalyst

Click the corresponding **Pathway Name** to view its graphical presentation; click **Match Status** to view the pathway members (with matched ones highlighted).

Download Results Table | Download Matched Features Table

1 2 3 4

Pathway Name	Match Status	p	-log(p)	Holm p	FDR	Impact	Link
Glycolysis or Gluconeogenesis	28/61	1.2805E-12	11.893	1.0756E-10	1.0756E-10	1.8167	KEGG
Fructose and mannose metabolism	19/40	3.1764E-9	8.4981	2.6364E-7	1.3341E-7	1.5128	KEGG
Pentose phosphate pathway	20/47	1.2988E-8	7.8865	1.065E-6	3.6367E-7	1.9348	KEGG
Starch and sucrose metabolism	15/43	1.7621E-5	4.754	0.0014273	3.7004E-4	1.4286	KEGG
Galactose metabolism	16/51	4.1966E-5	4.3771	0.0033573	6.5122E-4	0.96	KEGG
Arginine biosynthesis	11/27	4.6516E-5	4.3324	0.0036748	6.5122E-4	1.0385	KEGG
Retinol metabolism	15/47	5.8685E-5	4.2315	0.0045774	7.0422E-4	1.2826	KEGG
beta-Alanine metabolism	14/44	1.082E-4	3.9658	0.0083311	0.0010314	0.74419	KEGG
Pantothenate and CoA biosynthesis	12/34	1.1051E-4	3.9566	0.0083989	0.0010314	1.0	KEGG
Lysine degradation	14/49	3.8705E-4	3.4122	0.029029	0.0032513	0.75	KEGG
Amino sugar and nucleotide sugar metabolism	19/79	4.3262E-4	3.3639	0.032014	0.0033036	0.94872	KEGG
Ascorbate and aldarate metabolism	6/13	0.001268	2.8969	0.092562	0.0088758	1.0833	KEGG
Glutathione metabolism	14/56	0.0016645	2.7787	0.11984	0.010755	0.72727	KEGG
Butanoate metabolism	9/29	0.0023213	2.6343	0.16481	0.013928	0.71429	KEGG
Neomycin, kanamycin and gentamicin biosynthesis	3/4	0.0044608	2.3506	0.31225	0.02498	2.0	KEGG
Pentose and glucuronate interconversions	9/32	0.0048735	2.3122	0.33627	0.025586	1.0968	KEGG
Pyruvate metabolism	11/45	0.0062287	2.2056	0.42355	0.030777	0.75	KEGG
Arginine and proline metabolism	16/78	0.0068754	2.1627	0.46065	0.032085	0.71429	KEGG
D-Glutamine and D-glutamate metabolism	4/10	0.015946	1.7973	1.0	0.0705	1.2222	KEGG
Biotin metabolism	6/21	0.019191	1.7169	1.0	0.080601	1.45	KEGG

1 2 3 4

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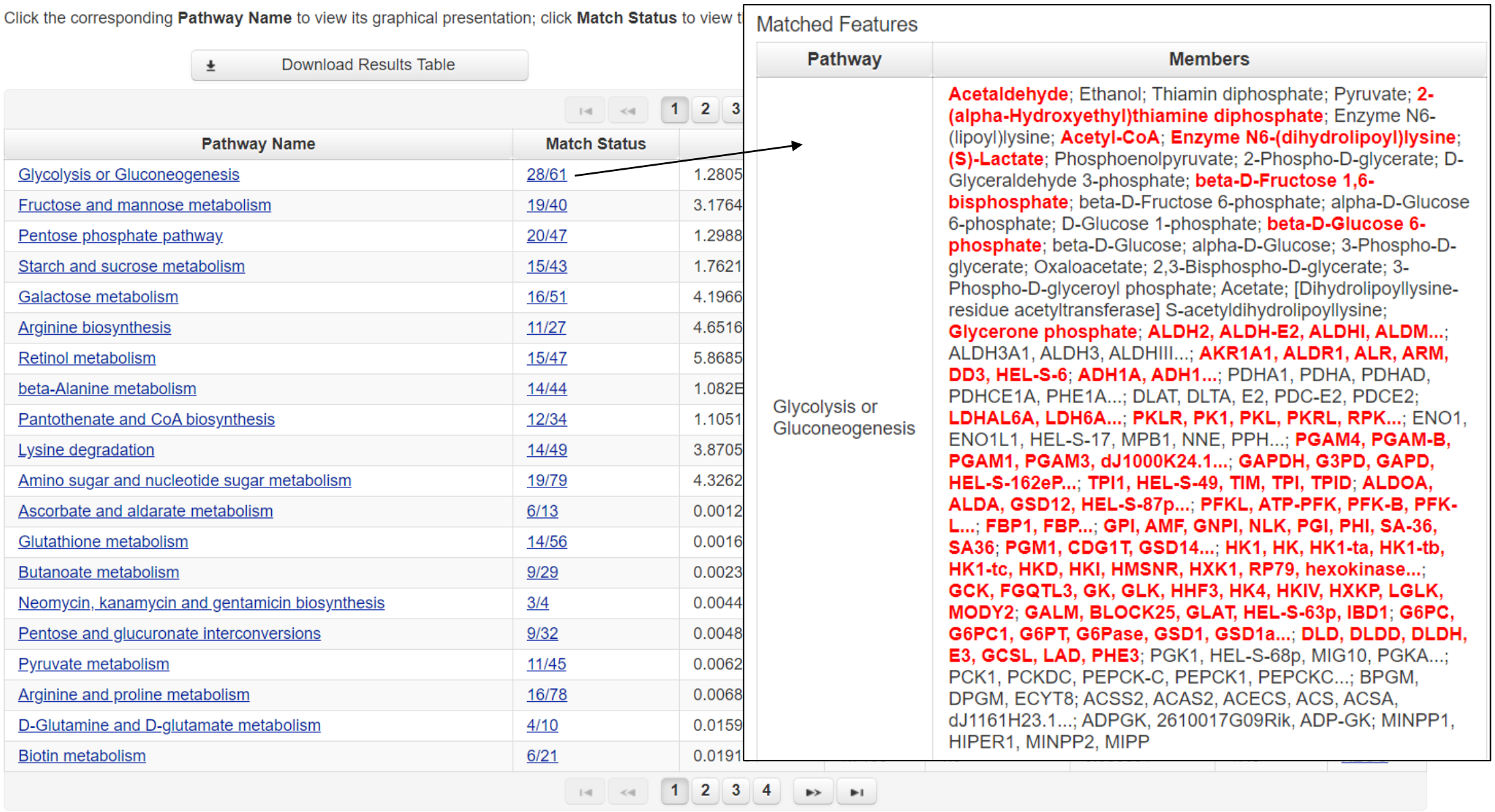
Integrated analysis in MetaboAnalyst



Click the corresponding **Pathway Name** to view its graphical presentation; click **Match Status** to view t

Download Results Table

1 2 3

Pathway Name	Match Status	
Glycolysis or Gluconeogenesis	28/61	1.2805
Fructose and mannose metabolism	19/40	3.1764
Pentose phosphate pathway	20/47	1.2988
Starch and sucrose metabolism	15/43	1.7621
Galactose metabolism	16/51	4.1966
Arginine biosynthesis	11/27	4.6516
Retinol metabolism	15/47	5.8685
beta-Alanine metabolism	14/44	1.082E
Pantothenate and CoA biosynthesis	12/34	1.1051
Lysine degradation	14/49	3.8705
Amino sugar and nucleotide sugar metabolism	19/79	4.3262
Ascorbate and aldarate metabolism	6/13	0.0012
Glutathione metabolism	14/56	0.0016
Butanoate metabolism	9/29	0.0023
Neomycin, kanamycin and gentamicin biosynthesis	3/4	0.0044
Pentose and glucuronate interconversions	9/32	0.0048
Pyruvate metabolism	11/45	0.0062
Arginine and proline metabolism	16/78	0.0068
D-Glutamine and D-glutamate metabolism	4/10	0.0159
Biotin metabolism	6/21	0.0191

1 2 3 4

Matched Features

Pathway	Members
Glycolysis or Gluconeogenesis	**Acetaldehyde**; Ethanol; Thiamin diphosphate; Pyruvate; **2-(alpha-Hydroxyethyl)thiamine diphosphate**; Enzyme N6-(lipoyl)lysine; **Acetyl-CoA**; **Enzyme N6-(dihydrolipoyl)lysine**; **(S)-Lactate**; Phosphoenolpyruvate; 2-Phospho-D-glycerate; D-Glyceraldehyde 3-phosphate; **beta-D-Fructose 1,6-bisphosphate**; beta-D-Fructose 6-phosphate; alpha-D-Glucose 6-phosphate; D-Glucose 1-phosphate; **beta-D-Glucose 6-phosphate**; beta-D-Glucose; alpha-D-Glucose; 3-Phospho-D-glycerate; Oxaloacetate; 2,3-Bisphospho-D-glycerate; 3-Phospho-D-glyceroyl phosphate; Acetate; [Dihydrolipoyllysine-residue acetyltransferase] S-acetyldihydrolipoyllysine; **Glycerone phosphate**; **ALDH2, ALDH-E2, ALDHI, ALDM...**; ALDH3A1, ALDH3, ALDHIII...; **AKR1A1, ALDR1, ALR, ARM, DD3, HEL-S-6**; **ADH1A, ADH1...**; PDHA1, PDHA, PDHAD, PDHCE1A, PHE1A...; DLAT, DLTA, E2, PDC-E2, PDCE2; **LDHAL6A, LDH6A...**; **PKLR, PK1, PKL, PKRL, RPK...**; ENO1, ENO1L1, HEL-S-17, MPB1, NNE, PPH...; **PGAM4, PGAM-B, PGAM1, PGAM3, dJ1000K24.1...**; **GAPDH, G3PD, GAPD, HEL-S-162eP...**; **TPI1, HEL-S-49, TIM, TPI, TPID**; **ALDOA, ALDA, GSD12, HEL-S-87p...**; **PFKL, ATP-PFK, PFK-B, PFK-L...**; **FBP1, FBP...**; **GPI, AMF, GNPI, NLK, PGI, PHI, SA-36, SA36**; **PGM1, CDG1T, GSD14...**; **HK1, HK, HK1-ta, HK1-tb, HK1-tc, HKD, HKI, HMSNR, HXK1, RP79, hexokinase...**; **GCK, FGQTL3, GK, GLK, HHF3, HK4, HKIV, HXKP, LGLK, MODY2**; **GALM, BLOCK25, GLAT, HEL-S-63p, IBD1**; **G6PC, G6PC1, G6PT, G6Pase, GSD1, GSD1a...**; **DLD, DLDD, DLDH, E3, GCSL, LAD, PHE3**; PGK1, HEL-S-68p, MIG10, PGKA...; PCK1, PCKDC, PEPCK-C, PEPCK1, PEPCKC...; BPGM, DPGM, ECYT8; ACSS2, ACAS2, ACECS, ACS, ACSA, dJ1161H23.1...; ADPGK, 2610017G09Rik, ADP-GK; MINPP1, HIPER1, MINPP2, MIPP

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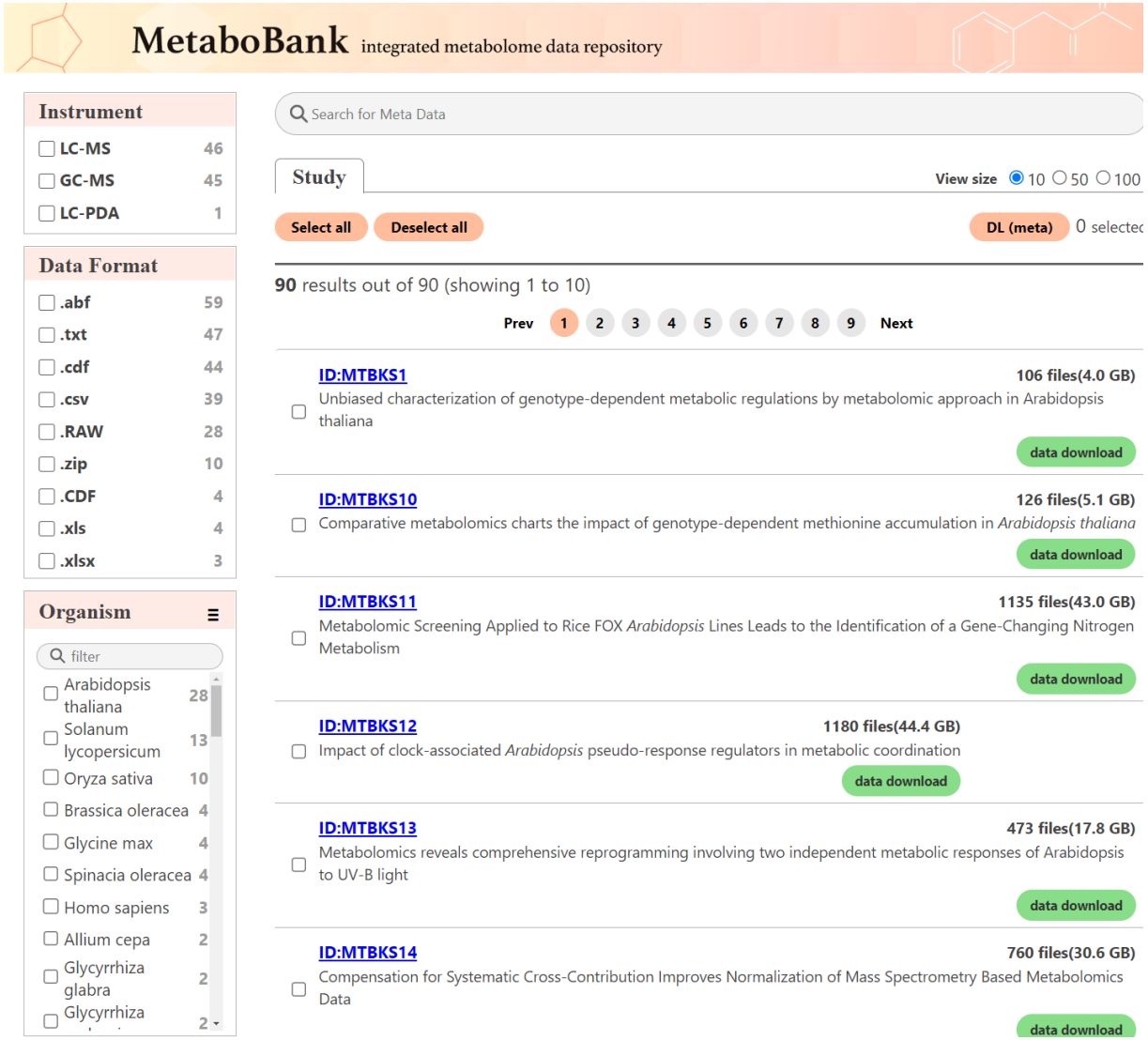
質量分析データの性質を理解し、データ再解析により新たな知見を創出



Project ID	Project Title	Institute (Experimental)	Institute (Analysis)	Number Of Studies
PR001483	Dietary inclusion of nitrite-containing frankfurter exacerbates colorectal cancer pathology, increases oxidative stress, alters metabolism and causes gut dybiosis in APCmin mice	Institute for Global Food Security	Institute for Global Food Security	1
PR001457	Machine Learning Reveals Lipidome Dynamics in a Mouse Model of Ovarian Cancer	Georgia Institute of Technology	Georgia Institute of Technology	1
PR001455	1-deoxysphingolipid synthesis compromises anchorage-independent growth and plasma membrane endocytosis in cancer cells	TU Braunschweig	Salk Institute for Biological Studies	1
PR001425	Application of Artificial Intelligence to Plasma Metabolomics Profiles to Predict Response to Neoadjuvant Chemotherapy in Triple-Negative Breast Cancer	University of Texas MD Anderson Cancer Center	University of Texas MD Anderson Cancer Center	1
PR001418	Dynamic partitioning of branched-chain amino acids-derived nitrogen supports renal cancer progression	CECAD Research Center, University Hospital Cologne	CECAD Research Center	8
PR001416	The microbiome-derived metabolite TMAO drives immune activation and boosts response to immune checkpoint blockade in pancreatic cancer	The Wistar Institute	The Wistar Institute	2

メタボロームデータを出す側と使う側

本日取り扱った内容

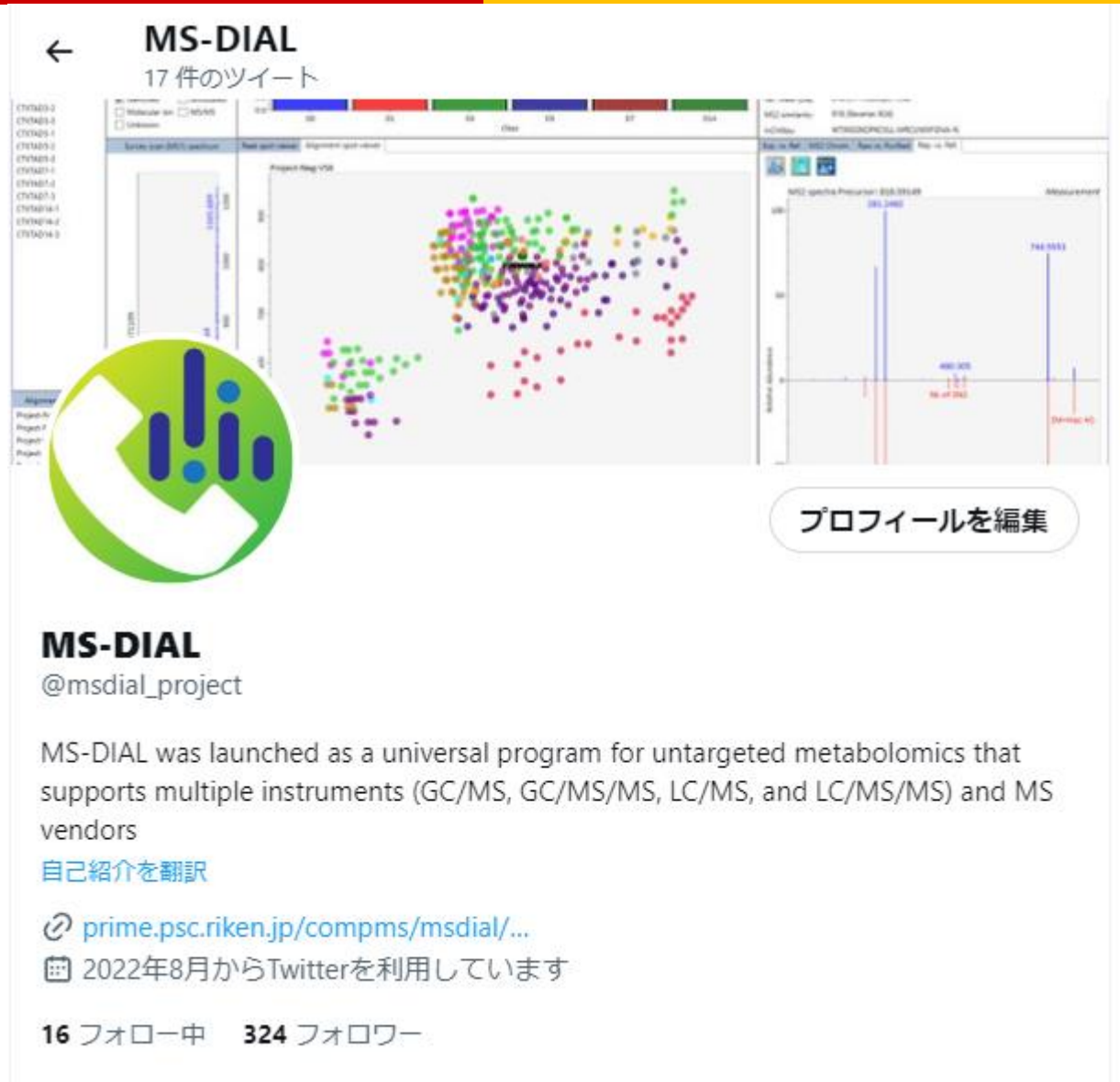
出す側

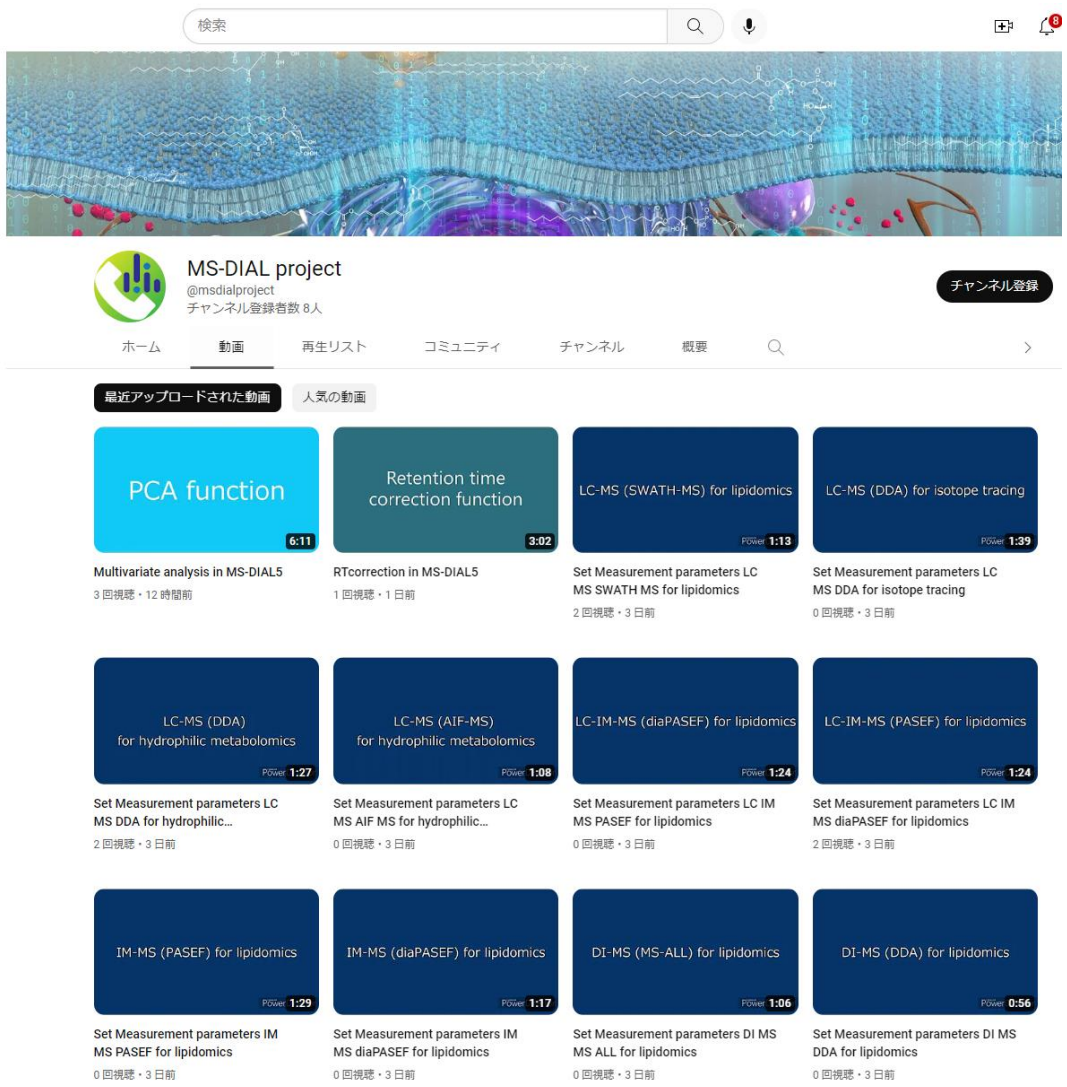
- 分析化学
- 質量分析
- イオン
- マススペクトル
- 質量分析インフォマティクス
- アノテーション
- データ標準化

使う側

- データの特徴理解
- 化合物IDの取得
- データの正規化
- 統計・多変量解析
- データベース検索
- 代謝マップ投影
- 適切な数理モデルの選択
- オミクスモジュールへ統合

最後に





質量分析の情報計測で新しいバイオロジーを探求したい方→ htsugawa@go.tuat.ac.jp