Metabolomics and Bioactive compound Discovery: The Foundation for Future Medicine

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Head of Centre of Biopharmaceutical Science for Healthy Ageing

Herbal medicine market:

https://www.fortunebusinessinsights.com/amp/herbal-medicine-market-106320

Biodiversity in Thailand:

สำนักงานนโยบายและแผนทรัพยากรธรรมชาติและสิ่งแวดล้อม
Office of Natural Resources and Environmental Policy and Planning

Mahidol University
Faculty of Pharmacy

Plant-derived natural medicinal products

Plant-Derived Natural Products	Botanical Source	Medicinal Application
Atropine	*Atropa belladonna* L.	Anticholinergic
Berberine	*Berberis vulgaris* L.	Bacillary dysentery
Caffeine	*Camellia sinensis* (L.) Kuntze	Neuroprotection
Camptothecin	*Camptotheca acuminata* Decne.	Anticancer
Cocaine	*Erythroxylum coca* Lam.	Anesthetic
Colchicine	*Colchicum autumnale* L.	Antigout, antitumor
Convallatoxin	*Convallaria majalis* L.	Cardiotonic
Digitoxin	*Digitalis purpurea* L.	Cardiotonic
Digoxin	*Digitalis lanata* Ehrh.	Cardiotonic
Ephedrine	*Ephedra sinica* Stapf	Sympathomimetic
Glaucine	*Glaucium flavum* Crantz	Antitussive
Glycyrrhizin	*Glycyrrhiza glabra* L.	Treatment of Addison's disease
Morphine	*Papaver somniferum* L.	Analgesic
Ouabain	*Strophanthus gratus* (Wall. & Hook.) Baill.	Cardiotonic
Quinine	*Cinchona officinalis* L.	Antimalarial
Reserpine	*Rauvolfia serpentina* (L.) Benth. ex Kurz	Antihypertensive
Salicin	*Salix alba* L.	Analgesic
Scopolamine	*Datura metel* L.	Sedative
Silymarin	*Silybum marianum* (L.) Gaertn.	Antihepatotoxic
Taxol	*Taxus brevifolia* Nutt.	Anticancer
Theophylline	*Theobroma cacao* L.	Diuretic
Thymol	*Thymus vulgaris* L.	Topical antifungal
Vinblastine	*Catharanthus roseus* (L.) G.Don	Anticancer
Vincristine	*Catharanthus roseus* (L.) G.Don	Anticancer
Yuanhuacine	*Daphne genkwa* Siebold & Zucc.	Abortifacient

Drugs Drug Candidates 2024, 3(1), 184-207; https://doi.org/10.3390/ddc3010011

Traditional workflow to elucidate herbal bio-active compound:

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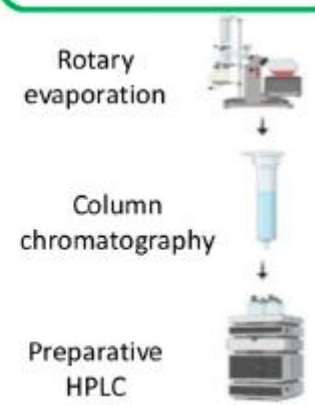
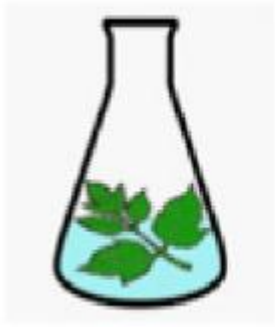
1 Plant Collection

2 Extraction

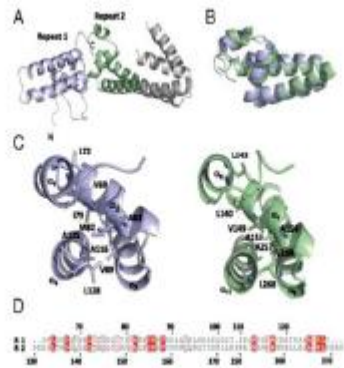
3 Isolation and Purification



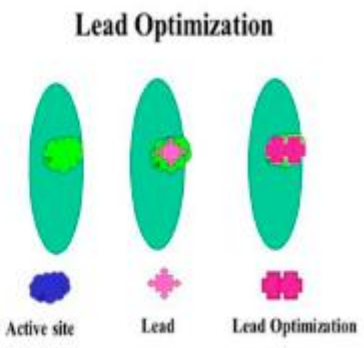
4 Bioassays



5 Structural Characterization



6 Lead Optimization



Drugs Drug Candidates 2024, 3(1), 184-207; https://doi.org/10.3390/ddc3010011

Metabolomics and Network Pharmacology: New drug discovery workflow

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scientific reports

OPEN

Integrated network pharmacology and metabolomics reveal the mechanisms of *Jasminum elongatum* in anti-ulcerative colitis

Jinyan Qiu[1], Guanlin Xiao[2], Minjuan Yang[1], Xuejun Huang[2], Dake Cai[2], Canhui Xie[1], Zhao Chen[2], Xiaoli Bi[1,2✉] & Aili Xu[1,2✉]

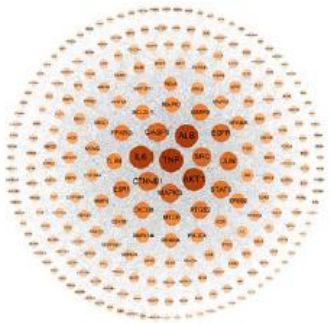
Jasminum elongatum

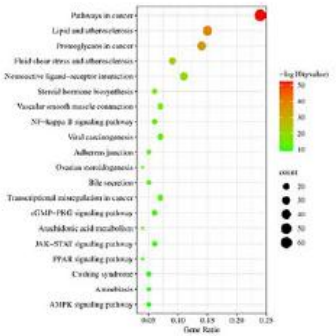
Components

UPLC-Q-TOF-MS

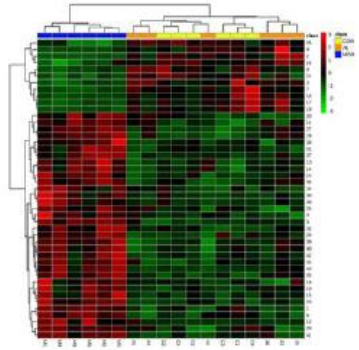
C57BL/6J mice

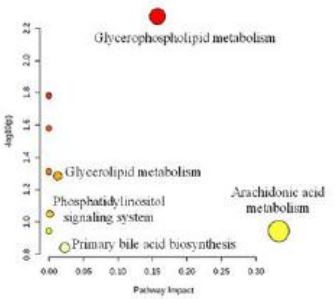
Network pharmacology



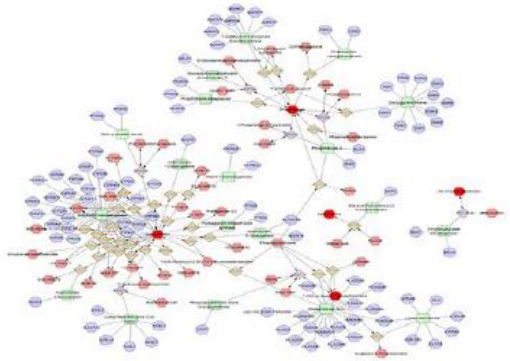


Metabolomics

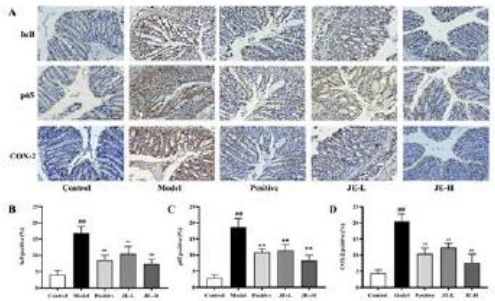




Compound-Reaction-Enzyme-Gene Networks



Immunohistochemistry verification



Qiu, J., Xiao, G., Yang, M. *et al. Sci Rep* 13, 22449 (2023).
https://doi.org/10.1038/s41598-023-49792-w

Metabolomics for plant metabolite identification

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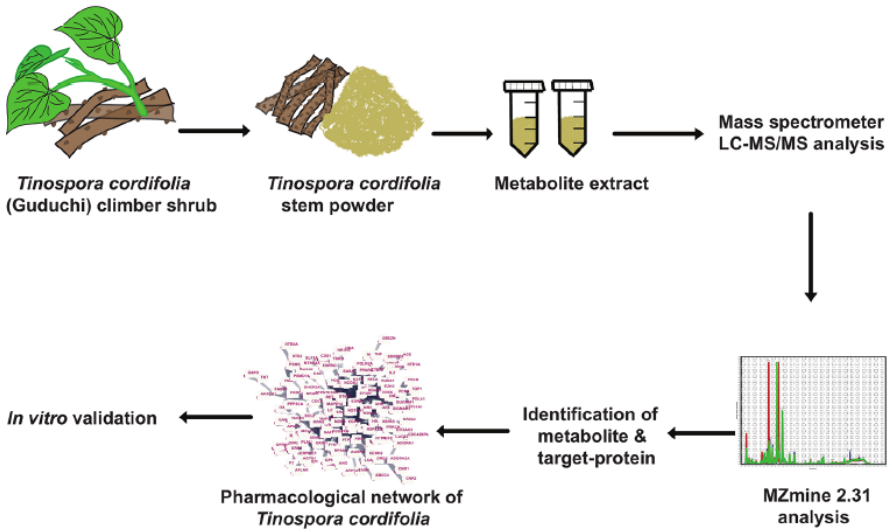
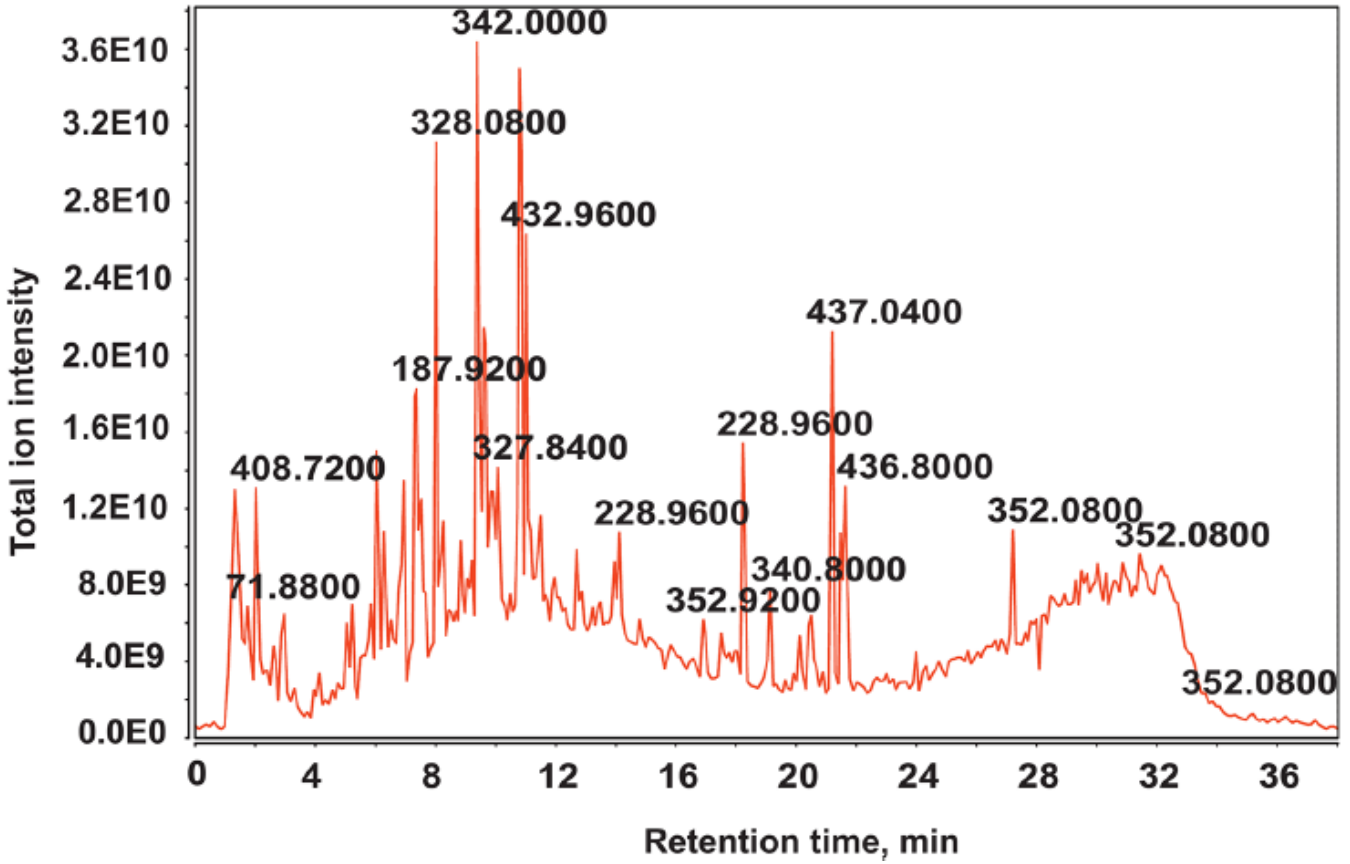
Network pharmacology and metabolomics analysis of *Tinospora cordifolia* reveals BACE1 and MAOB as potential therapeutic targets for neuroprotection in Alzheimer's disease



Workflow of metabolite extraction from T. *cordifolia* stem poder, LC-MS/MS followed by MZmine tool and subsequent bioinformatics analysis and *in vitro* validation of neuroprotective activity



Representative of total ion chromatogram of T. *cordifolia* metabolite analysis in positive mode

Amrutha, S., Abhinand, C.S., Upadhyay, S.S. *et al. Sci Rep* **15**, 8103 (2025).
https://doi.org/10.1038/s41598-025-92756-5

Metabolomics for plant metabolite identification

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scientific reports

OPEN **Network pharmacology and metabolomics analysis of *Tinospora cordifolia* reveals BACE1 and MAOB as potential therapeutic targets for neuroprotection in Alzheimer's disease**

S. Amrutha[1], Chandran S. Abhinand[1], Shubham Sukerndeo Upadhyay[1], Ravishankar Parvaje[2], Thottethodi Subrahmanya Keshava Prasad[1,3] & Prashant Kumar Modi[1]

List of Intense Metabolite Identified in T. *cordifolia*

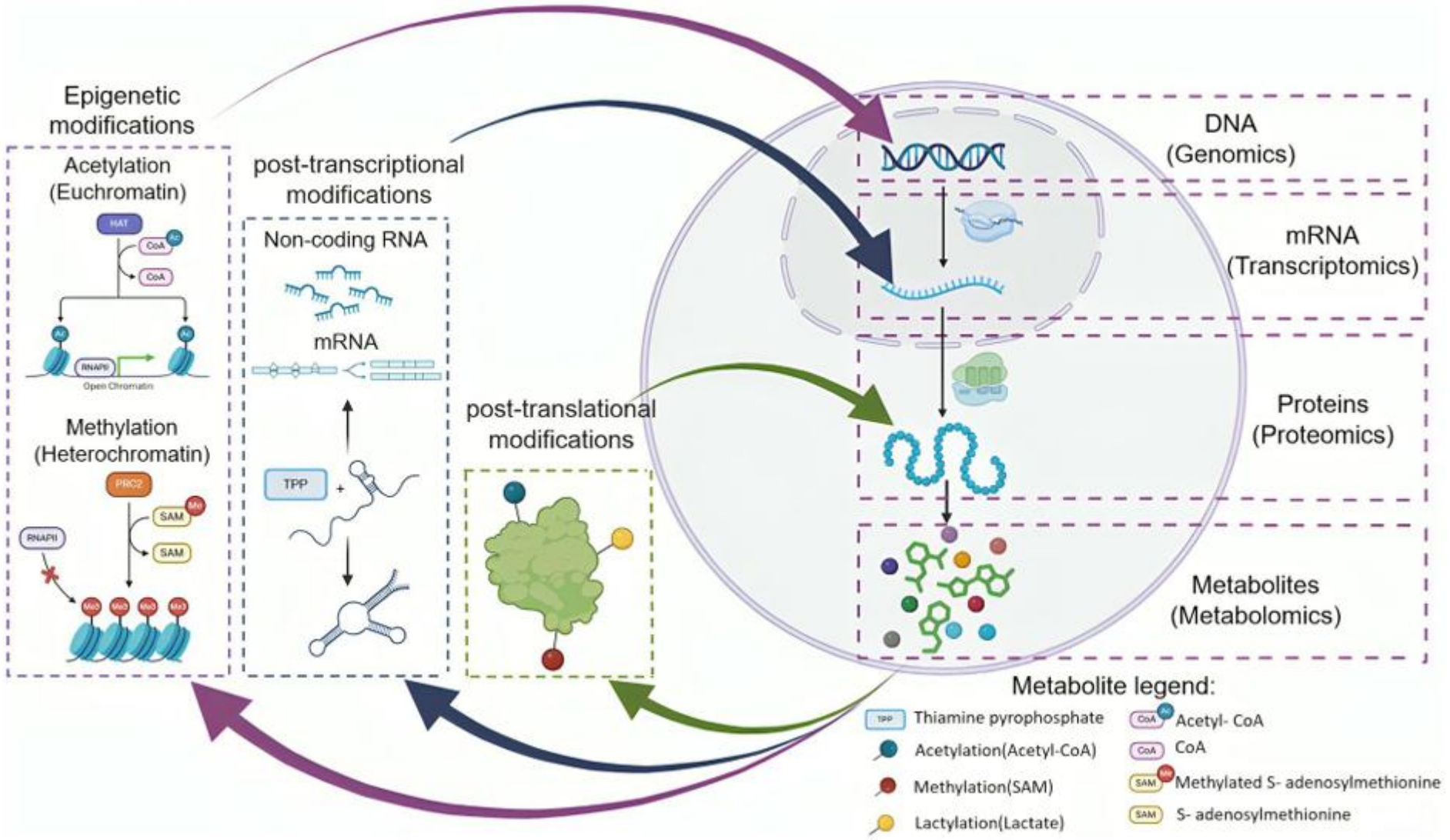
m/z, (Da)	Retention time, minutes	Metabolite identification	Peak intensity	Polarity
432.84	10.81	3-(3,5-Diiodo-4-hydroxyphenyl)pyruvate	3.27E+10	+
414.96	10.81	Perfluorooctanoic acid	3.8E+10	+
785.88	29.62	1-Cyclohexyl-11-heneicosanone	3.7E+10	+
605.16	32.05	5,7,3'-Trihydroxy-4'-methoxyflavanone	3.5E+10	+
757.8	30.67	Erucoylacetone	3.2E+10	+
352.2	29.02	O-sinapoylcholine	9.21E+09	+
338.16	32.33	Deoxynivalenol	3.2E+09	+
542.76	1.36	Cyclolinopeptide F	2.7E+09	+
271.92	7.36	Di-2-thienyl disulfide	5.13E+09	+
383.16	9.88	Cassythine	1.4E+09	+
144.96	7.55	thioacrolein	1.4E+09	+
183.96	30.07	Arsenate	1.3E+09	+
339.48	31.88	N-Dodecane	2.1E+08	-
742.32	30.96	Agavoside F	1.9E+08	-
309.12	25.54	Ilicifolinoside A	1.4E+07	-
692.76	16.48	Captafol	2.3E+07	-
343.2	14.28	corynantheal	2.4E+07	-
387.12	8.56	Dictyoquinazol C	3.7E+08	-
175.2	1.01	Putrescine	2.4E+07	-
293.04	7.98	Wasalexin A	3.2E+07	-
315.12	6.04	Hypoglycin B	1.1E+08	-
371.06	15.87	psoralen	3.3E+07	-
328.08	12.81	Avenanthramide 1p	5.6E+07	-
369.12	8.44	Linusitamarin	6.2E+07	-
71.88	1.70	Unassigned	3.4E+09	+
609.72	11.09	Unassigned	7.8E+08	+
83.88	1.42	Unassigned	7.6E+08	+
788.88	30.31	Unassigned	1.4E+09	+
585.84	13.09	Unassigned	3E+08	+
83.88	4.10	Unassigned	2.9E+07	+
682.8	9.38	Unassigned	1.6E+08	+
788.88	28.31	Unassigned	1.5E+09	+
338.42	13.50	Unassigned	5E+07	-
608.82	10.36	Unassigned	1E+08	-
357.72	9.94	Unassigned	2E+07	-
326.52	9.13	Unassigned	3E+07	-
686.88	10.47	Unassigned	2E+07	-
135.24	1.25	Unassigned	5E+07	-
413.64	10.95	Unassigned	2E+07	-
406.44	8.80	Unassigned	1E+07	-

List of Metabolite that are not Identified in T. *cordifolia*

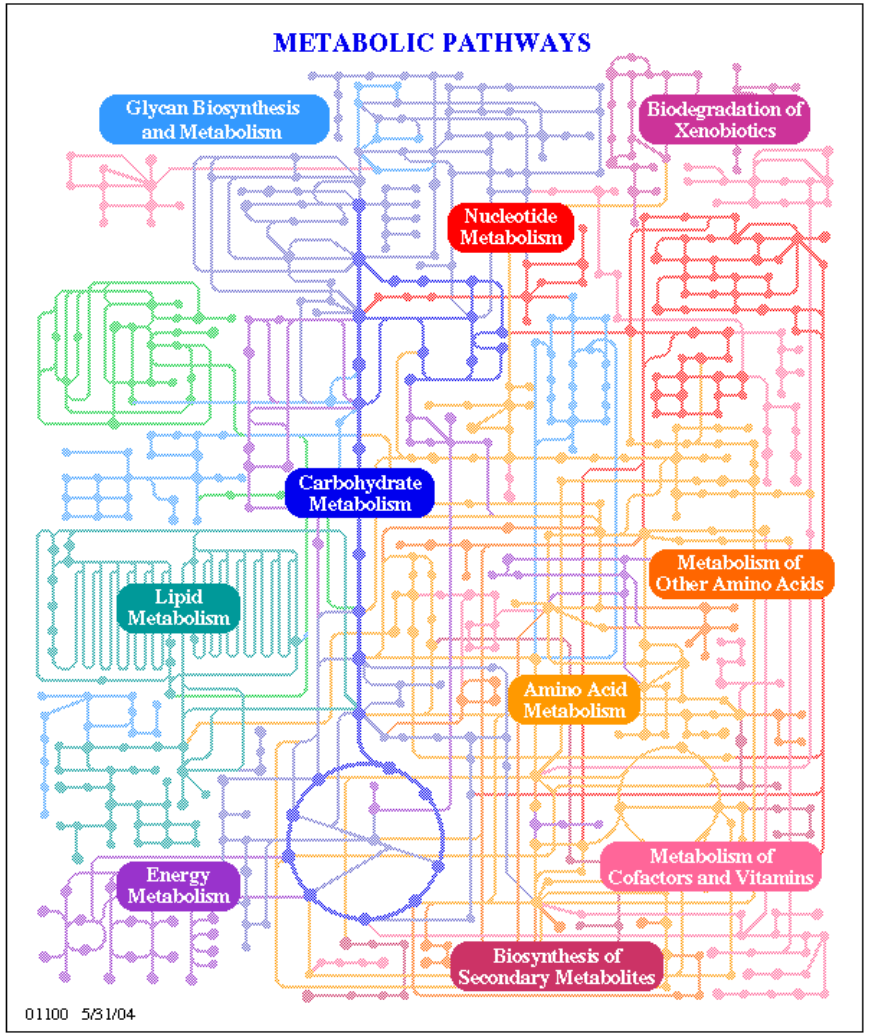
m/z, (Da)	Retention time, minutes	Metabolite identification	Peak intensity	Polarity
352.32	32.05	11Z-Eicosenoic acid	1.69E+10	+
198	20.84	Selenomethionine	6.2E+07	+
201	18.24	Poppy acid	1.7E+09	+
159.12	4.87	Betaine	1E+08	+
758.16	31.69	Theaflavin-3-gallate	4.99E+09	+
366.96	10.81	Se-Methylselenocysteine	3.78E+09	+
504	32.86	Quercetin 3,3'-bissulfate	1.22E+09	+
194.04	4.87	Shoyuflavone A	1.15E+09	+
720.12	31.69	Norbadione A	7.59E+08	+
438.72	20.87	Gliadorphin	4.65E+08	+
312.12	30.79	pinostrobin	4.02E+09	+
164.04	8.96	Fertaric acid	1.09E+08	+
339.24	30.93	Plastoquinone 3	2.45E+08	-
417.12	12.25	Liquiritin	1.3E+07	-
430.92	10.82	Nitroprusside	2.1E+09	-
743.04	32.40	Gluconapin	8.3E+07	-
538.92	12.11	Chymopapain	1.7E+07	-
179.52	36.15	Glucoputranjivin	1.7E+07	-
711.62	4.71	Conessine	1.1E+07	-
889.08	33.10	Baicalin	5E+06	-
133.08	1.56	3-Butenenitrile	1.5E+08	-

Amrutha, S., Abhinand, C.S., Upadhyay, S.S. *et al. Sci Rep* **15**, 8103 (2025).
https://doi.org/10.1038/s41598-025-92756-5

Four major omics fields, genomics, transcriptomics, proteomics and metabolomics



Metabolomics: The challenges of analytical



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- Diversity in structures and physical chemical properties
  - Require multiple technologies to capture a metabolome
- Many isomeric and isobaric species
  - Require high resolving power for correct ID
- Very low to very high concentrations
  - Require High sensitivity and wide dynamic range
- No single database to identify all unknown metabolites
  - Require extensive library or fragment ion prediction based on compound structure

Metabolomics: The challenges of analytical

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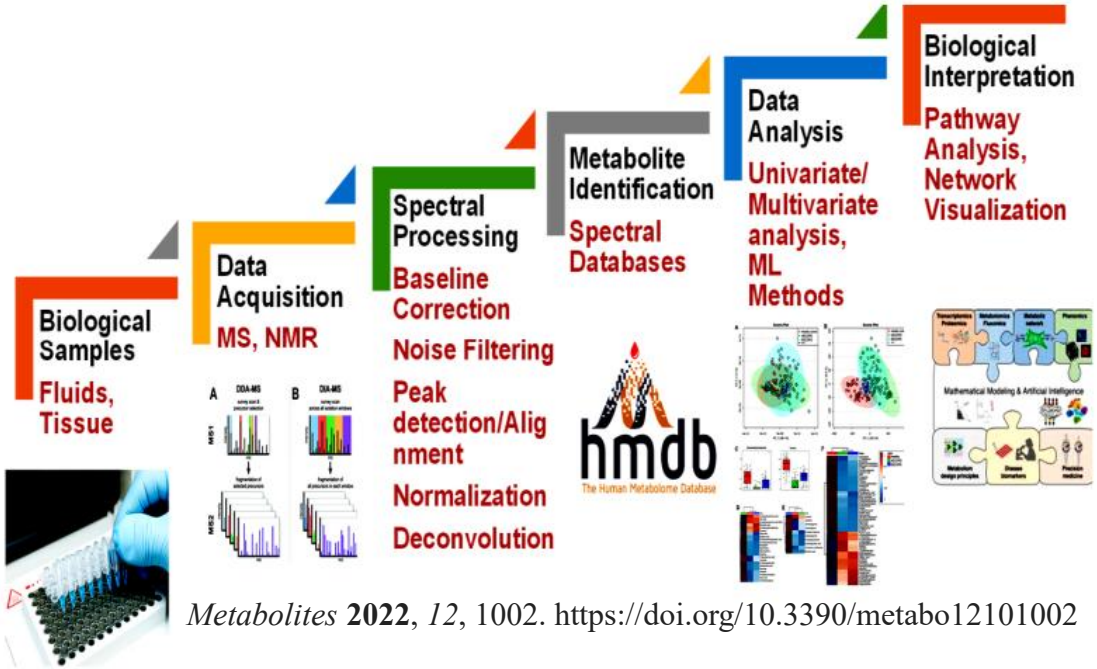
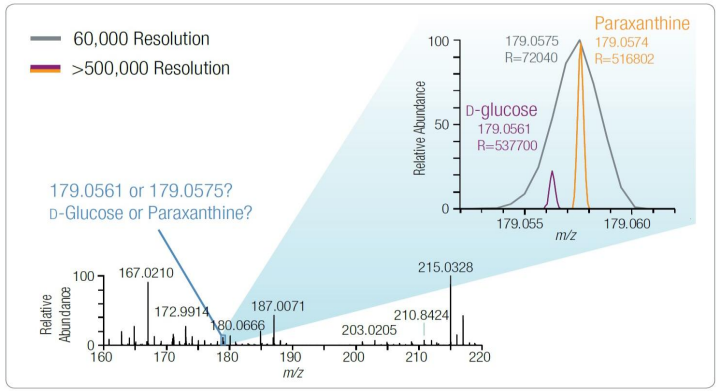
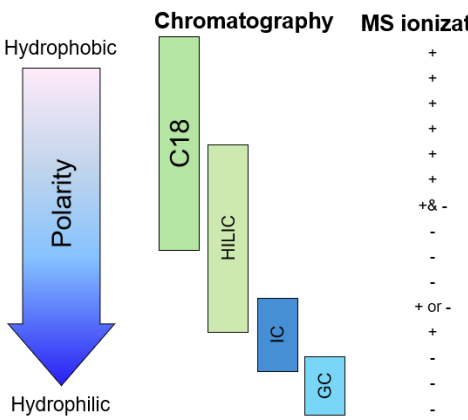


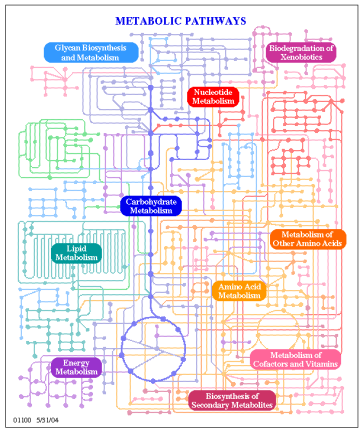
Metabolites **2022**, *12*, 1002. https://doi.org/10.3390/metabo12101002



Metabolites

- triglycerides
- cholesterol esters
- diacylglycerols
- sphingomyelines
- phosphatidylcholines
- phosphatidylethanolamines
- other phospholipids
- fatty acids
- eicosanoids & metabolites
- bile acids
- bilirubin
- amino acids, amines
- organic acids
- sugars
- Other polar:
- e.g. purines & pyrimidines





All the images shown in this frame are downloaded or parsed from KEGG

Database	Organisms	Database Descriptions	Coverage	Accessibility	Link	Y.O.R
Reactome Knowledgebase	Homo-sapiens	It contains visualization, interpretation, and analysis of pathway knowledge. Available tools: SkyPainter, PathFinder, BioMart, Reactome Gene Set Analysis (ReactomeGSA) and Reactome IDG Portal.	Human Pathways:2546 Reactions:13890 Proteins:1020 Small Molecules:1940 Drugs:507	Free	Reactome.org (accessed on 1 April 2022)	2005
BioCyc	Eukaryotes Bacteria and Archaea.	A comprehensive reference containing listed data from 130,000 publications—available tools: Pathologic, Genome browser, Pathway Tools, BLAST search, and SmartTables.	Pathway/Genome Databases (PGDBs): 19,494 Archaea: 465 databases Bacteria: 18,956 databases Eukaryota: 37 databases MetaCyc: Metabolic Encyclopedia	EcoCyc and MetaCyc databases: free access. Others: Paid subscription	Biocyc.org (accessed on 1 April 2022)	1997
MetaCyc	Eukaryotes Bacteria and Archaea.	Serves as a comprehensive reference to metabolic pathways and enzymes. Available tools: Pathologic, Genome browser, BLAST search, Pathways Tools, Google™.	Multi-organisms: 3295 Metabolic pathways:2937 Enzymatic reactions:17,310	Free	MetaCyc.org (accessed on 1 April 2022)	1999
EcoCyc	Bacterial organism: Escherichia coli K-12 MG1655	Contains Metabolic Network Explorer, Circular Genome Viewer	Genes:4518 Enzymes:1682 Metabolic reactions:2151	Free	EcoCyc.org (accessed on 1 April 2022)	1995

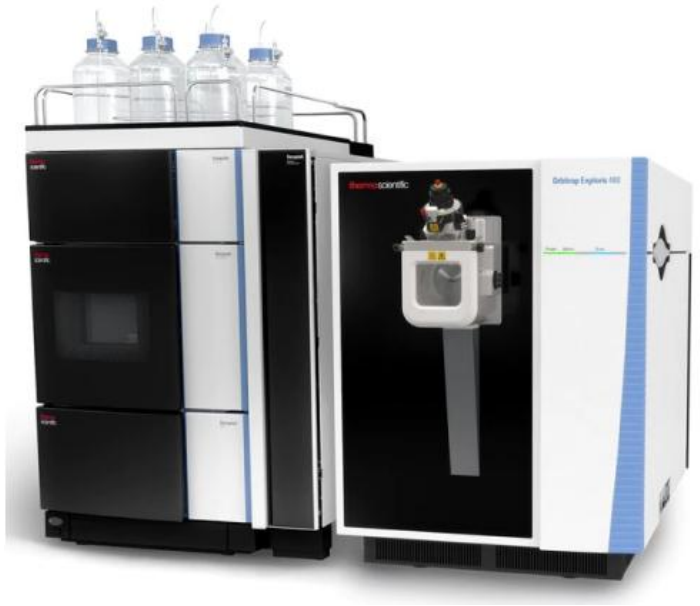
Database	Organisms	Database Descriptions	Coverage	Accessibility	Link	Y.O.R
HMDB	Homo-sapiens	A human metabolomics database. It has spectral and pathway visualization tools. Available tools: Data Extractor, ChemSketch, BLAST search, MetaboCard, MS and NMR spectral search utility, MetaboLIMS.	Annotated metabolite entries: 217,920	Free	https://hmdb.ca (accessed on 1 April 2022)	2007
ChemSpider	Eukaryotes Bacteria and Archaea	A chemical structure database.	Chemical entities:114 Million	Free	chemspider.com (accessed on 1 April 2022)	2007
MetaboLights	Eukaryotes Bacteria and Archaea	An open-access database repository for cross-platform and cross-species metabolomics research.	Different organisms: 6510 Reference compounds:27,475 Metabolite annotation features:2016,457	Free	https://www.ebi.ac.uk/metabolights (accessed on 1 April 2022)	2012
Metabolomics Workbench	Eukaryotes Bacteria and Archaea	A repository for metabolomics data and metadata and provides analysis tools and access to metabolite standards, protocols, tutorials, training, and more.	Discrete structures:136,000 Genes:7300 Proteins:15,500	Free	metabolomicsworkbench.org (accessed on 1 April 2022)	2016
SMPDB	Eukaryotes Bacteria and Archaea	A pathway database for different model organisms such as humans, mice, E. coli, yeast, and Arabidopsis thaliana.	Pathways Number: 48,690 Metabolites Number (non-redundant): 55,700	Free	https://smpdb.ca/ (accessed on 1 April 2022)	2009
MetSigDis	Homo-sapiens, Rat, Mouse, Drosophila melanogaster, Triatomine, Mice, Pig, and Mus musculus.	A manually curated resource that aims to provide a comprehensive resource of metabolite alterations in various disease.	Curated relationships:6849 Metabolites:2420 Diseases:129 Species: 8	Free	http://www.bio-annotation.cn/MetSigDis/ (accessed on 1 April 2022)	2017

Database	Organisms	Database Descriptions	Coverage	Accessibility	Link	Y.O.R
BIGG Models	Eukaryotes, Prokaryotes, and Photosynthetic Eukaryotes.	Provides pathway visualization with Escher. It also offers standardized identifiers for metabolites, reactions, and genes.	It contains more than 75 high-quality manually-curated genome-scale metabolic models.	Free	BIGG.ucsd.edu (accessed on 1 April 2022)	2007
KEGG	Eukaryotes Bacteria and Archaea.	PATHWAY database, KEGG NETWORK database, KO annotation and taxonomy, drug information, and virus-cell interaction. Available tools: KEGG Atlas, KegHier, KegArray, KegDraw, KegTools, KEGG2, KEGG API.	KEGG organisms: 7760 (Eukaryotes: 695, Bacteria:6694, Archaea:371). KEGG modules: 456 Reaction modules:46	Free	www.kegg.jp/ (accessed on 1 April 2022)	1995
BRENDA	Eukaryotes Bacteria and Archaea.	Comprises disease-related data, protein sequences, 3D structures, genome annotations, ligand information, taxonomic, bibliographic, and kinetic data.	Number of different enzymes: 8197	Free	www.brenda-enzymes.org (accessed on 1 April 2022)	1987
PubChem	Eukaryotes Bacteria and Archaea	Provides chemical and physical properties, biological activities, safety and toxicity information, patents, literature citations, and more. Available tools: PubChem Structure Editor, Entrez, PubChem3D, PubChem Download Facility, ToxNet.	Compounds:110 million, Substances:277 million, Bioactivities:293 million.	Free	PubChem.ncbi.nlm.nih.gov (accessed on 1 April 2022)	2004
ChEBI	Eukaryotes Bacteria and Archaea	A database and ontology containing information about chemical entities of biological interest.	Annotated compounds: 59,708	Free	www.ebi.ac.uk/chebi (accessed on 1 April 2022)	2010

Database	Organisms	Database Descriptions	Coverage	Accessibility	Link	Y.O.R
Virtual Metabolic Human	Homo-sapiens	Captures human and gut microbial metabolism information and links it to hundreds of diseases and nutritional data.	Reactions:19,313 Metabolites:5607 Human genes:3695 Diseases:255 Foodstuff:8790	Free	www.vmh.life (accessed on 1 April 2022)	2018
Pathway Commons	Eukaryotes Bacteria and Archaea	Aims to collect and disseminate biological pathway and interaction data	Pathways:5772 Interactions:2,424,055 Databases:22	Free	https://www.pathwaycommons.org (accessed on 1 April 2022)	
WikiPathways	Eukaryotes Bacteria and Archaea	A public, collaborative platform devoted to the curation of biological pathways	Human genes: 11,532 Number of pathways: 3013	Free	wikipathways.org (accessed on 1 April 2022)	2008
RaMP	Eukaryotes Bacteria and Archaea	A multi-database integration approach for gene/metabolite enrichment analysis providing interactive tables of query results, interactive tables of pathway analysis results, and clustering of enriched pathways by pathway similarity	Pathways: 51,526 (from KEGG, Reactome, SMPDB, and WikiPathways) Genes: 23,077 Metabolites: 113,725	Free	https://github.com/mathelab/RaMP-DB/or https://github.com/mathelab/RaMP-DB/inst/extdata/ (accessed on 1 April 2022)	
MENDA	Organisms include: Human, Rat, Mouse, and Non-human primates.	A comprehensive metabolic characterization database for depression.	Differential expressed metabolites: 5675. (Humans:1347 Rat:3127 Mouse:1105 Non-human primates:96)	Free	Menda.cpmu.edu.cn:8080/index.php (accessed on 1 April 2022)	2020

What is Mass Spectrometry?

The basis in mass spectrometry (MS) is the production of **ions**, that are subsequently separated or filtered according to their **mass-to-charge (m/z) ratio** and detected.



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Separation : Mass detector

Chromatography

UHPLC-nano flow

UHPLC-micro flow

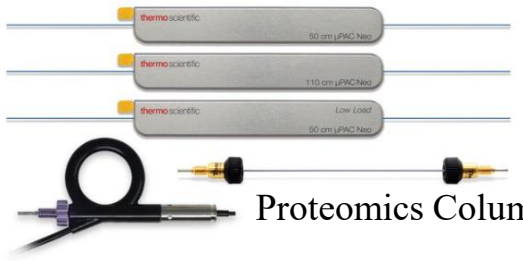
GC

MS/MS

Quadrupole-TOF

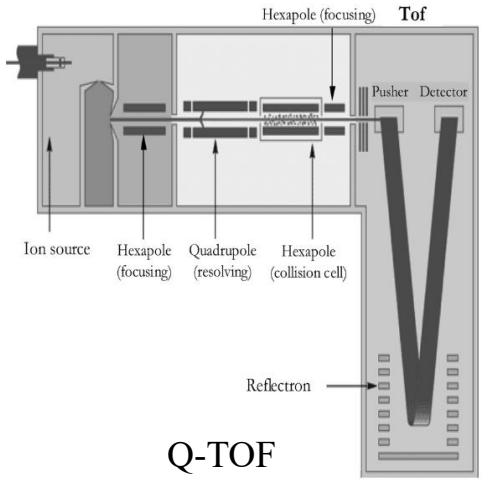
Quadrupole-Orbitrap

Tribrid

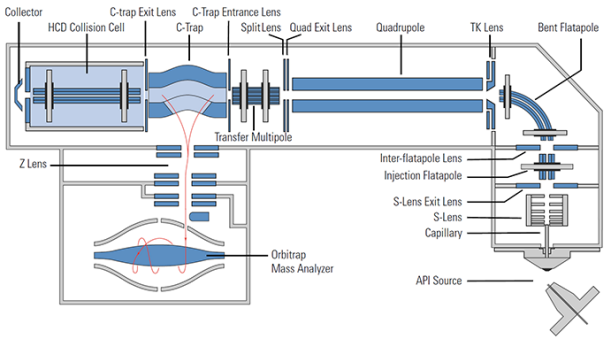


Proteomics Column

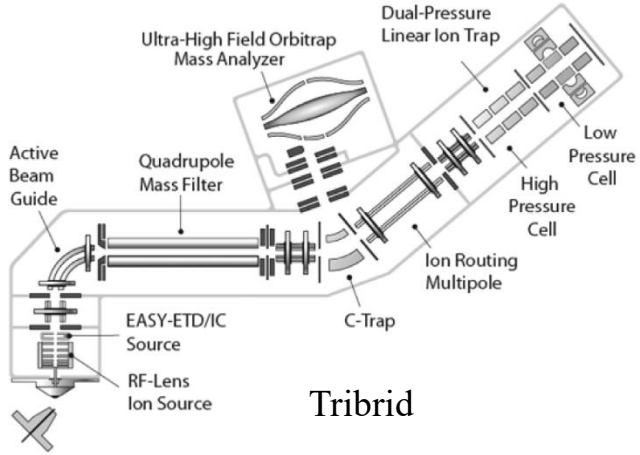
Metabolomics Column



Q-TOF

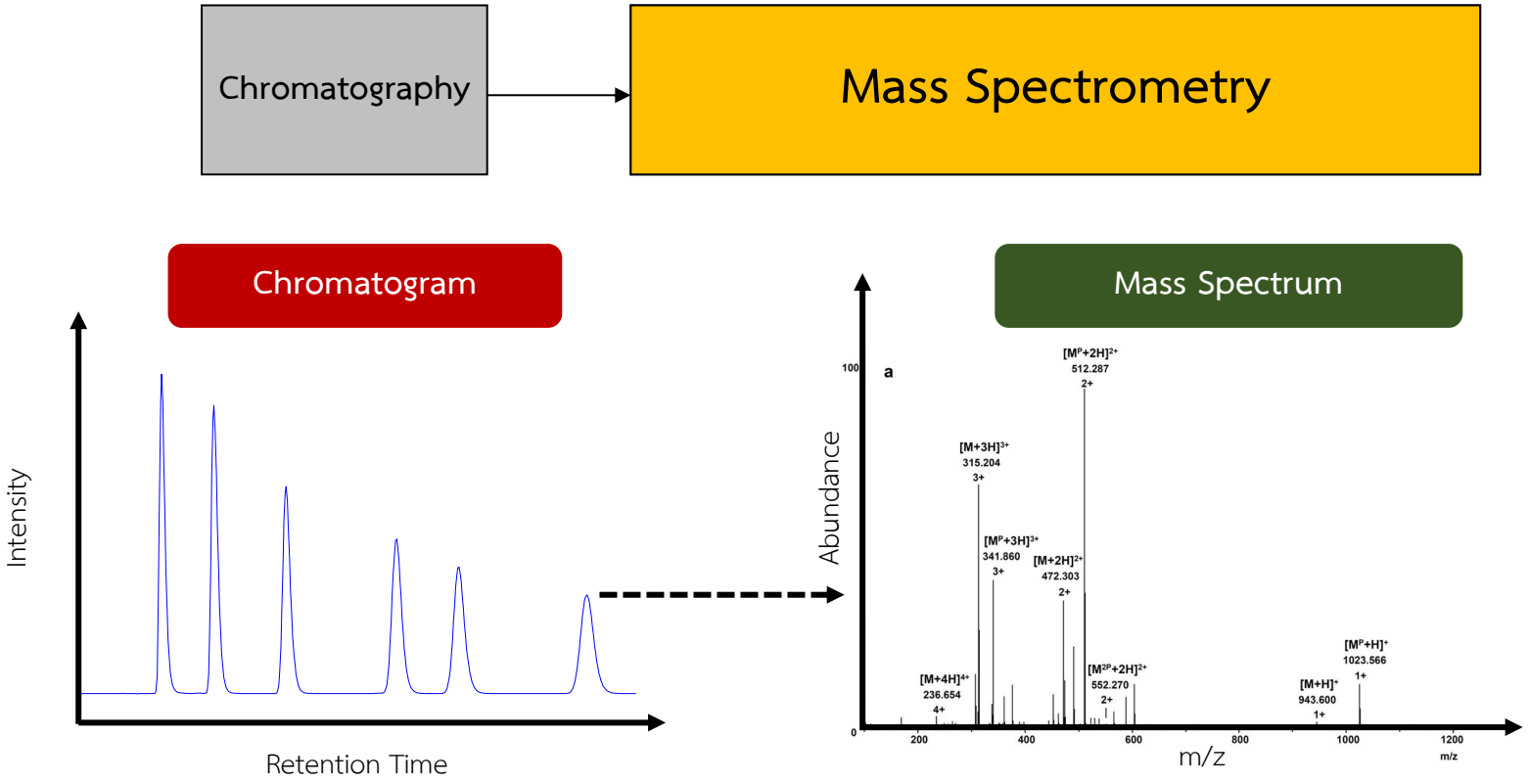


Q-Orbitrap

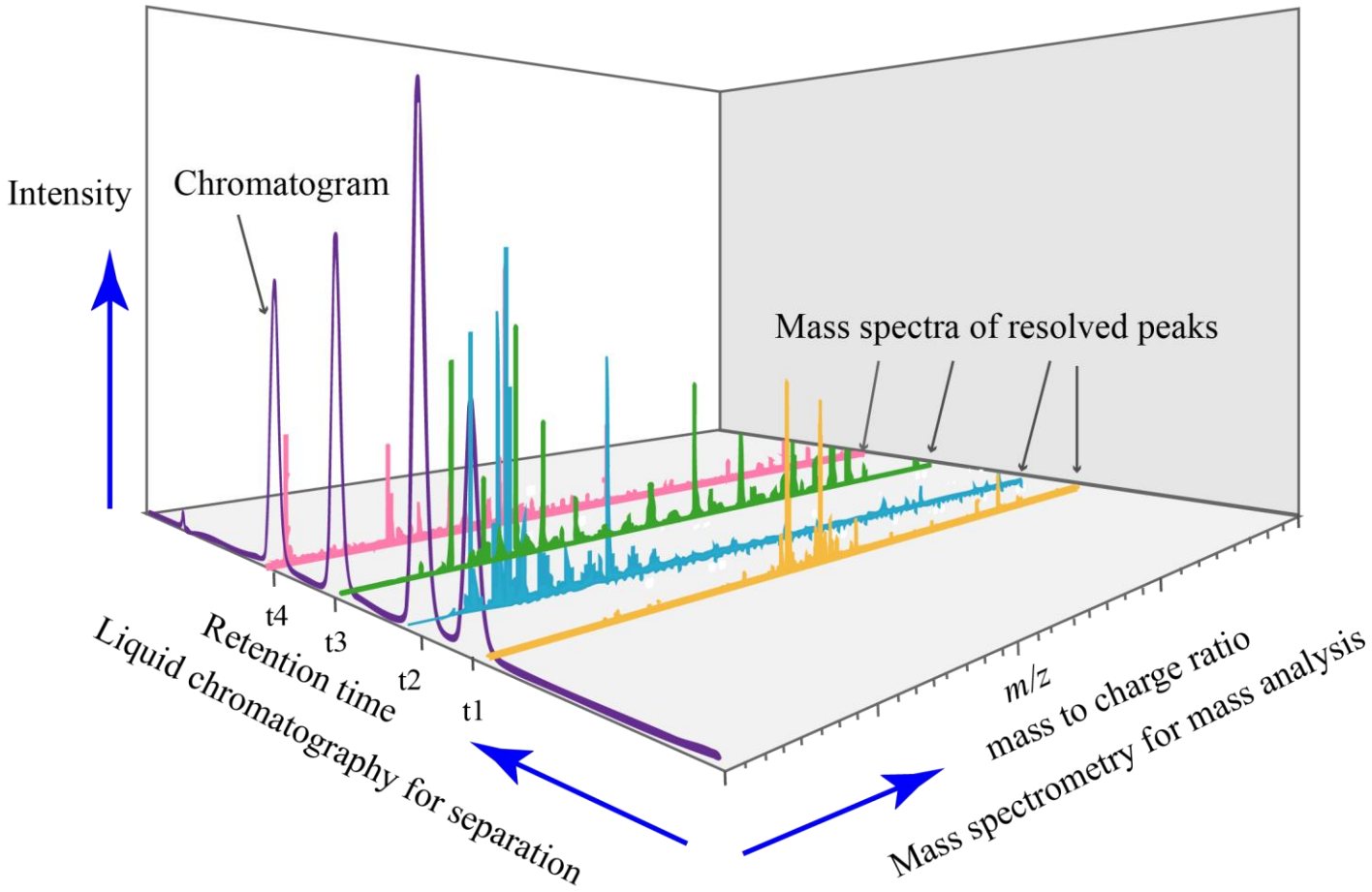


Tribrid

LCMS-Diagram



Data from LCMS



Mass spectra-m/z

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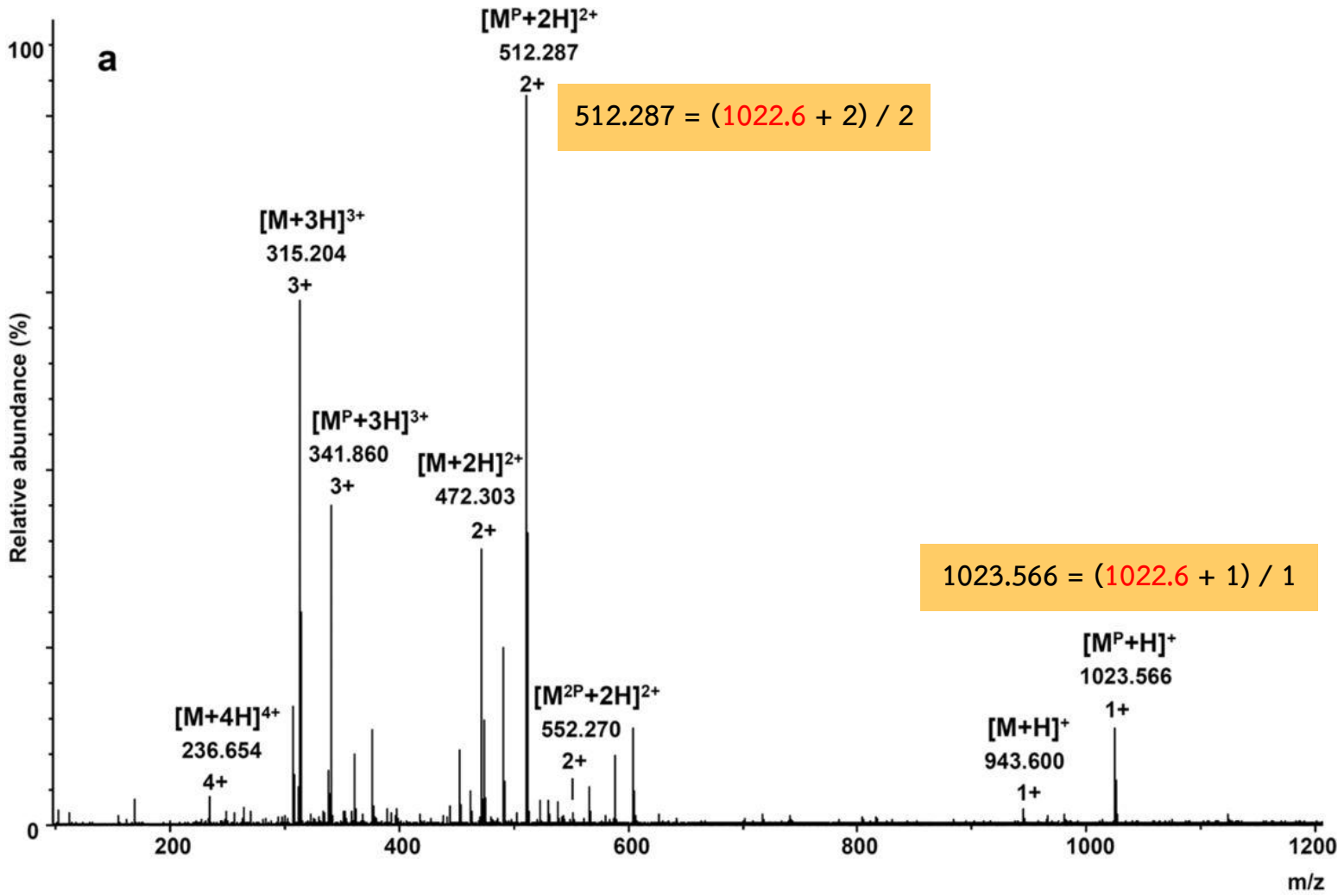
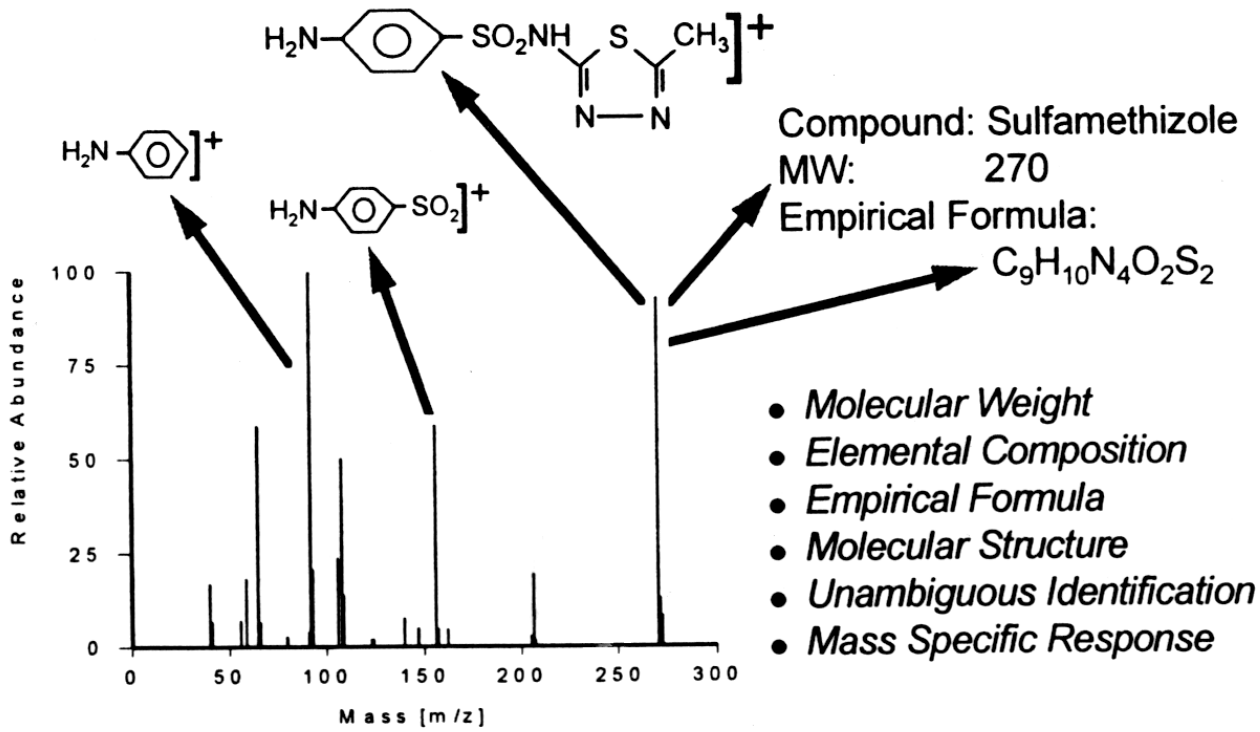
$$m/z = (\text{molecular weight} + \text{charge}) / \text{charge}$$

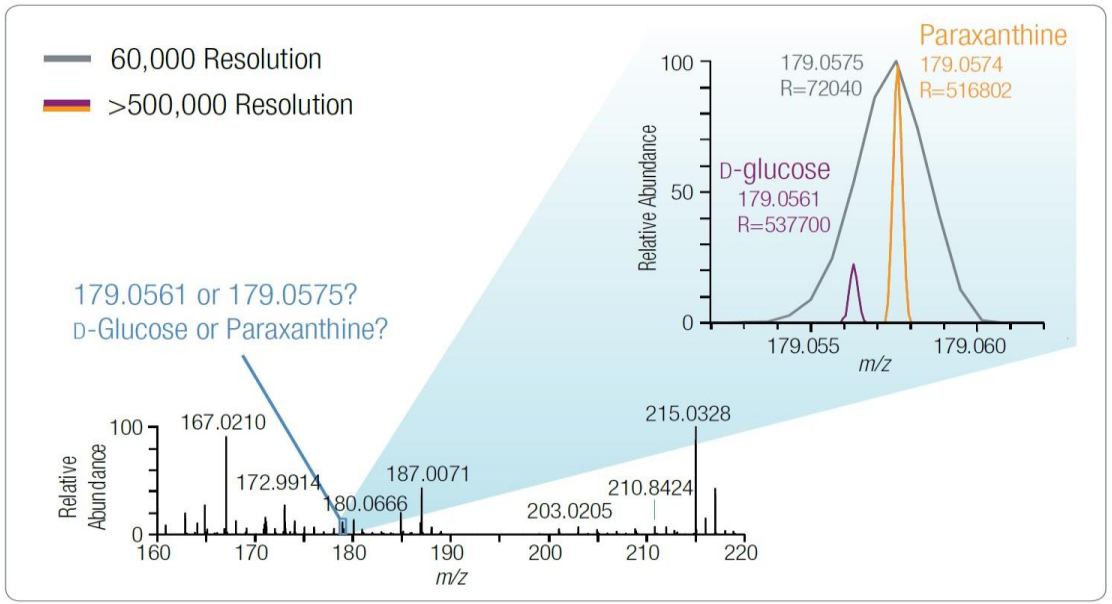


512.287 = (1022.6 + 2) / 2

1023.566 = (1022.6 + 1) / 1

MS/MS data


Relative Abundance
Mass [m/z]
Compound: Sulfamethizole
MW: 270
Empirical Formula:
$C_9H_{10}N_4O_2S_2$
Molecular Weight
Elemental Composition
Empirical Formula
Molecular Structure
Unambiguous Identification
Mass Specific Response


60,000 Resolution
>500,000 Resolution
179.0561 or 179.0575?
D-Glucose or Paraxanthine?
D-glucose
179.0561
R=537700
179.0575
R=72040
Paraxanthine
179.0574
R=516802
Relative Abundance
m/z
167.0210
172.9914
180.0666
187.0071
203.0205
210.8424
215.0328

Metabolomics database

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Database	Organisms	Database Descriptions	Coverage	Accessibility	Link	Y.O.R
Reactome Knowledgebase	Homo-sapiens	It contains visualization, interpretation, and analysis of pathway knowledge. Available tools: SkyPainter, PathFinder, BioMart, Reactome Gene Set Analysis (ReactomeGSA) and Reactome IDG Portal.	Human Pathways:2546 Reactions:13890 Proteins:1020 Small Molecules:1940 Drugs:507	Free	Reactome.org (accessed on 1 April 2022)	2005
BioCyc	Eukaryotes Bacteria and Archaea.	A comprehensive reference containing listed data from 130,000 publications—available tools: Pathologic, Genome browser, Pathway Tools, BLAST search, and SmartTables.	Pathway/Genome Databases (PGDBs): 19,494 Archaea: 465 databases Bacteria: 18,956 databases Eukaryota: 37 databases MetaCyc: Metabolic Encyclopedia	EcoCyc and MetaCyc databases: free access. Others: Paid subscription	Biocyc.org (accessed on 1 April 2022)	1997
MetaCyc	Eukaryotes Bacteria and Archaea.	Serves as a comprehensive reference to metabolic pathways and enzymes. Available tools: Pathologic, Genome browser, BLAST search, Pathways Tools, Google™.	Multi-organisms: 3295 Metabolic pathways:2937 Enzymatic reactions:17,310	Free	MetaCyc.org (accessed on 1 April 2022)	1999
EcoCyc	Bacterial organism: Escherichia coli K-12 MG1655	Contains Metabolic Network Explorer, Circular Genome Viewer	Genes:4518 Enzymes:1682 Metabolic reactions:2151	Free	EcoCyc.org (accessed on 1 April 2022)	1995

Database	Organisms	Database Descriptions	Coverage	Accessibility	Link	Y.O.R
HMDB	Homo-sapiens	A human metabolomics database. It has spectral and pathway visualization tools. Available tools: Data Extractor, ChemSketch, BLAST search, MetaboCard, MS and NMR spectral search utility, MetaboLIMS.	Annotated metabolite entries: 217,920	Free	https://hmdb.ca (accessed on 1 April 2022)	2007
ChemSpider	Eukaryotes Bacteria and Archaea	A chemical structure database.	Chemical entities:114 Million	Free	chemspider.com (accessed on 1 April 2022)	2007
MetaboLights	Eukaryotes Bacteria and Archaea	An open-access database repository for cross-platform and cross-species metabolomics research.	Different organisms: 6510 Reference compounds:27,475 Metabolite annotation features:2016,457	Free	https://www.ebi.ac.uk/metabolights (accessed on 1 April 2022)	2012
Metabolomics Workbench	Eukaryotes Bacteria and Archaea	A repository for metabolomics data and metadata and provides analysis tools and access to metabolite standards, protocols, tutorials, training, and more.	Discrete structures:136,000 Genes:7300 Proteins:15,500	Free	metabolomicsworkbench.org (accessed on 1 April 2022)	2016
SMPDB	Eukaryotes Bacteria and Archaea	A pathway database for different model organisms such as humans, mice, E. coli, yeast, and Arabidopsis thaliana.	Pathways Number: 48,690 Metabolites Number (non-redundant): 55,700	Free	https://smpdb.ca/ (accessed on 1 April 2022)	2009
MetSigDis	Homo-sapiens, Rat, Mouse, Drosophila melanogaster, Triatomine, Mice, Pig, and Mus musculus.	A manually curated resource that aims to provide a comprehensive resource of metabolite alterations in various disease.	Curated relationships:6849 Metabolites:2420 Diseases:129 Species: 8	Free	http://www.bio-annotation.cn/MetSigDis/ (accessed on 1 April 2022)	2017

Database	Organisms	Database Descriptions	Coverage	Accessibility	Link	Y.O.R
BIGG Models	Eukaryotes, Prokaryotes, and Photosynthetic Eukaryotes.	Provides pathway visualization with Escher. It also offers standardized identifiers for metabolites, reactions, and genes.	It contains more than 75 high-quality manually-curated genome-scale metabolic models.	Free	BIGG.ucsd.edu (accessed on 1 April 2022)	2007
KEGG	Eukaryotes Bacteria and Archaea.	PATHWAY database, KEGG NETWORK database, KO annotation and taxonomy, drug information, and virus-cell interaction. Available tools: KEGG Atlas, KegHier, KegArray, KegDraw, KegTools, KEGG2, KEGG API.	KEGG organisms: 7760 (Eukaryotes: 695, Bacteria:6694, Archaea:371). KEGG modules: 456 Reaction modules:46	Free	www.kegg.jp/ (accessed on 1 April 2022)	1995
BRENDA	Eukaryotes Bacteria and Archaea.	Comprises disease-related data, protein sequences, 3D structures, genome annotations, ligand information, taxonomic, bibliographic, and kinetic data.	Number of different enzymes: 8197	Free	www.brenda-enzymes.org (accessed on 1 April 2022)	1987
PubChem	Eukaryotes Bacteria and Archaea	Provides chemical and physical properties, biological activities, safety and toxicity information, patents, literature citations, and more. Available tools: PubChem Structure Editor, Entrez, PubChem3D, PubChem Download Facility, ToxNet.	Compounds:110 million, Substances:277 million, Bioactivities:293 million.	Free	PubChem.ncbi.nlm.nih.gov (accessed on 1 April 2022)	2004
ChEBI	Eukaryotes Bacteria and Archaea	A database and ontology containing information about chemical entities of biological interest.	Annotated compounds: 59,708	Free	www.ebi.ac.uk/chebi (accessed on 1 April 2022)	2010

Database	Organisms	Database Descriptions	Coverage	Accessibility	Link	Y.O.R
Virtual Metabolic Human	Homo-sapiens	Captures human and gut microbial metabolism information and links it to hundreds of diseases and nutritional data.	Reactions:19,313 Metabolites:5607 Human genes:3695 Diseases:255 Foodstuff:8790	Free	www.vmh.life (accessed on 1 April 2022)	2018
Pathway Commons	Eukaryotes Bacteria and Archaea	Aims to collect and disseminate biological pathway and interaction data	Pathways:5772 Interactions:2,424,055 Databases:22	Free	https://www.pathwaycommons.org (accessed on 1 April 2022)	
WikiPathways	Eukaryotes Bacteria and Archaea	A public, collaborative platform devoted to the curation of biological pathways	Human genes: 11,532 Number of pathways: 3013	Free	wikipathways.org (accessed on 1 April 2022)	2008
RaMP	Eukaryotes Bacteria and Archaea	A multi-database integration approach for gene/metabolite enrichment analysis providing interactive tables of query results, interactive tables of pathway analysis results, and clustering of enriched pathways by pathway similarity	Pathways: 51,526 (from KEGG, Reactome, SMPDB, and WikiPathways) Genes: 23,077 Metabolites: 113,725	Free	https://github.com/mathelab/RaMP-DB/or https://github.com/mathelab/RaMP-DB/inst/extdata/ (accessed on 1 April 2022)	
MENDA	Organisms include: Human, Rat, Mouse, and Non-human primates.	A comprehensive metabolic characterization database for depression.	Differential expressed metabolites: 5675. (Humans:1347 Rat:3127 Mouse:1105 Non-human primates:96)	Free	Menda.cqmu.edu.cn:8080/index.php (accessed on 1 April 2022)	2020

npatlas

PMDB
Plant Metabolite DataBase

Plant Metabolite PM hub

compound databases commonly used for compound identification.

Database	Targets	Description
PubChem [32]	All small molecules	Small molecules, metadata
ChemSpider [33]	All small molecules	Small molecules, curated data
KEGG [34]	Metabolites	Pathway database, multiple species
MetaCyc [35]	Metabolites	Pathway database, multiple species
BRENDA [36]	Enzymes	Enzyme and metabolism data
HMDB [37]	Metabolites	Human metabolites
CHEBI [38]	Small molecules	Molecules of biological interest
UNPD [39]	Metabolites	Secondary plant metabolites
MINE [40]	Metabolites	In silico predicted metabolites

PubChem, ChemSpider or the Chemical Abstracts Database is larger than 120 million compounds.
The number of compounds with biological relevance is estimated at 1–2 million

Metabolites 2018, 8(2), 31; https://doi.org/10.3390/metabo8020031

mass spectral databases commonly used for compound annotations

Database	Targets	Description
NIST	EI-MS, CID-MS/MS	Curated DB, graphical interface
WILEY	EI-MS, CID-MS/MS	Largest collection of EI-MS data
METLIN [51]	CID-MS/MS	Developed for QTOF instruments
MoNA	EI, MS/MS, MSn	Autocurated collection of spectra
MassBank [52]	EI, MS/MS, MSn	Longest standing community database
mzCloud [53]	MSn	Multiple stage MSn
GNPS [54]	MS/MS	Community database
ReSpect [55]	MS/MS, RT	Plant metabolomics database

Metabolomics for plant metabolite identification

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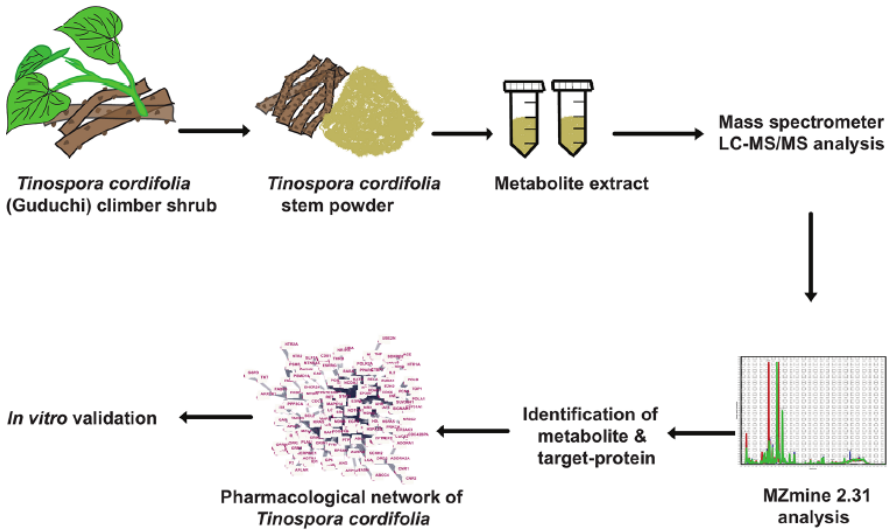
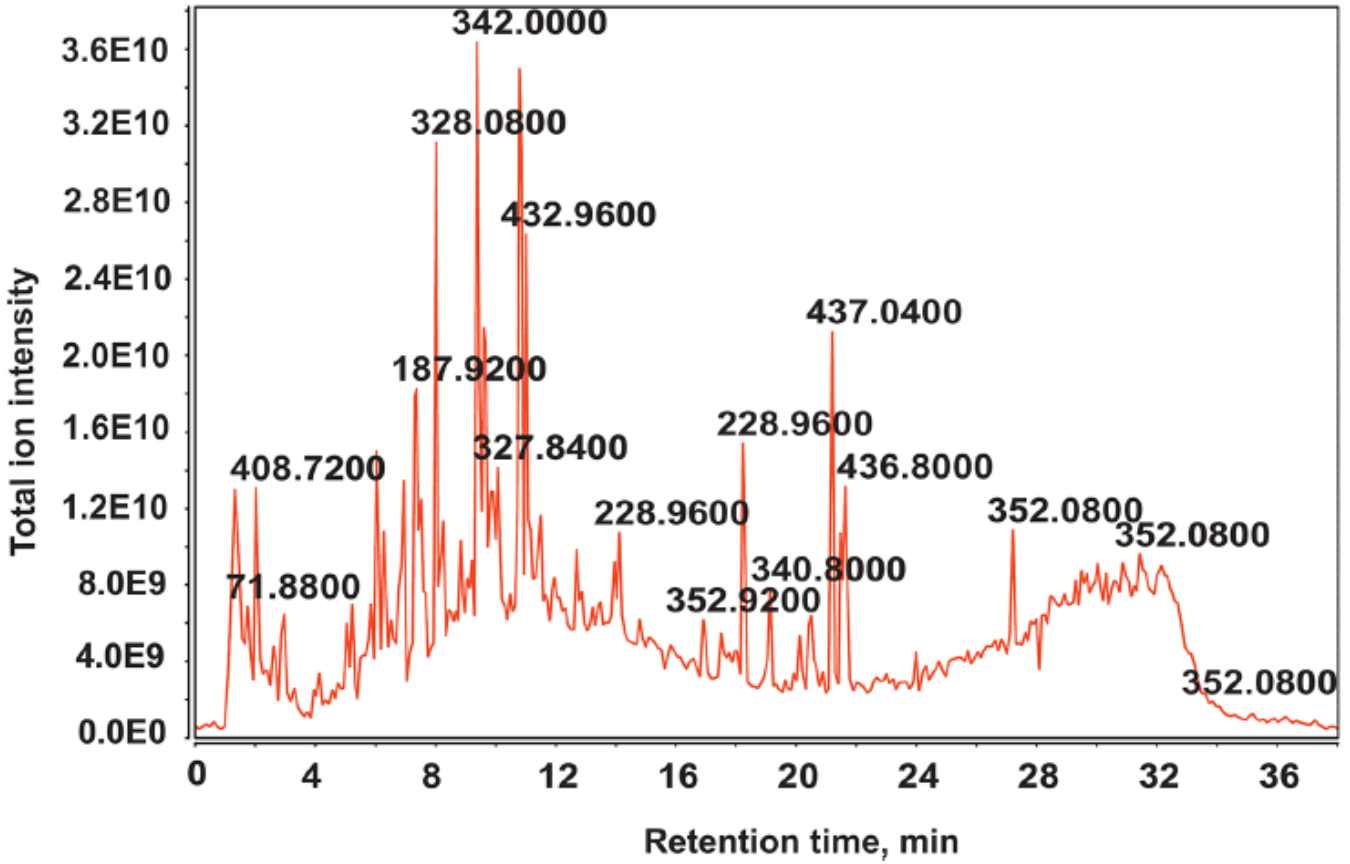
scientific reports

OPEN

Network pharmacology and metabolomics analysis of *Tinospora cordifolia* reveals BACE1 and MAOB as potential therapeutic targets for neuroprotection in Alzheimer's disease



Workflow of metabolite extraction from T. *cordifolia* stem poder, LC-MS/MS followed by MZmine tool and subsequent bioinformatics analysis and *in vitro* validation of neuroprotective activity



Representative of total ion chromatogram of T. *cordifolia* metabolite analysis in positive mode

Amrutha, S., Abhinand, C.S., Upadhyay, S.S. *et al. Sci Rep* **15**, 8103 (2025).
https://doi.org/10.1038/s41598-025-92756-5

Network Pharmacology: Protein targets of *T. cordifolia* metabolites

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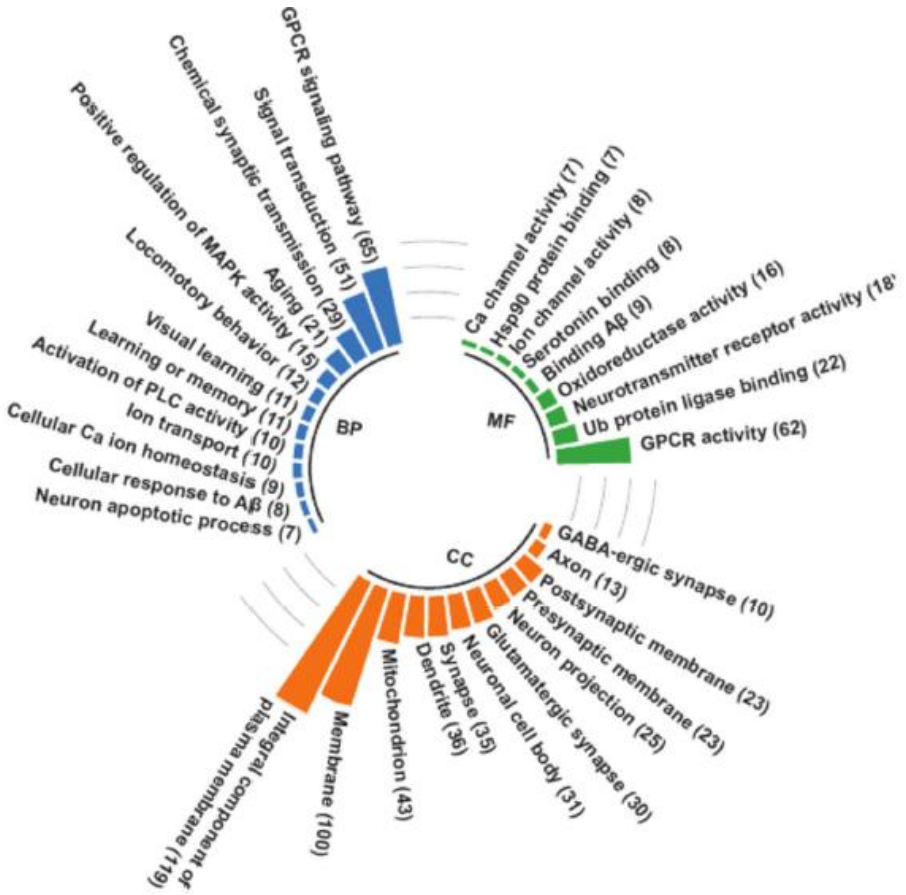


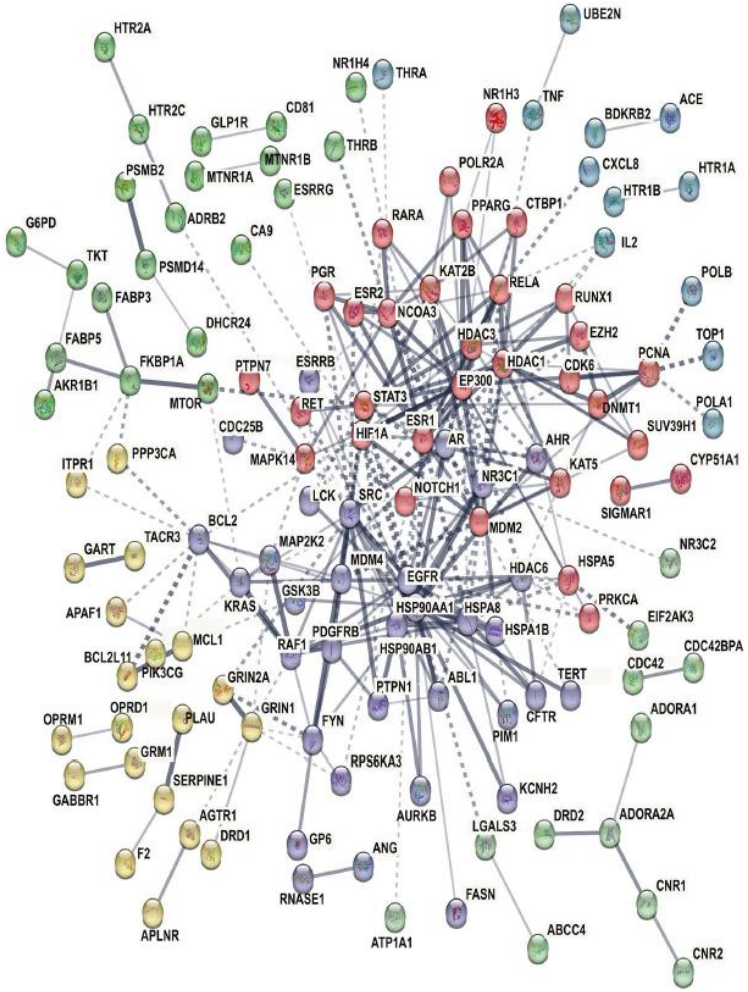
1546 protein interactions

- **346 proteins: exact structural matches**
- **1200 proteins: similarity matches**

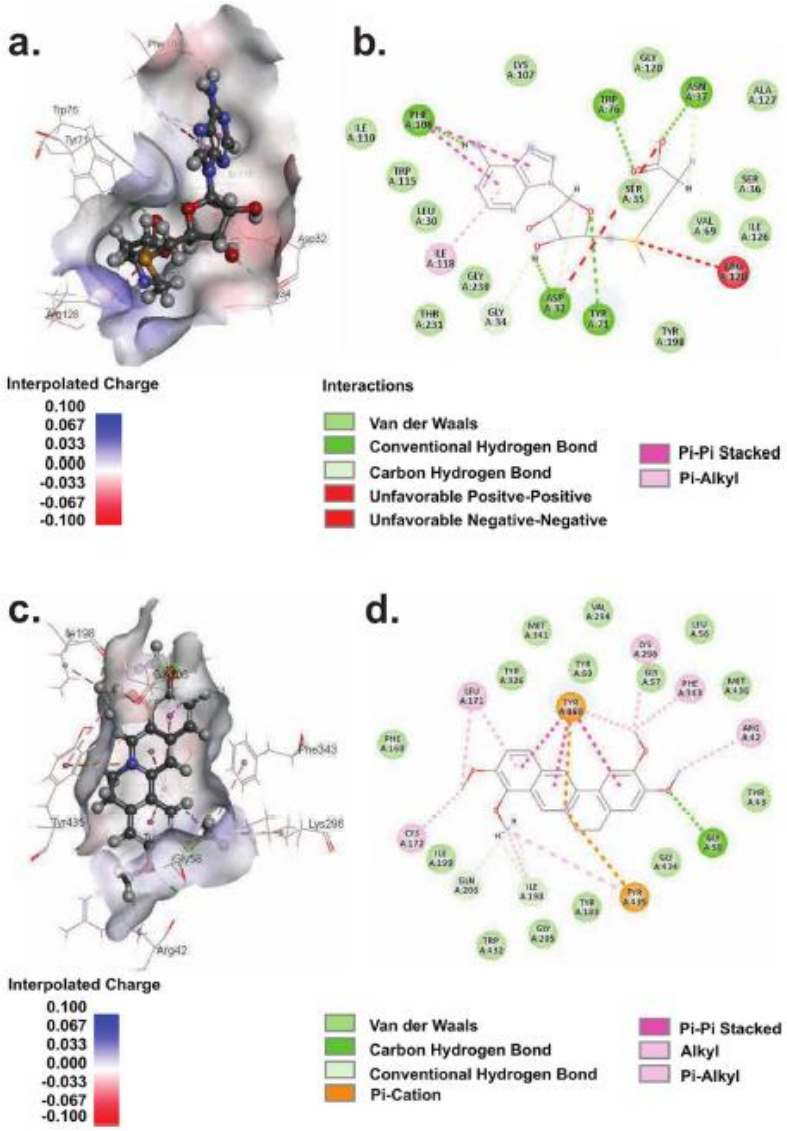
Human protein classification based on molecular function, biological process and cellular localization

Amrutha, S., Abhinand, C.S., Upadhyay, S.S. *et al. Sci Rep* **15**, 8103 (2025).
https://doi.org/10.1038/s41598-025-92756-5

Network Pharmacology: Protein targets of *T. cordifolia* metabolites



Protein-protein interacting network of protein targets of T. *cordifolia*

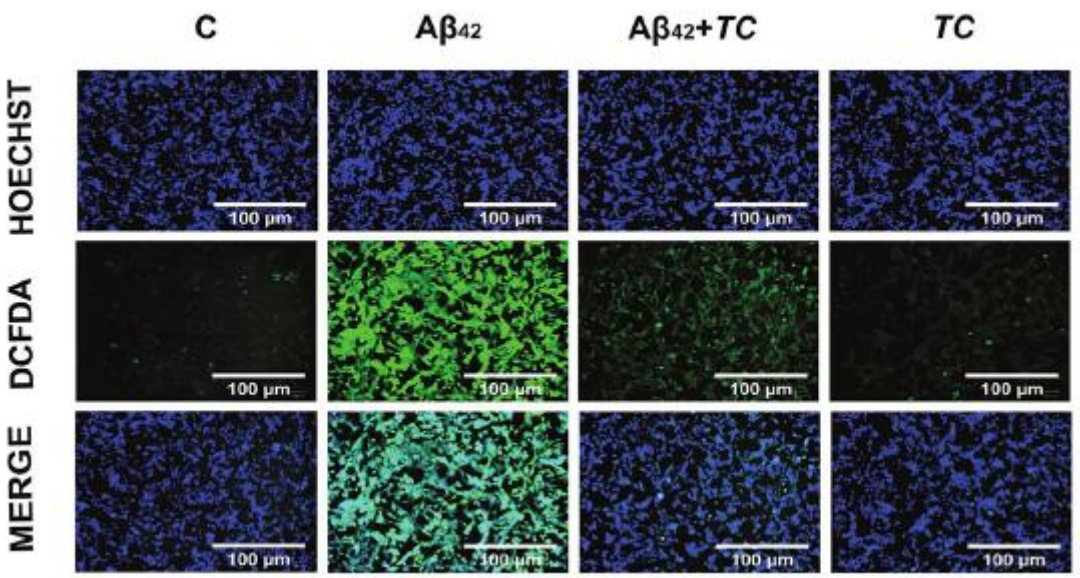


a-b.
S-adenosyl-L-methionine against BACE1

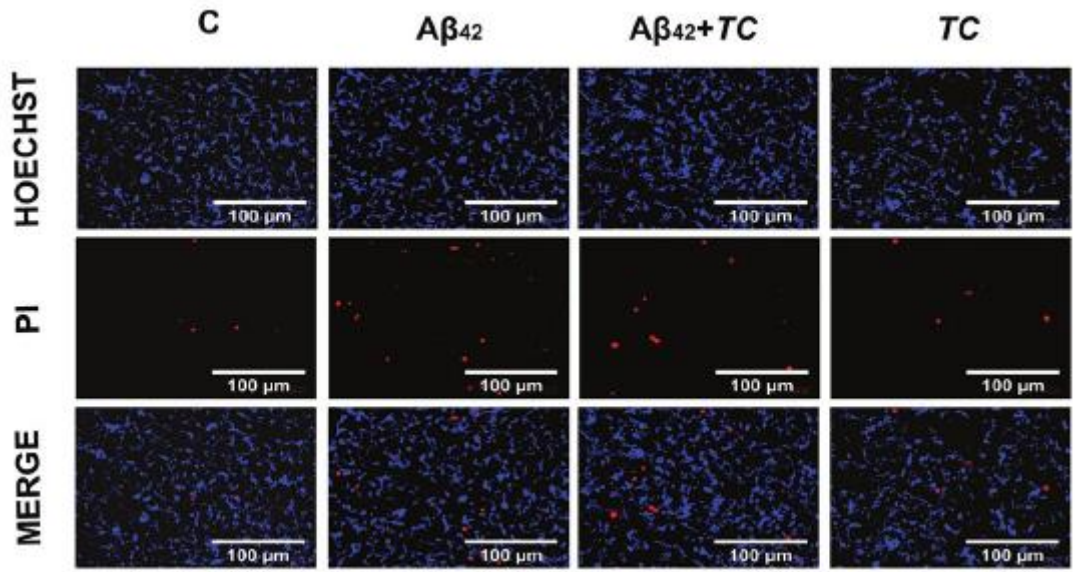
c-d.
Palmatine against MAO-B

Amrutha, S., Abhinand, C.S., Upadhyay, S.S. *et al. Sci Rep* **15**, 8103 (2025).
https://doi.org/10.1038/s41598-025-92756-5

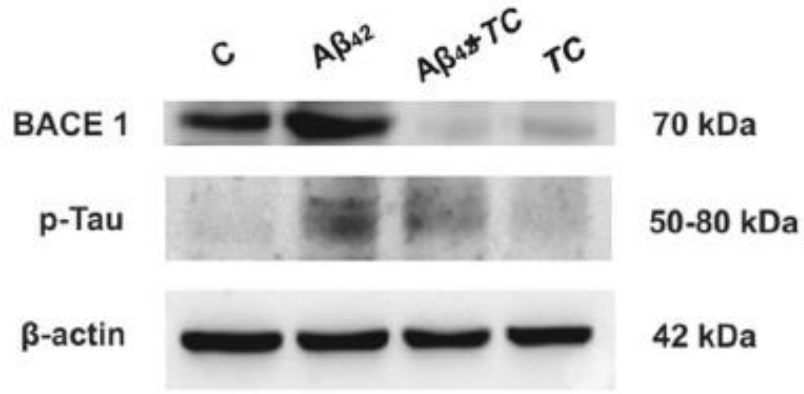
In vitro validation



ROS production



Cell death assay



Western blot analysis

Amrutha, S., Abhinand, C.S., Upadhyay, S.S. *et al. Sci Rep* **15**, 8103 (2025).
https://doi.org/10.1038/s41598-025-92756-5

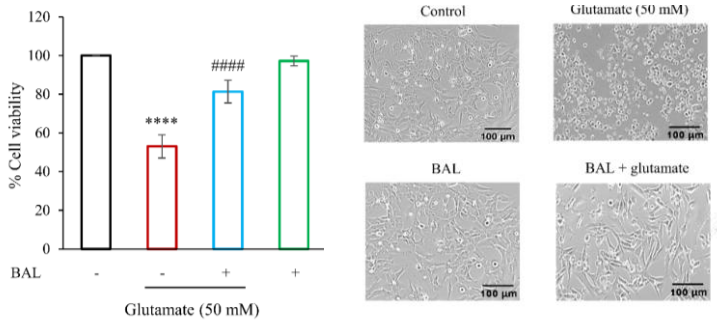
Metabolomics: Bioavailable (BAL) fraction of *Albizia lebbeck* (L.) Benth.

Mahidol University
Faculty of Pharmacy

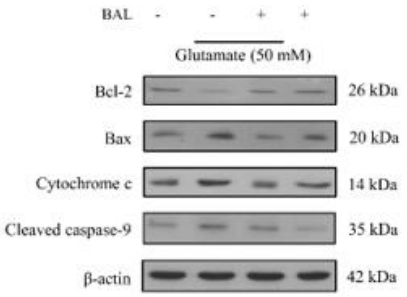
มหาวิทยาลัยมหิดล
สถาบันโภชนาการ

รศ.ดร.มลฤดี สุขประสานทรัพย์
หน่วยพิษวิทยาทางอาหาร
สถาบันโภชนาการ
มหาวิทยาลัยมหิดล

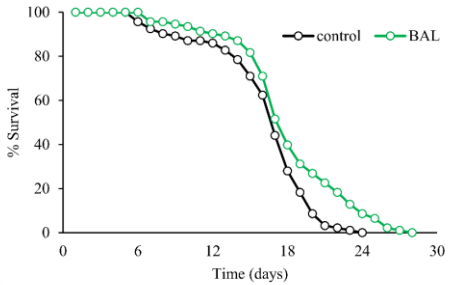
International Journal of Food Science and Technology
Bioavailable fraction from the edible leaf of *Albizia lebbeck* (L.) Benth. inhibits neurotoxicity in human microglial HMC3 cells and promotes lifespan in *Caenorhabditis elegans*



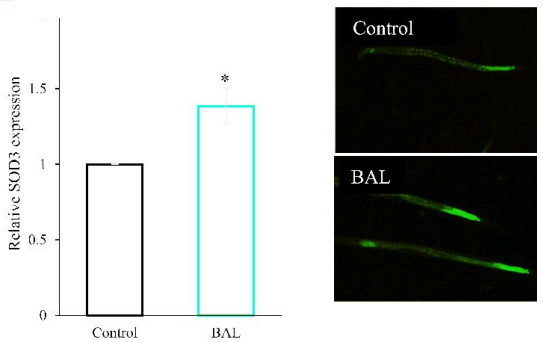
Protective effect of BAL on glutamate-induced toxicity in HMC3 cells



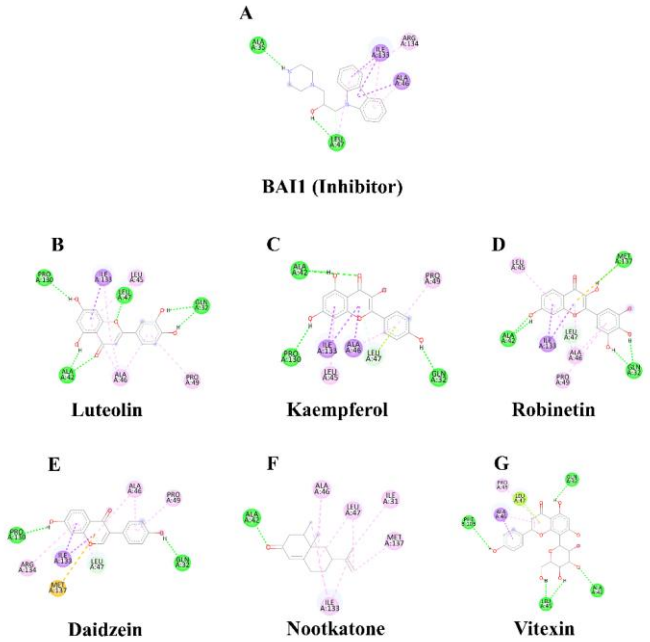
Effect of BAL on glutamate-induced apoptotic signaling activation in HMC3 cells



Effect of BAL on longevity of *C. elegans*



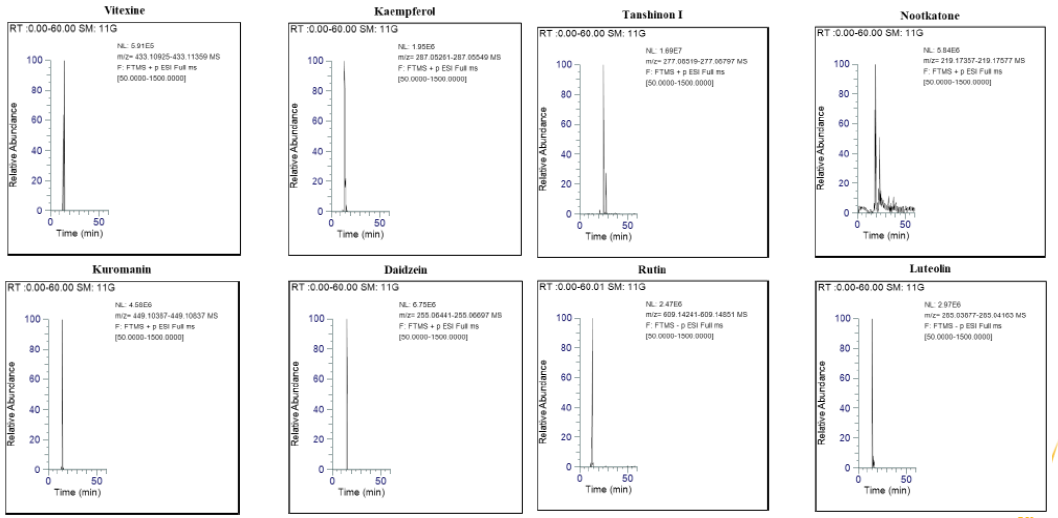
Effect of BAL on SOD-3 expression in *C. elegans*



Amino acid interactions of Bax with candidate ligands

Identification of bioactive compounds in BAL using UHPLC-Q-Orbitrap-(Exploris 480)

Ion mode	Compound name	Molecular formula	Rt (min)	m/z calculated	m/z observed	Error (ppm)
Positive	Quercetin-3β-D-glucoside	$C_{21}H_{20}O_{12}$	13.324	464.09379	465.10107	-3.63
	Robinetin	$C_{15}H_{10}O_7$	13.498	302.0416	303.04887	-3.5
	Vitexin	$C_{21}H_{20}O_{10}$	13.749	432.10414	433.11142	-3.48
	Kaempferol	$C_{15}H_{10}O_6$	14.062	286.04678	287.05405	-3.36
	Kuromanin	$C_{21}H_{20}O_{11}$	14.765	448.09884	449.10612	-3.84
	Daidzein	$C_{15}H_{10}O_4$	15.66	254.05841	255.06569	1.98
	Tanshinon I	$C_{18}H_{12}O_3$	21.174	276.0793	277.08658	2.38
	Nootkatone	$C_{15}H_{22}O$	38.014	218.16739	219.17467	1.49
Negative	Rutin	$C_{27}H_{30}O_{16}$	13.665	610.15274	609.14546	-1.06
	Luteolin	$C_{15}H_{10}O_6$	14.772	286.04748	285.0402	-0.9

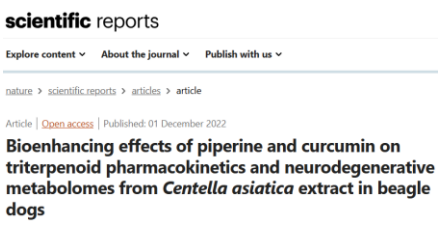


Metabolomics: Beagle dog's plasma metabolome-PK-omics correlation

Mahidol University
Faculty of Pharmacy

CNMI
RAMATHIBODI
The Incubator of Change Agents

รศ.ดร.ภก.พิสิฐ เขมาวุฒฆ์
สถาบันการแพทย์จักรีนฤบดินทร์
โรงพยาบาลรามาธิบดี



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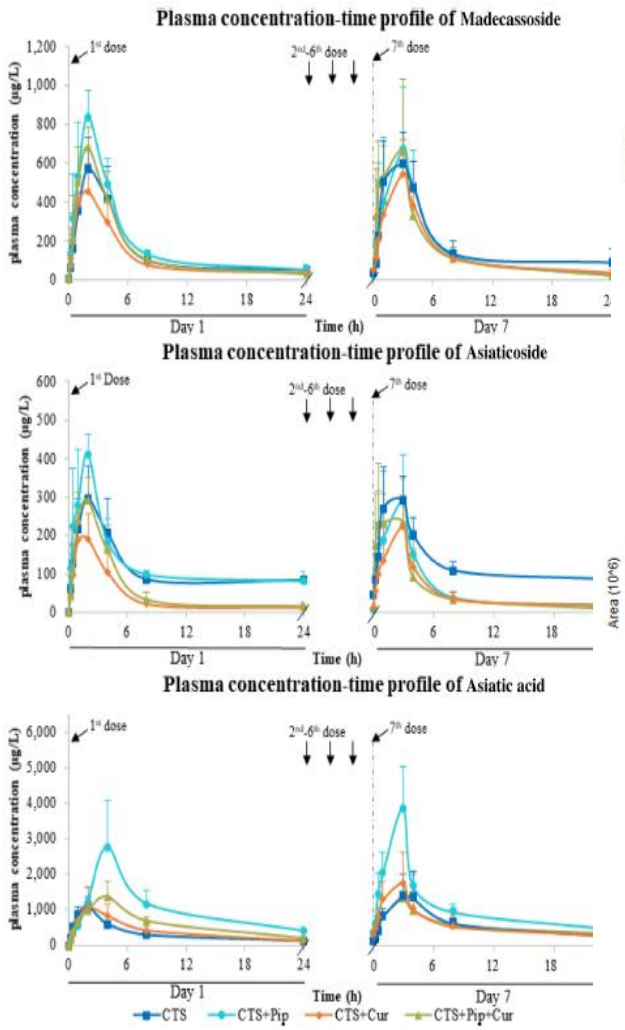
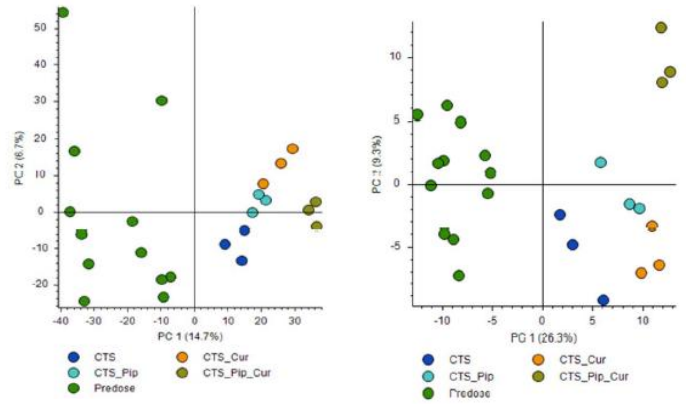
Article | Open access | Published: 01 December 2022

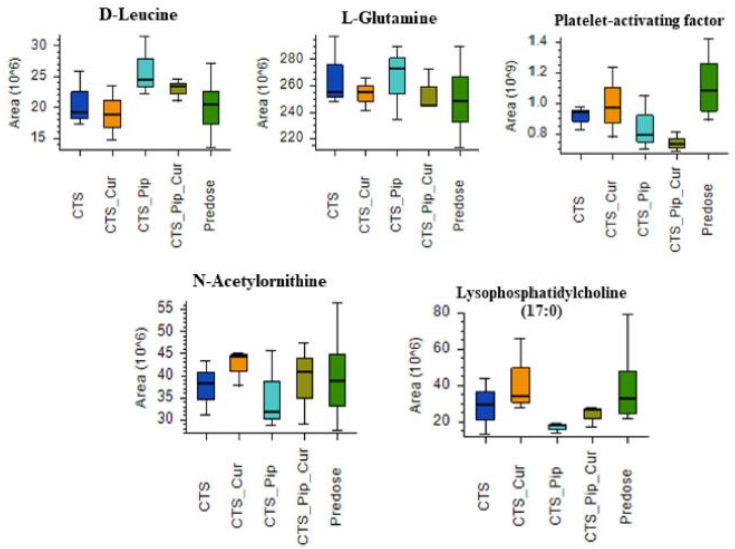
Bioenhancing effects of piperine and curcumin on triterpenoid pharmacokinetics and neurodegenerative metabolomes from *Centella asiatica* extract in beagle dogs



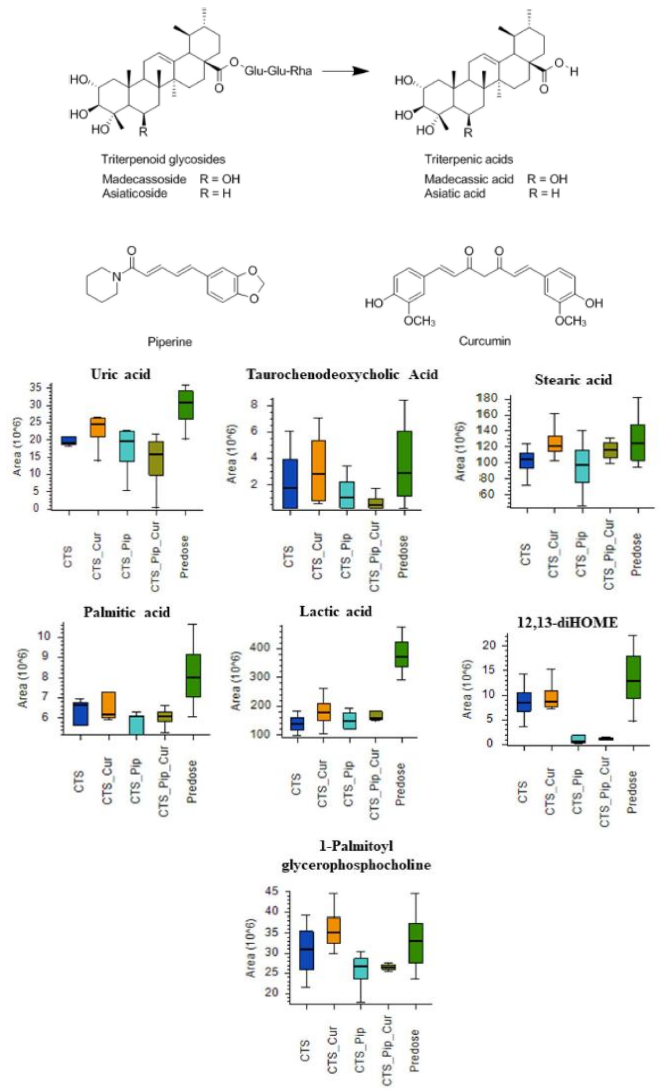
Plasma concentration–time profiles of major bioactive triterpenoids from *Centella asiatica* extract alone and in combination with curcumin and/or piperine



The PCA plot of metabolites from positive mode and negative mode of each plasma sample group



Boxplots of the metabolite biomarkers that changed 4 h after administration of *Centella asiatica* (CTS) in the positive mode of detection



Boxplots of the metabolite biomarkers that changed 4 h after administration of *Centella asiatica* (CTS) in the negative mode of detection


Thank you