

# **Tutorial for browsing, searching, and visualizing the Human Microbial Metabolome Database MiMeDB**

**August 15th, 2022**

**Updated on September 16th, 2025**

## Structure and design of the MimeDB

In simple terms, the Human Microbial Metabolome Database or MiMeDB (<https://mimedb.org>) contains data about human microbes, their associated metabolites, and the effects these metabolites have on humans.

The MiMeDB (<https://mimedb.org>) is a comprehensive, multi-omic, microbiome resource that connects:

- 1) microbes to microbial genomes
- 2) microbial genomes to microbial metabolites
- 3) microbial metabolites to the human exposome
- 4) all of these “omes” to human health.

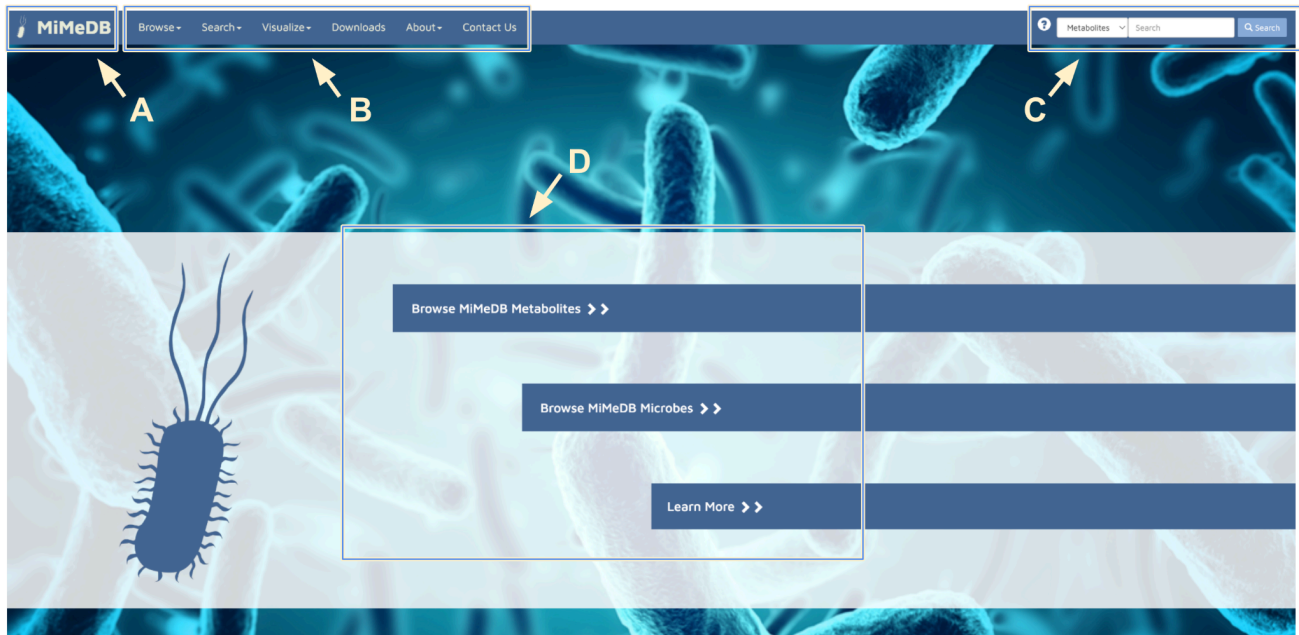
While the general content of MiMeDB can be grouped into three broad classes (microbes, metabolites, and effects), MiMeDB is actually divided into six smaller categories for more facile browsing, searching, and viewing. These six categories include:


- 1) Metabolites
- 2) Microbial Sources
- 3) Biospecimens & Location
- 4) Health Effects
- 5) Exposure Sources
- 6) Metabolic Reactions

The following sections provide details about how to “**Browse**” and “**Search**” the MiMeDB. The last section provides details on how to use the “**Visualize**” tabs, “**Genome Viewer**” and “**Network Viewer**”.

First, to access MiMeDB, open your preferred browser and type “<https://mimedb.org>” or simply “mimedb.org” into the search bar and press the “Enter” key. You will be first taken to the homepage.

## Navigating the Homepage



- A** – Clicking the MiMeDB logo at the top left brings you back to the homepage
- B** – At the top of the page there are 6 menu headings, each with their own pulldown menu: **Browse**, **Search**, **Visualize**, **Downloads**, **About** and **Contact Us**.
- C** – At the top right corner there is a Search box that enables you to search the entire database. Here, you can either search for a microbe or a metabolite by name by selecting either **Metabolites** or **Microbes** from the pulldown menu. Clicking on the  button returns a list of results that match your query.
- D** – There are hyperlinked bars at the center of the homepage that allow you to **Browse MiMeDB Metabolites**, **Browse MiMeDB Microbes**, or **Learn More** about MiMeDB.

# Search Box

## Some general searches using the Search box

If you enter “succinate” in the search box and select **Metabolites** from the pulldown menu, 40 results are returned where “succinate” is found in the name or description.

Metabolites

succinate

Search

MiMeDB

Browse

Search

Visualize

Downloads

About

Contact Us

Metabolites

succinate

Search

Search Results for metabolites

Searching metabolites for succinate returned 40 results.

1

2

Next

Last

MMDB-003440

925-15-5

CC(=O)OCC(=O)O

dipropyl succinate

Matched name: ... dipropyl succinate ...

MMDB-003441

1070-34-4

CCOC(=O)CC(=O)O

monoethyl succinate

Matched name: ... monoethyl succinate ...

If you enter *Escherichia coli* O157 in the Search box and select **Microbes** from the pulldown menu, 5744 results are returned containing “Escherichia”, “coli” or “O157” in the microbe name.

Microbes

Escherichia coli O157

Search

MiMeDB

Browse

Search

Visualize

Downloads

About

Contact Us

Microbes

Escherichia coli O157

Search

Search Results for microbes

Searching microbes for Escherichia coli O157 returned 5744 results.

1

2

3

4

5

...

Next

Last

MMDB-054346

Escherichia coli O157

Matched name: ... Escherichia coli O157 ...

MMDB-054349

Escherichia coli O157:H43

Matched name: ... Escherichia coli O157:H43 ...

MMDB-054341

Escherichia coli O157:H45

Matched name: ... Escherichia coli O157:H45 ...

MMDB-054350

Escherichia coli O157:H9

Matched name: ... Escherichia coli O157:H9 ...

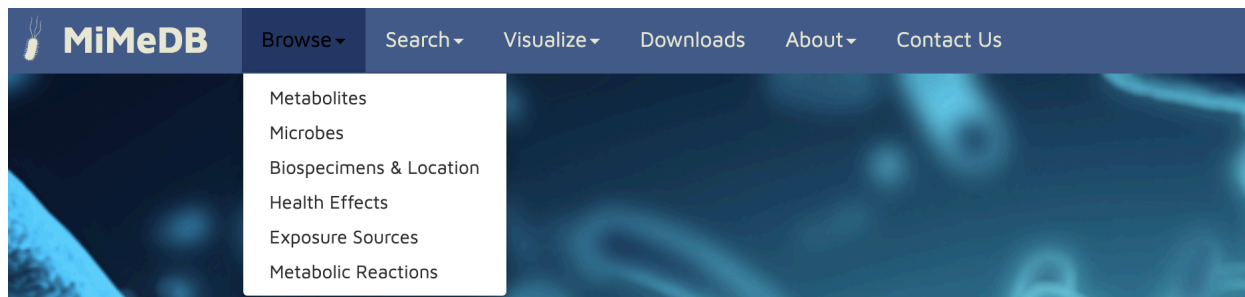
MMDB-054370

Escherichia coli O157:HNM

Matched name: ... Escherichia coli O157:HNM ...

# Browse

Browse at the top left of the homepage reveals a pulldown menu with 6 options.



## I. Metabolites

**Metabolites** in the pulldown menu will bring you to the Metabolites table.

**Browsing Metabolites**

Filter by:



Metabolite Origin:  Structure Class:  Host:

Microbial Metabolism:  Health Outcome:  Biospecimen:

Status in Biospecimen:  Bioactivity:

[Download All](#)

Displaying microbes 1 - 25 of 20061 in total

Metabolite ID	Name	Molecular Formula	Average Mass	Monoisotopic Mass	Structure	Structure Class	Host and Biospecimen	# Microbes	Metabolite Origin	Health Effects	Detection Status
<a href="#">MIMDB-0000001</a>	Indoxyl sulfate	$C_{10}H_7NO_3S$	213.21	213.009578407		<a href="#">Organic sulfuric acids and derivatives</a>	Human Urine Human Blood Human Faces Human Cerebrospinal Fluid (CSF) Human Bone Marrow Human Brain	0	Co-metabolite Food	Uremia Eosinophilic esophagitis Mild cognitive impairment Uremic toxin Liver damage Pro-inflammatory	Detected and Quantified
<a href="#">MIMDB-0000002</a>	p-Cresol sulfate	$C_7H_7O_2S$	188.201	188.014329434		<a href="#">Organic sulfuric acids and derivatives</a>	Human Blood Human Urine Human Saliva Human Faces Human Cerebrospinal Fluid (CSF) Human Placenta	8	Food Industrial exposure	Uremia Eosinophilic esophagitis Mild cognitive impairment Liver damage Chronic kidney disease Uremic toxin	Detected and Quantified

Here there are various filters that can narrow your metabolite search such as **specific metabolite origin, structure class, host, microbial metabolism, health outcome, biospecimen, status in biospecimen, and bioactivity**. These each have their own corresponding pulldown menu, where you can then click **Apply Filter** to return a shorter table that matches your filter preferences.

Clicking on the MiMeDB compound button or the compound name will take you to the MiMeDB MetaboCard for that compound or metabolite. The MiMeDB MetaboCard for indoxyl sulfate (MMDBc0000001) is shown below.

MIMeDB

[Browse](#) | 
 [Search](#) | 
 [Visualize](#) | 
 [Downloads](#) | 
 [About](#) | 
 [Contact Us](#)

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### Showing metabocard for Indoxyl sulfate (MMDBc0000001)

Microbial

Human

**Co-metabolite**

Plant

Animal

Pharmaceutical

Xenobiotic


Record information															
Version	1.0														
Status	Detected and Quantified														
Creation Date	2021-12-11 00:18:36 UTC														
Update Date	2024-10-11 04:59:25 UTC														
Metabolite ID	MMDBc0000001														
Metabolite Identification															
Common Name	Indoxyl sulfate														
Description	<p>Indoxyl sulfate, also known as 3-indoxyl sulfate, is a member of the class of organic compounds known as arylsulfates. These are organic compounds containing a sulfate group that carries an aryl group through an ether group. Indoxyl sulfate is a metabolite of the common amino acid tryptophan and is derived through the consumption, digestion and microbial processing of protein-rich foods. Indoxyl sulfate is technically a bacterial co-metabolite, meaning that it is derived from both bacterial and host metabolism. Specifically, it is generated from dietary L-tryptophan which is converted to indole in the large intestine via tryptophanase-expressing gastrointestinal bacteria (PMID: 27102537 <a href="#">↗</a>). The resulting indole is converted to indoxyl in the liver via enzyme-mediated hydroxylation by the CYP450 enzyme CYP2E1 (PMID 1183685 <a href="#">↗</a>). Subsequently, indoxyl is converted into indoxyl sulfate by the SULT1A1 sulfotransferase enzyme in the liver (PMID: 12084372 <a href="#">↗</a>). Indoxyl sulfate has been identified as a uremic toxin according to the European Uremic Toxin Working Group (PMID: 22626821 <a href="#">↗</a>) and is classified as a protein-bound uremic solute. Indoxyl sulfate is known to bind to serum albumin (PMID: 22626821 <a href="#">↗</a>), to be transported by the OAT1 transporter (PMID: 34678967 <a href="#">↗</a>) and to be an agonist for the arylhydrocarbon receptor (AhR) (PMID: 32527975 <a href="#">↗</a>). High concentrations of indoxyl sulfate in whole blood or blood plasma are known to be associated with the development and progression of chronic kidney disease (CKD) as well as the development of cardiovascular disease (CVD) in humans and other mammals (PMID: 28754616 <a href="#">↗</a>). As a uremic toxin, indoxyl sulfate is known to stimulate</p>														
Structure	 <div> <input checked="" type="checkbox"/> MOL           <input type="checkbox"/> 3D MOL           <input type="checkbox"/> SDF           <input type="checkbox"/> 3D SDF           <input type="checkbox"/> PDB           <input type="checkbox"/> 3D PDB           <input type="checkbox"/> SMILES           <input type="checkbox"/> InChI         </div>														
Synonyms	<table border="1"> <thead> <tr> <th>Value</th> <th>Source</th> </tr> </thead> <tbody> <tr> <td>3-Indoxyl hydrogen sulfate</td> <td>CHEBI</td> </tr> <tr> <td>3-Indoxyl sulfate</td> <td>CHEBI</td> </tr> <tr> <td>3-Indoxyl sulfate</td> <td>CHEBI</td> </tr> <tr> <td>3-Indoxylsulfuric acid</td> <td>CHEBI</td> </tr> <tr> <td>Indican</td> <td>CHEBI</td> </tr> <tr> <td>Indoxyl 3-sulfate</td> <td>CHEBI</td> </tr> </tbody> </table>	Value	Source	3-Indoxyl hydrogen sulfate	CHEBI	3-Indoxyl sulfate	CHEBI	3-Indoxyl sulfate	CHEBI	3-Indoxylsulfuric acid	CHEBI	Indican	CHEBI	Indoxyl 3-sulfate	CHEBI
Value	Source														
3-Indoxyl hydrogen sulfate	CHEBI														
3-Indoxyl sulfate	CHEBI														
3-Indoxyl sulfate	CHEBI														
3-Indoxylsulfuric acid	CHEBI														
Indican	CHEBI														
Indoxyl 3-sulfate	CHEBI														
Molecular Formula	C <sub>9</sub> H <sub>7</sub> NO <sub>4</sub> S														
Average Mass	213.21														

Each MiMeDB MetaboCard contains 16 data fields: **Record Information**; **Metabolite Identification**; **Chemical Taxonomy**; **Functional Ontology**; **Physical Properties**; **Spectra**; **Biological Properties**; **Human Proteins and Enzymes**; **Human Pathways**; **Metabolic Reactions**; **Health Effect and Bioactivity**; **Microbial Sources**; **Exposure Sources**; **Host Biospecimen and Location**; **External Links**; and **References**. The Record Information and Metabolite Information sections are expanded by default.

For any collapsed section, clicking on the down arrow on the righthand side expands it and reveals further information about that metabolite. Clicking on the up arrow for any expanded section collapses that section.

## II. Microbes

From the top selection bar under **Browse, Microbes** in the pulldown menu will bring you to the Microbes table.

 **MiMeDB**

[Browse](#) [Search](#) [Visualize](#) [Downloads](#) [About](#) [Contact Us](#)

Metabolites

Search

Search

Browsing Microbes

Filter by:

Host:

Human

Body Site:

All

Biospecimen:

All

Pathogen:

All

Superkingdom:

All

Phylum:

All

Oxygen Preference:

All

Energy Production:

All

Gram Stain:

All

Cell shape:

All

Cell arrangement:

All

Clear

Apply Filter

Download All

Displaying microbes 1 - 25 of 2410 in total

1

2

3

4

5

...

Next

Last

Microbe ID	Organism	Superkingdom	Kingdom	Phylum	Oxygen Preference	Energy Production	Host & Site	Pathogenicity Status
MMDBn0000009	Acinetobacter baumannii	Bacteria	Eubacteria	Proteobacteria	Aerobe	Prototrophic	Human Human Thigh Human Lower respiratory tract Human Lung Human Trachea Human Gingiva	Pathogenic
MMDBn0000014	Akkermansia muciniphila	Bacteria	Eubacteria	Verrucomicrobia	Anaerobe	Saccharolytic, fermentative	Human Gut Human Large intestine Human Bladder	Pathogenic
MMDBn0000021	Anaerostipes caccae	Bacteria	Eubacteria	Firmicutes	Anaerobe	Saccharolytic, fermentative, acetate and lactate converted to butyrate	Human Large intestine	Pathogenic
MMDBn0000022	Anaerostipes hadrus	Bacteria	Eubacteria	Firmicutes	Anaerobe	Saccharolytic, fermentative	Human Gut Human Large intestine	Pathogenic
MMDBn0000031	Bacillus subtilis	Bacteria	Eubacteria	Firmicutes	Facultative	Not Available	Human Human Large intestine	Pathogenic
MMDBn0000032	Bacillus timonensis	Bacteria	Eubacteria	Firmicutes	Facultative anaerobe	Respiration or fermentation of carbohydrates and central metabolism intermediates	Human Gut	Pathogenic

The Microbes table contains 11 filters that can specify your microbe search: **Host**, **Body site**, **Biospecimen**, **Pathogen**, **Superkingdom**, **Phylum**, **Oxygen Preference**, **Energy Preference**, **Energy Production**, **Gram Stain**, **Cell shape**, **Cell arrangement**. These each have their own corresponding pulldown menu, where you can then click **Apply Filter** to return a shorter table that matches your filter preferences.

Clicking on the MiMeDB microbe ID button or the Microbe name, will take you to the MiMeDB MicrobeCard for that organism. *Acinetobacter baumannii* (MMDBm0000006) is shown below.

MiMeDB

Browse

Search

Visualize

Downloads

About

Contact Us

Metabites

Search

Search

Acinetobacter baumannii (MMDBm0000006)

Microbe Identification

Microbe name

Acinetobacter baumannii

NCBI Taxonomy ID

470

Description

Acinetobacter baumannii is classified as a mesophile, a chemoheterotroph, capable of energy production through aerobic respiration, a Gram-negative bacterium, typically appearing as a coccobacillus, found across various body sites such as the skin, respiratory tract, and urinary tract, and is categorized as a facultative anaerobe. This opportunistic pathogen thrives optimally at moderate temperatures, making it well-suited for survival in human hosts. As a chemoheterotroph, A. baumannii derives its energy from organic compounds, utilizing a variety of carbon sources, which contributes to its adaptability in diverse environments. Its Gram-negative nature is characterized by a thin peptidoglycan layer and an outer membrane containing lipopolysaccharides, which can elicit strong immune responses. The coccobacillus shape allows for efficient colonization and biofilm formation, facilitating its persistence in hospital settings. A. baumannii is commonly found colonizing skin and mucosal surfaces, particularly in critically ill patients. Its ability to survive in harsh conditions, including desiccation and the presence of disinfectants, enhances its transmission in healthcare environments, leading to outbreaks in intensive care units and among patients with compromised immune systems. Furthermore, this microbe poses a significant challenge in clinical settings due to its remarkable antibiotic resistance, often exhibiting multi-drug resistance profiles that complicate treatment options. Research into its genomic features has revealed mechanisms that confer resistance, allowing it to thrive despite aggressive antimicrobial therapies. Understanding A. baumannii's adaptability and resistance mechanisms is crucial for developing effective infection control strategies and treatment modalities, especially as it continues to emerge as a formidable nosocomial pathogen.

Microbe Taxonomy

Superkingdom

Bacteria

Kingdom

Eubacteria

Phylum

Proteobacteria

Class

Gammaproteobacteria

Order

Pseudomonadales

Family

Moraxellaceae

Genus

Acinetobacter

Species

baumanni

Microbe Properties

Gram staining properties

Negative

Shape

Bacilli

Mobility

No

Flagellar presence

No

Number of membranes

2

Oxygen preference

Aerobe

Optimal temperature

37

Temperature range

Mesophilic

Habitat

Multiple

Biotic relationship

Free living

Cell arrangement

Singles

Sporelation

Singles

Each MiMeDB MicrobeCard contains nine data fields: **Microbe Identification**; **Microbe Taxonomy**; **Microbe Properties**; **Hosts and Biospecimens**; **Health Effects**; **Related Metabolites**; **Metabolic Reactions**; **Genome Data**; and **Source Links**.

For any collapsed section, clicking on the down arrow on the righthand side expands it and reveals further information about that microbe. Clicking on the up arrow for any expanded section collapses that section.

*Acinetobacter baumannii* (MMDBm0000006)

Microbe Identification	▼
Microbe Taxonomy	▼
Microbe Properties	▼
Host and Biospecimens	▼
Health Effects	▼
Related Metabolites	▼
Metabolic Reactions	▼
Genome Data	▼
Source Links	▼

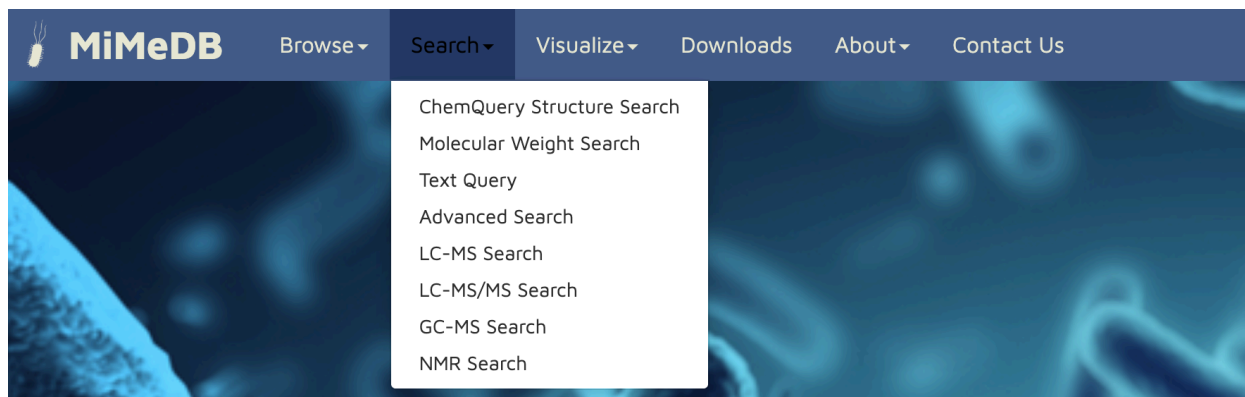
### III. Other Browsing Options

Similar browsing options, similar layouts, and similar data tables are also available for each of the other Browse menu options including “Biospecimens & Locations”, “Health Effects”, “Exposure Sources” and “Metabolic Reactions”, each with their MiMeDB identifiers (named BiospeCard, HealthCard and Exposocard, ReactCard respectively), filterable and sortable tables, and section-expandable viewing cards.



## Search

Clicking on the “Search” option at the top left of the homepage reveals a pulldown menu with 8 options.



### I. ChemQuery searches

The MarvinView applet from ChemAxon allows you to interactively draw structures or paste InChI or SMILES strings onto a palette (shown below).

If you were

searching for the

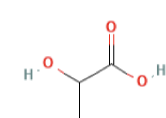
metabolite lactic

acid, using the

interactive palette,

you could draw its

chemical structure as



insert its InChI

(InChI=1S/C3H6O3/c

1-2(4)3(5)6/h2,4H,

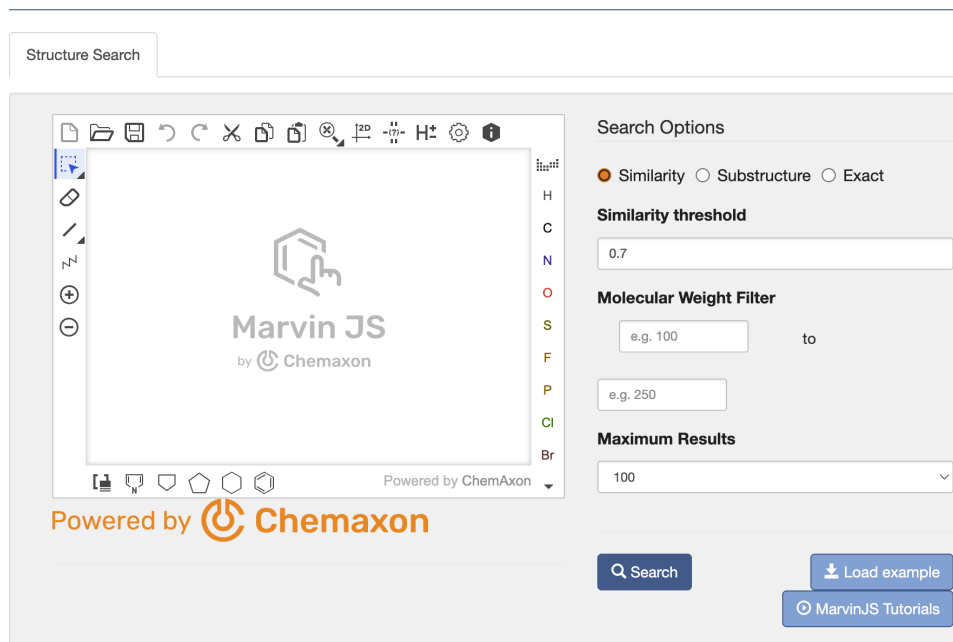
1H3,(H,5,6)); or

insert one of its

SMILES strings (e.g.,

CC(C(=O)O)O).

#### ChemQuery Search by structure



Selections for a narrowed search are also provided to specify the similarity threshold, add a range of molecular weight, and limit maximum results.

## II. Text Query

Using the provided instructions on the text query page, you can match strings you provide to data in MiMeDB.

### Searching MiMeDB

MiMeDB supports advanced searching using a powerful search engine based on the [Lucene query language](#). The MiMeDB text search supports boolean logic (AND, OR, NOT operations). To match a string exactly, place quotes around your search term (for example "acetic acid" will only match the acetic followed by acid, it will not match acetic or acid alone). You can also search using "wild cards" by inserting a "\*" in your search term. For example, searching for "acet\*" will match all words starting with "acet". In addition, text search supports parenthetical groupings, and prepended +plus and -minus operators.

Example	Description
<code>methylhistidine AND poultry</code>	Find all entries containing <b>both</b> methylhistidine and poultry in MiMeDB
<code>(histidine OR poultry) AND NOT glycolylneuraminic</code>	Find all metabolites containing histidine, poultry or both, but not containing glycolylneuraminic
<code>"acetic acid"</code>	Find all metabolites where the <b>entire term</b> "acetic acid" is found. In other words, don't match "acetic" or "acid" alone.

## III. Spectra Search

 **MiMeDB** [Browse](#) [Search](#) [Visualize](#) [Downloads](#) [About](#) [Contact Us](#) [?](#) [Metabolites](#)

### Spectra Search Mass Spectrum

[LC-MS Search](#) [LC-MS/MS Search](#) [GC-MS Search](#) [NMR Search](#)

**Query Masses (Da) and Collision Cross Section ( $\text{\AA}^2$ ):**



Enter one mass and CCS value (optional) per line  
(maximum 700 query masses per request)

**Ion Mode:**

Positive

**Adduct Type:**

Unknown  
M+H  
M+H-2H<sub>2</sub>O  
M+H-H<sub>2</sub>O  
M+NH<sub>4</sub>-H<sub>2</sub>O  
M+Li  
M+NH<sub>4</sub>


Hold Ctrl (  ) or Command (  ) to select multiple adducts.


**Molecular Weight Tolerance  $\pm$ :**

e.g. 0.05

Da

**CCS Prediction Method:****Collision Cross Section Tolerance  $\pm$  (%):**

 Load Example with CCS

 Load Example without CCS

There are four available spectral searches available on MiMeDB, Mass spectrum, Tandem mass spectrum, GC mass spectrum, and NMR spectrum. Each of these searches include a load example that can be clicked to fill in the required information with an example spectral search. By clicking search, you are brought to a table with your search results. For example, this is the propagated search box for the LC-MS search example:

#### Spectra Search Mass Spectrum

[LC-MS Search](#)
[LC-MS/MS Search](#)
[GC-MS Search](#)
[NMR Search](#)

**Query Masses (Da) and Collision Cross Section (Å²):**

74.0785 122.21  
104.1045 126.73  
228.202 150.79

**Ion Mode:** Positive

**Adduct Type:**

Unknown  
M+H  
M+H-2H2O  
M+H-H2O  
M+NH4-H2O  
M+Li  
M+NH4

Hold Ctrl (⌘) or Command (⌘) to select multiple adducts.

**Molecular Weight Tolerance ±:** 0.05 Da

**CCS Prediction Method:** AllCCS

**Collision Cross Section Tolerance ± (%):** 5

[Load Example with CCS](#)
[Search](#)
[Reset](#)

[Load Example without CCS](#)

When clicking search, this is the result:

#### Spectra Search Mass Spectrum

[LC-MS Search](#)
[LC-MS/MS Search](#)
[GC-MS Search](#)
[NMR Search](#)

[Search options](#)

**Search Results**
[Download Results As CSV](#)

**MS search for 74.0785 m/z** Delta = (abs(query mass - adduct mass)/adduct mass)\*1000000

Show 10 entries

Search

Compound	Name	Formula	Monoisotopic Mass	Adduct	Adduct M/Z	Delta (ppm)	CCS
<a href="#">MMDBc0030360</a>	Isobutylamine	C <sub>4</sub> H <sub>11</sub> N	73.0891	M+H	74.0964 <a href="#">m/z calculator</a>	242	120.6
<a href="#">MMDBc0029683</a>	Aminoacetone	C <sub>3</sub> H <sub>7</sub> NO	73.0528	M+H	74.060 <a href="#">m/z calculator</a>	249	120.8
<a href="#">MMDBc0029557</a>	3-Aminopropionaldehyde	C <sub>3</sub> H <sub>7</sub> NO	73.0528	M+H	74.060 <a href="#">m/z calculator</a>	249	122.312
<a href="#">MMDBc0054592</a>	N,N-dimethylformamide	C <sub>3</sub> H <sub>7</sub> NO	73.0528	M+H	74.060 <a href="#">m/z calculator</a>	249	123.2195

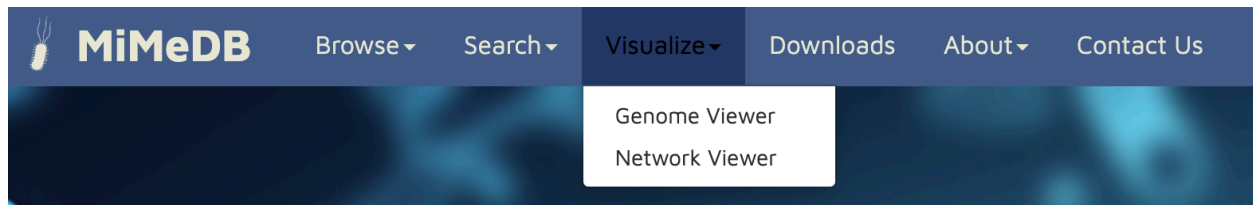
Showing 1 to 4 of 4 entries

[Previous](#)
[Next](#)

**MS search for 104.1045 m/z** Delta = (abs(query mass - adduct mass)/adduct mass)\*1000000

# Visualize

Clicking on the “Visualize” at the top left of the homepage reveals a pulldown menu with 2 options: “Genome Viewer” and “Network Viewer”



## I. Genome Viewer

Selecting the “Chromosome Viewer” returns a default list of microbes with genomes that are available. One can scroll through the list to find a microorganism of interest.

The image shows the MiMeDB homepage with the search bar and the default list of microbes. The search bar is labeled 'Microbe Name' and contains the text 'Acidaminococcus fermentans DSM 20731'. The search button is labeled 'Search'.

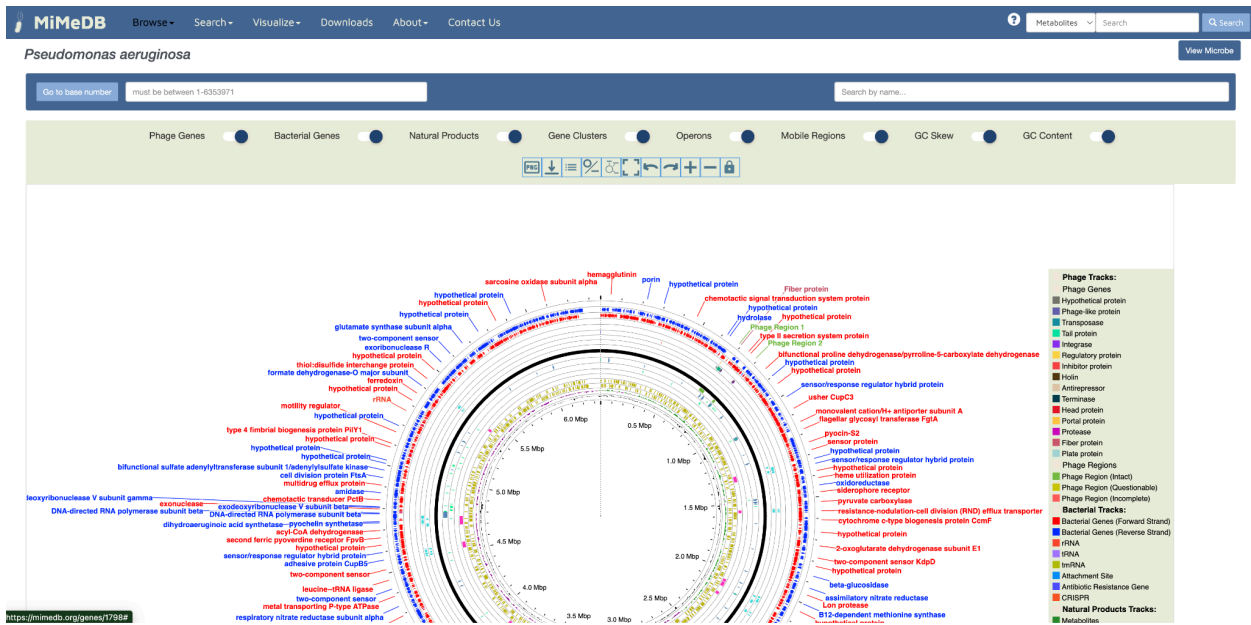
Genome ID	Number of Chromosomes	Name	Superkingdom	Phylum	NCBI Tax-ID	Oxygen Requirement	Shape
<a href="#">View Genome</a>	1	Micromonospora aurantiaca ATCC 27029	Bacteria	Actinobacteria	644283	Aerobe	Bacilli
<a href="#">View Genome</a>	1	Acidaminococcus fermentans DSM 20731	Bacteria	Firmicutes	591001	Anaerobe	Cocci
<a href="#">View Genome</a>	1	Acidaminococcus intestini RYC-MR95	Bacteria	Firmicutes	568816	Anaerobe	Cocci
<a href="#">View Genome</a>	1	Acinetobacter baumannii	Bacteria	Proteobacteria	470	Aerobe	Bacilli
<a href="#">View Genome</a>	1	Acinetobacter pittii ANC 4052	Bacteria	Proteobacteria	1217689	Aerobe	Not Available
<a href="#">View Genome</a>	1	Acinetobacter radioresistens NIPH 2130	Bacteria	Proteobacteria	1217674	Aerobe	Not Available
<a href="#">View Genome</a>	1	Adlercreutzia equolifaciens DSM 19450	Bacteria	Actinobacteria	1384484	Anaerobe	Not Available
<a href="#">View Genome</a>	1	Aeromonas jandael Riv2	Bacteria	Proteobacteria	1458276	Facultative anaerobe	Not Available
<a href="#">View Genome</a>	1	Aggregatibacter aphrophilus NJ8700	Bacteria	Proteobacteria	634176	Facultative	Bacilli
<a href="#">View Genome</a>	1	Agrobacterium tumefaciens F2	Bacteria	Proteobacteria	1050720	Aerobe	Bacilli
<a href="#">View Genome</a>	1	Akkermansia muciniphila	Bacteria	Verrucomicrobia	239935	Anaerobe	Cocci
<a href="#">View Genome</a>	1	Akkermansia muciniphila ATCC BAA-835	Bacteria	Verrucomicrobia	349741	Anaerobe	Cocci
<a href="#">View Genome</a>	1	Alcaligenes faecalis subsp. faecalis NBRC 13111	Bacteria	Proteobacteria	1218102	Aerobe	Not Available
<a href="#">View Genome</a>	1	Alistipes finegoldii DSM 17242	Bacteria	Bacteroidetes	679535	Anaerobe	Not Available
<a href="#">View Genome</a>	1	Alistipes shahii WAL 8301	Bacteria	Bacteroidetes	717959	Anaerobe	Not Available
<a href="#">View Genome</a>	1	Anaerococcus prevotii DSM 20548	Bacteria	Firmicutes	525919	Anaerobe	Cocci
<a href="#">View Genome</a>	1	Anaerostipes caccae	Bacteria	Firmicutes	105841	Anaerobe	Not Available

Alternatively, one can search for a specific microorganism by entering the name in the **Microbe Name** search box and clicking “Search”. Shown below are the 6 results returned when “Pseudomonas aeruginosa” is entered in the “Microbe Name” box.

The image shows the search results for 'Pseudomonas aeruginosa'. The search bar is labeled 'Microbe Name' and contains the text 'Pseudomonas aeruginosa'. The search button is labeled 'Search'. The results table shows 6 entries for 'Pseudomonas aeruginosa' with various strains and their corresponding genome IDs.

Genome ID	Number of Chromosomes	Name	Superkingdom	Phylum	NCBI Tax-ID	Oxygen Requirement	Shape
<a href="#">View Genome</a>	1	Pseudomonas aeruginosa	Bacteria	Proteobacteria	287	Aerobe	Bacilli
<a href="#">View Genome</a>	1	Pseudomonas aeruginosa PAO1	Bacteria	Proteobacteria	208964	Aerobe	Bacilli
<a href="#">View Genome</a>	1	Pseudomonas aeruginosa UCBPP-59.14	Bacteria	Proteobacteria	208963	Aerobe	Bacilli
<a href="#">View Genome</a>	1	Pseudomonas aeruginosa PA7	Bacteria	Proteobacteria	381754	Aerobe	Bacilli
<a href="#">View Genome</a>	1	Pseudomonas aeruginosa LES558	Bacteria	Proteobacteria	557722	Aerobe	Bacilli
<a href="#">View Genome</a>	1	Pseudomonas aeruginosa NC042 S1	Bacteria	Proteobacteria	1089456	Aerobe	Not Available

By clicking **View Genome**, you are brought to the following page:



Widgets at the top of the genome viewer carry out the listed functions:



Download map snapshot as PNG



Download map snapshot as SVG



Toggle legends



Toggle Circular/Linear format



Toggle phage annotation labels



Reset view



Pan left



Pan right



Zoom in



Zoom out

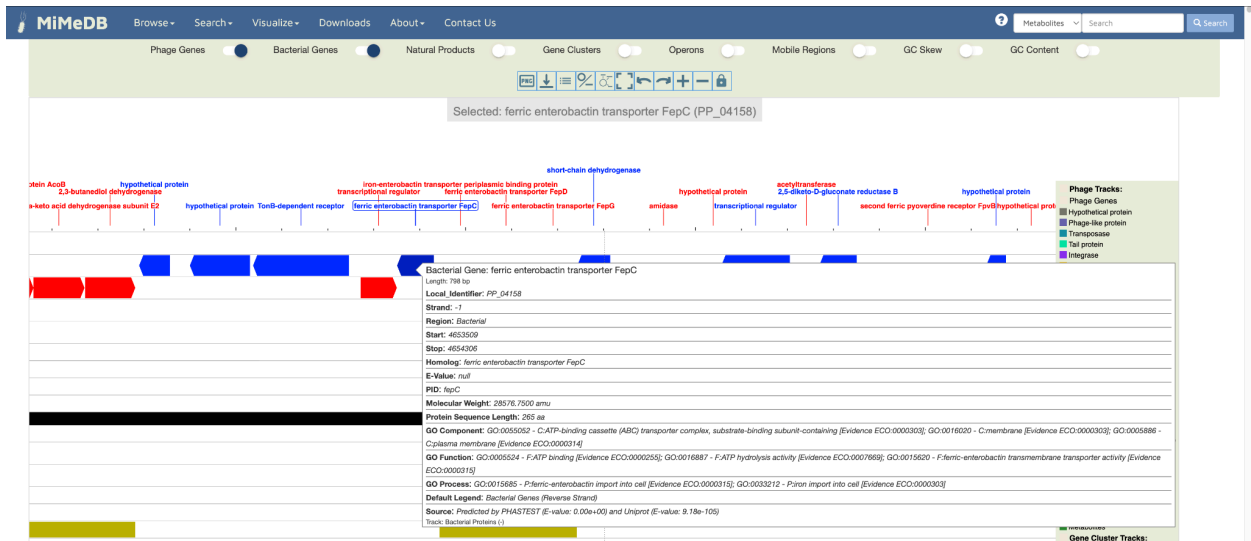


Lock zoom by scroll

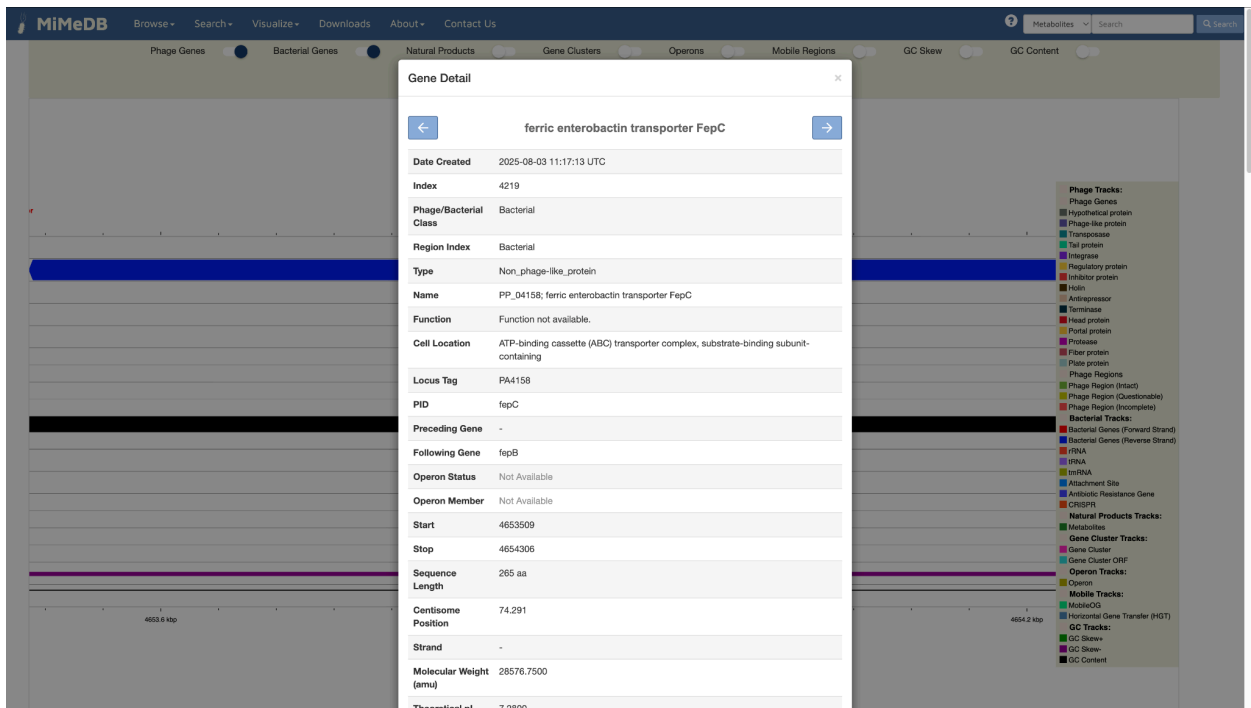
Above these widgets are switches that toggle to alter the data shown on the tracks of the genome viewer.



The Genome Viewer shows specific gene positions, names and orientations. Each chromosome is zoomable and each gene is clickable. By hovering over a gene you see the following popup:



By clicking on this same gene you are provided a page with richer information on the gene, seen below:



Genes can also be searched for underneath the genome viewer:

Search by:

Full Gene/Protein Name  Short Gene Name  COG Functional Category

OR,

Paste your query sequence to BLAST against the genes in this chromosome

Expected BLAST input:

1. must be a coding sequence
2. must be at least 9 characters long
3. may contain residue position numbers
4. may be either nucleotide or amino acid sequence (but not both)

MMuDB ID	Locus Tag	Short Name	Full Name	Functional Category	E-value	Start	Stop	Strand	Protein Sequence
<a href="#">MMDBg4534517</a>	<a href="#">PA0658</a>	Gph	Phosphoglycolate phosphatase, HAD superfamily	Energy production and conversion	3.79E-57	670369	670937	+	MSAAEPFFATRL...
<a href="#">MMDBg4534619</a>	<a href="#">PA0659</a>	TopE	Antitranilate/para-aminobenzoate synthase component I	Coenzyme transport and metabolism	1.47E-177	670960	672406	+	MNREERLRLAA...
<a href="#">MMDBg4534613</a>	<a href="#">PA0610</a>	Not Available	Not Available	Not Available	Not Available	672777	673091	-	MQPSAPSTPL...
<a href="#">MMDBg4534625</a>	<a href="#">PA0611</a>	Not Available	Phage repressor protein C, contains Cys/C1-type HTH and peptidase s24 domains	Mobility: prophages, transposons	1.23E-42	673191	673961	-	MCKSTQIPPOS...
<a href="#">MMDBg4534621</a>	<a href="#">PA0612</a>	DksA	RNA polymerase-binding transcription factor DksA	Transcription	9.27E-09	674419	674419	+	MADLADHANEL...
<a href="#">MMDBg4534622</a>	<a href="#">PA0613</a>	Not Available	Not Available	Not Available	Not Available	674667	675026	+	MKADEMLJL...

Here you can search using the full gene name, short gene name, COG functional category or by sequence. Shown below is an example of a BLAST search by sequence, on the right side is a popup of the BLAST results.

Search by:

Full Gene/Protein Name  Short Gene Name  COG Functional Category

OR,

Expected BLAST input:

1. must be a coding sequence
2. must be at least 9 characters long
3. may contain residue position numbers
4. may be either nucleotide or amino acid sequence (but not both)

#	MMuDB ID	E-Value
1	MMDBg4534517	0.0
2	MMDBg4537857	2.07e-36
3	MMDBg4537653	2.19e-13
4	MMDBg4534640	3.85e-13

Clicking on any eye icon will bring you to the exact location of the gene on the chromosome map.

## II. Network Viewer

The network viewer allows you to see connections of metabolites to health effects to exposure to microbes to body sites. It is a tool to decipher/depict/visualize the relationship and interaction between metabolites and microbes. Clicking on Network viewer in the **Visualize** pulldown menu brings you to another page.

The following information is required for generating your network viewer:



The screenshot shows the MiMeDB Network Viewer form. It includes a header with navigation links: Browse, Search, Visualize, Downloads, About, and Contact Us. The form fields are: Metabolite Name (with a placeholder 'Type & Select Metabolite'), five Microbe selection boxes (Microbe 1 to Microbe 5), a Degree of Connectivity dropdown (set to 5), and two buttons: View and Load Example. Blue arrows labeled A through E point to these specific elements: A points to the Metabolite Name box, B points to the Microbe selection boxes, C points to the Degree of Connectivity dropdown, D points to the View button, and E points to the Load Example button.

**A) Metabolite:** Enter the metabolite of interest in the Metabolite Name box. Begin typing and a pulldown list of metabolites will appear below to select.

**B) Microbe(s):** Enter the names of up to 5 microbe(s) in the “Select Microbe” boxes. You must enter the scientific name or partial name and auto-select will reveal a list for you to choose your microbe of interest.

**C) Degree of Connectivity:** You must also select the degree of connectivity (default is “5”). The degree of connectivity affects the density of the network graph: the higher the connectivity, then more data (more interactivity) is loaded into the graph. From the pull-down menu, “1, 3, 5, 8 or 10” degrees of connectivity can be selected.

**D) View:** Once you have filled all desired boxes, click on view to be taken to the network viewer.

**E) Load Example:** To see an example of the network viewer, or how the boxes can be filled, click load example. All options will be filled by an example, the result is shown below:

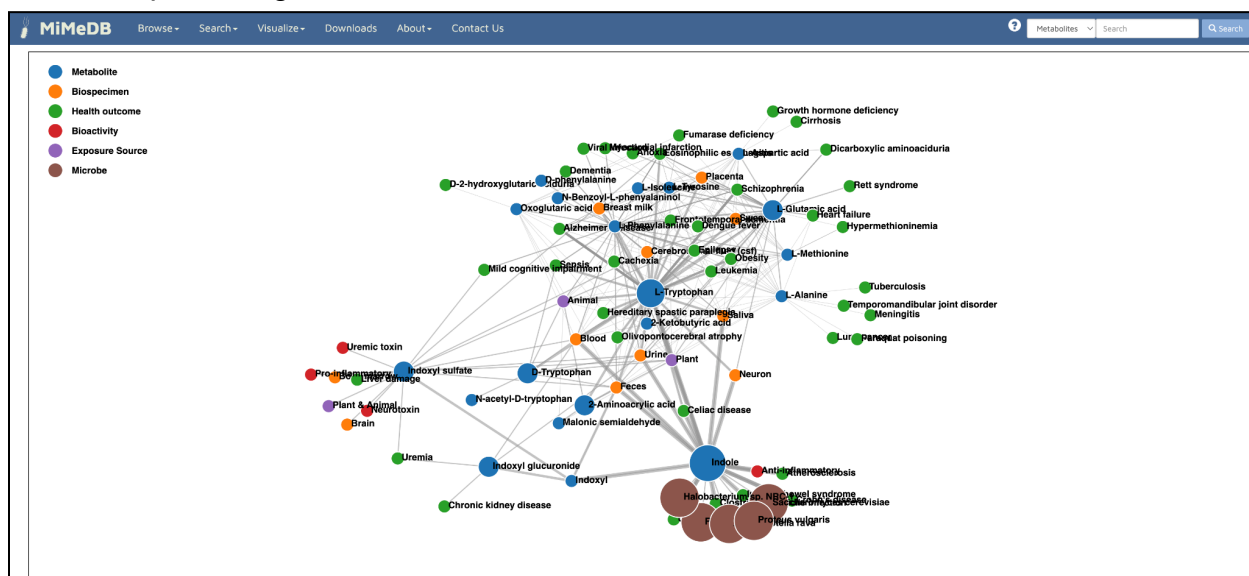


The screenshot shows the MiMeDB Network Viewer form with example data filled in. The header includes navigation links: Browse, Search, Visualize, Downloads, About, and Contact Us. The form fields are: Metabolite Name (Indole), five Microbe selection boxes (Microbe 1: Halobacterium sp. NRC-1, Microbe 2: Saccharomyces cerevisiae, Microbe 3: Alloprevotella rava, Microbe 4: Proteus vulgaris, Microbe 5: Ralstonia pickettii), a Degree of Connectivity dropdown (set to 5), and two buttons: View and Load Example.

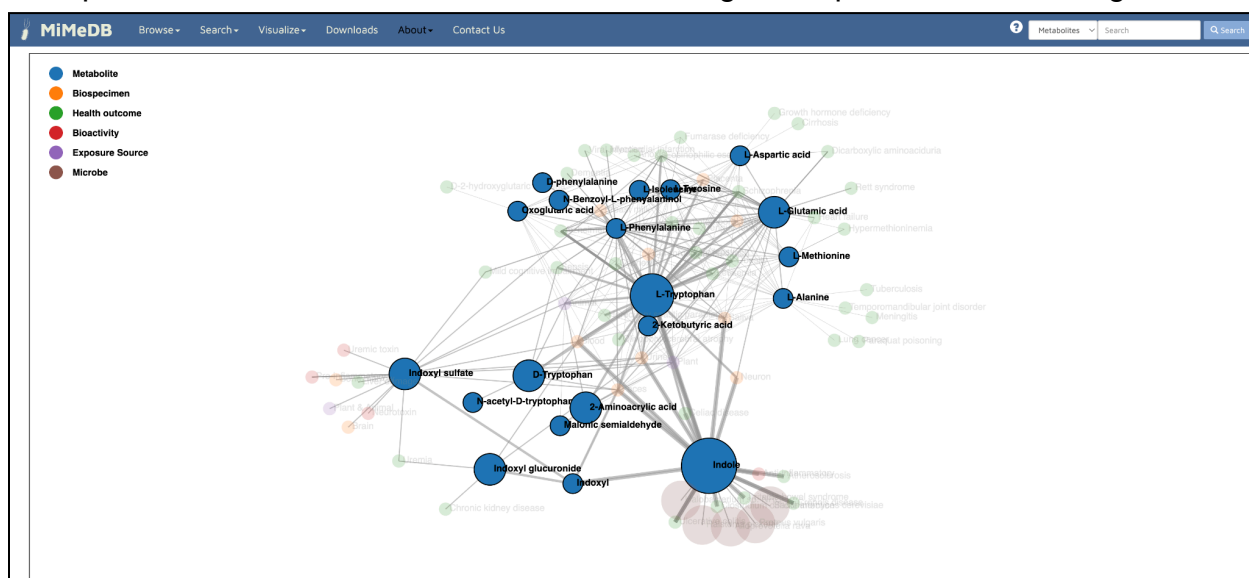


The generated network from the uploaded sample is shown below. All connections of metabolites, microbes, biospecimens and health effects within MiMeDB are shown. A color legend is provided on the top left to easily distinguish metabolites, biospecimens, health outcomes, bioactivity, exposure sources, and microbes within the network.

The viewer represents data in Nodes and Edges. **Nodes** are represented by metabolite, biospecimen, health outcome, exposure source and microbes. **Edges** depict the relationship among these different nodes. You can “Click” any of the nodes and edges. These nodes and edges can be adjusted or moved around to have a better view of the relationships among them.



Selecting on one of the labels in the legend isolates that specific data type. In the example below, Metabolite was clicked on in the legend to provide the following result



[illegible]


**MiMeDB**
Browse • Search • Visualize • Downloads • About • Contact Us

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### Showing metabocard for L-Tryptophan (MMDBc0000170)

Microbial
Plant
Animal
Pharmaceutical
Xenobiotic

Record Information	
Version	1.0
Status	Detected and Quantified
Creation Date	2020-10-27 23:38:26 UTC
Update Date	2024-09-27 23:08:57 UTC
Metabolite ID	MMDBc0000170

Metabolite Identification									
Common Name	L-Tryptophan								
Description	<p>Tryptophan is an essential amino acid that is the precursor of both serotonin and melatonin. Melatonin is a hormone that is produced by the pineal gland in animals, which regulates sleep and wakefulness. Serotonin is a brain neurotransmitter, platelet clotting factor, and neurohormone found in organs throughout the body. Metabolism of tryptophan into serotonin requires nutrients such as vitamin B6, niacin, and glutathione. Niacin (also known as vitamin B3) is an important metabolite of tryptophan. It is synthesized via kynurenine and quinolinic acids, which are products of tryptophan degradation. There are a number of conditions or diseases that are characterized by tryptophan deficiencies. For instance, fructose malabsorption causes improper absorption of tryptophan in the intestine, which reduces levels of tryptophan in the blood and leads to depression. High corn or other tryptophan-deficient diets can cause pellagra, which is a niacin-tryptophan deficiency disease with symptoms of dermatitis, diarrhea, and dementia. Hartnup's disease is a disorder in which tryptophan and other amino acids are not absorbed properly. Symptoms of Hartnup's disease include skin rashes, difficulty coordinating movements (cerebellar ataxia), and psychiatric symptoms such as depression or psychosis. Tryptophan supplements may be useful for treating Hartnup's. Assessment of tryptophan deficiency is done through studying excretion of tryptophan metabolites in the urine or blood. Blood may be the most sensitive test because the amino acid tryptophan is transported in a unique way. Increased urination of tryptophan breakdown products (such as kynurenine) correlates with increased tryptophan.</p> <p style="text-align: right;"><a href="#">Read more...</a></p>								
Structure	 <div style="margin-top: 10px;"> <input type="text" value="Search"/> <input type="button" value="MOL"/> <input type="button" value="3D MOL"/> <input type="button" value="SDF"/> <input type="button" value="3D SDF"/> <input type="button" value="PDB"/> <input type="button" value="3D PDB"/> <input type="button" value="SMILES"/> <input type="button" value="InChI"/> </div>								
Synonyms	<table style="width: 100%;"> <thead> <tr> <th style="text-align: left;">Value</th> <th style="text-align: left;">Source</th> </tr> </thead> <tbody> <tr> <td>(2S)-2-Amino-3-(1H-indol-3-yl)propanoic acid</td> <td>CHEBI</td> </tr> <tr> <td>(S)-alpha-Amino-1H-indole-3-propanoic acid</td> <td>CHEBI</td> </tr> <tr> <td>(S)-alpha-Amino-beta-(3-indolyl)-propionic acid</td> <td>CHEBI</td> </tr> </tbody> </table>	Value	Source	(2S)-2-Amino-3-(1H-indol-3-yl)propanoic acid	CHEBI	(S)-alpha-Amino-1H-indole-3-propanoic acid	CHEBI	(S)-alpha-Amino-beta-(3-indolyl)-propionic acid	CHEBI
Value	Source								
(2S)-2-Amino-3-(1H-indol-3-yl)propanoic acid	CHEBI								
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(S)-alpha-Amino-beta-(3-indolyl)-propionic acid	CHEBI								