

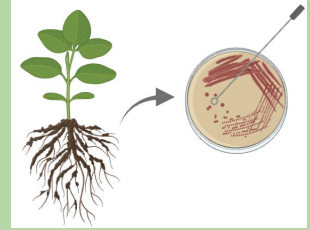
# ROOTOMICS DATABASE

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# INTRODUCTION

- Soil microbes drive global biogeochemical cycles
- We know little about their extracellular molecular functions
- RootOmics links gene presence to ecological function



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## What is Root Omics?

Root Omics is a functional enzyme database for microbial ecology research. It catalogs soil nutrient-cycling enzymes involved in carbon, nitrogen, and phosphorus transformations, with detailed annotations (EC, KO, GO) and pathway mappings. By integrating genomic and experimental data, it helps researchers assess enzyme distribution, pathway completeness, and functional potential across diverse soil microbial communities.

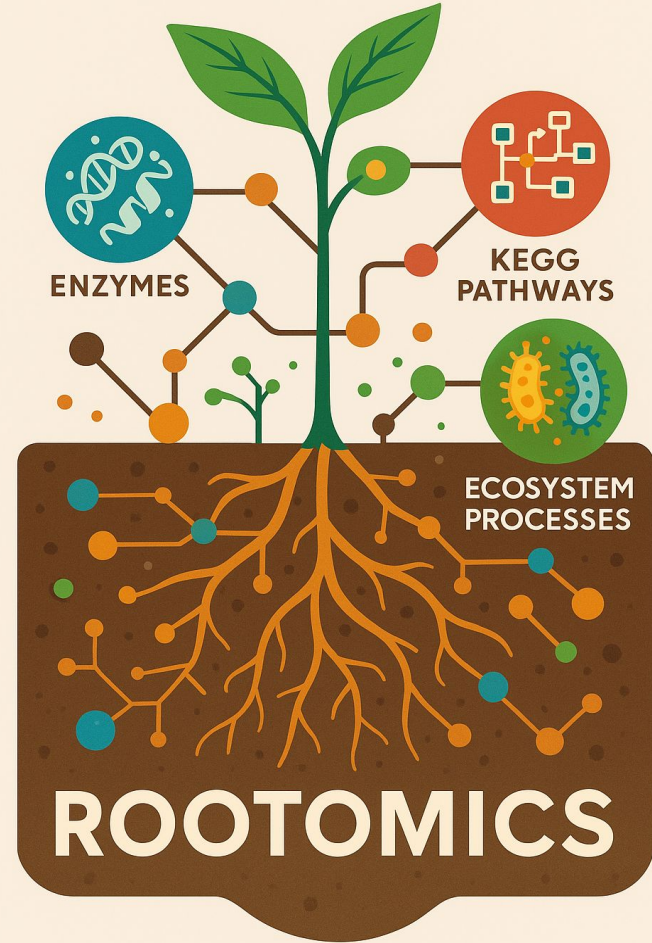
Developed by Team 13 at Boston University (BF768, Spring 2024) under Dr. G. Benson, Root Omics supports bioinformatics workflows, genomic analyses, and environmental functional gene studies, enabling insights into biogeochemical cycling and microbial ecosystem functions.

# MOTIVATION AND BACKGROUND

KEGG and GO focus mostly on intracellular processes

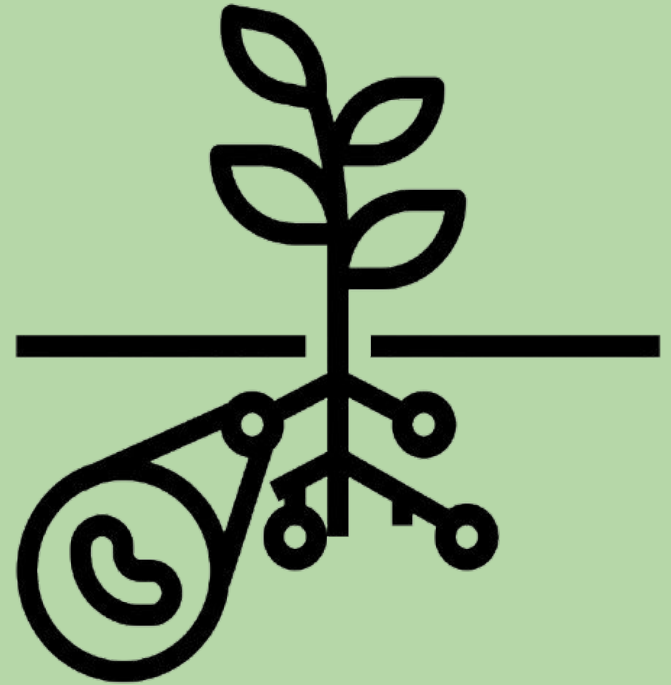
Environmental gene function remains under-characterized

No comprehensive tool links genes → ecological role



# What Can RootOmics Help Us Answer?

1. How do enzymes respond to environmental stressors?
2. What evidence supports a specific enzyme's role in nutrient cycling?
3. What are the dominant enzymes driving C, N, P transformations in soil?

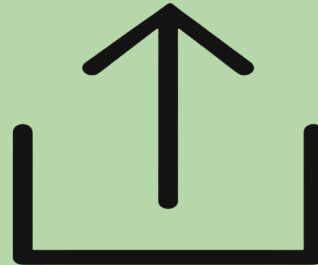


# Database Structure & Accessibility

- Open access and searchable—no login required.
- Each entry includes EC number, enzyme name, function, and evidence source.
- Contributor uploads are reviewed to ensure data quality.



Open access



# Data Model & ER Diagram

## Proteins

PID → Protein\_name, Enzyme\_Type, EC\_numbers,  
KO\_Numbers, GO\_terms

## Pathways

PAID → KEGG\_pathway, CAZyme\_class\_superfamily

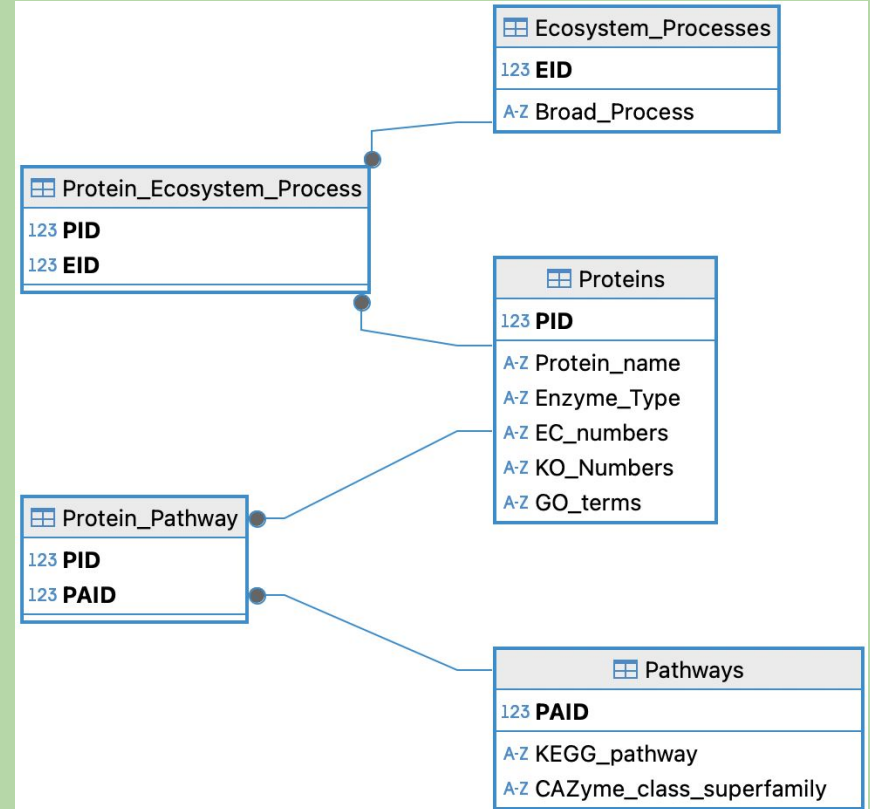
## Ecosystem\_Processes

EID → Broad\_Process

## Links

Protein\_Pathway (PID ↔ PAID) (many-to-many)

Protein\_Ecosystem\_Process (PID ↔ EID)



# Sample SQL Queries

-- 1) Search by protein name ("oxidase") and return full annotation

```
SELECT
  p.Protein_name,
  p.Enzyme_Type,
  p.EC_numbers,
  p.KO_Numbers,
  p.GO_terms,
  GROUP_CONCAT(DISTINCT pw.KEGG_pathway) AS Pathways,
  GROUP_CONCAT(DISTINCT ep.Broad_Process) AS Ecosystem_Processes
FROM Proteins p
LEFT JOIN Protein_Pathway pp ON p.PID = pp.PID
LEFT JOIN Pathways pw ON pp.PAID = pw.PAID
LEFT JOIN Protein_Ecosystem_Process pep ON p.PID = pep.PID
LEFT JOIN Ecosystem_Processes ep ON pep.EID = ep.EID
WHERE p.Protein_name LIKE '%oxidase%'
GROUP BY p.PID
LIMIT 100;
```

-- 3) Combine protein name and KEGG pathway filter

```
SELECT
  p.Protein_name,
  GROUP_CONCAT(DISTINCT pw.KEGG_pathway) AS Pathways
FROM Proteins p
JOIN Protein_Pathway pp ON p.PID = pp.PID
JOIN Pathways pw ON pp.PAID = pw.PAID
WHERE p.Protein_name LIKE '%oxidase%'
      AND pw.KEGG_pathway = '00010' -- Glycolysis / Gluconeogenesis
GROUP BY p.PID;
```

-- 2) Filter by EC number (e.g. "3.2.1.14")

```
SELECT
  p.Protein_name,
  p.Enzyme_Type,
  p.EC_numbers
FROM Proteins p
WHERE p.EC_numbers LIKE '%3.2.1.14%'
LIMIT 100;
```

# WEB INTERFACE



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Protein	Enzyme Type	EC #	KO #	GO term	KEGG
<input type="text" value="e.g. oxidase"/>	<input type="text" value="oxidase"/>	<input type="text" value="1.14"/>	<input type="text" value="e.g. K00844"/>	<input type="text" value="e.g. GO:0004672"/>	<input type="text" value="e.g. map00010"/>
<input type="button" value="Reset Filters"/>					

## Results

Protein Name	Enzyme Type	EC Numbers	KO Numbers	GO Terms	KEGG Pathways	Ecosystem Processes
Lignin peroxidase	Peroxidase	1.11.1.14				<a href="#">Soil C cycling; Soil N cycling</a> <a href="#">Soil N cycling</a>
Cytochrome P450	Polyphenol oxidase	1.14.14.1	K00490; K07408; K07409; K07410; K07411; K07412; K07413; K07414; K07416; K07418; K07420; K07424; K074	<a href="https://www.ebi.ac.uk/QuickGO/term/GO:0016682">https://www.ebi.ac.uk/QuickGO/term/GO:0016682</a>	<a href="https://www.kegg.jp/entry/K00490">https://www.kegg.jp/entry/K00490</a>	<a href="#">Soil C cycling; Soil N cycling</a>
Mono-oxygenase	Polyphenol oxidase	1.14.18	K00506		<a href="https://www.kegg.jp/entry/K00506">https://www.kegg.jp/entry/K00506</a>	<a href="#">Soil C cycling; Soil N cycling</a>

# PATHWAY MAPS

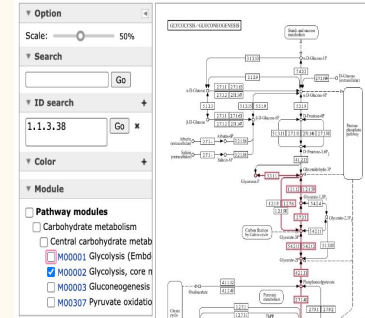
## Pathway Maps

### Glycolysis / Gluconeogenesis

#### KEGG Glycolysis / Gluconeogenesis - Reference pathway

[ Pathway menu | Organism group | Pathway entry | Show description | Download | Help ]

Change pathway type

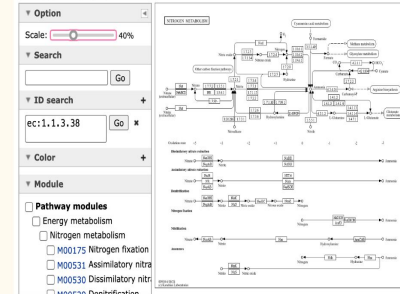


### Nitrogen metabolism

#### KEGG Nitrogen metabolism - Reference pathway

[ Pathway menu | Organism group | Pathway entry | Show description | Download | Help ]

Change pathway type

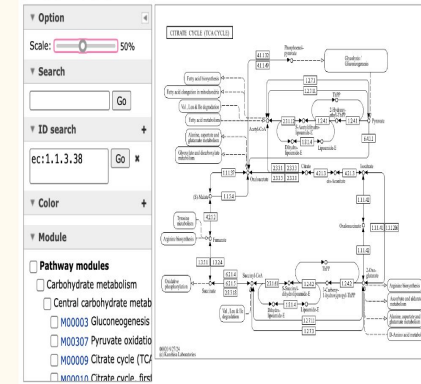


### TCA cycle

#### KEGG Citrate cycle (TCA cycle) - Reference pathway

[ Pathway menu | Organism group | Pathway entry | Show description | Download | Help ]

Change pathway type



# QUERY BASED DATA DOWNLOAD



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## Download Your Data

Export the current view (including any filters) as CSV or Excel:

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Download XLSX

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## Get in Touch

Have a suggestion, new dataset, or improvement for Root Omics? Fill out the form below and Dr. Jenny will get back to you.

Your Name

Your Email

Message

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## ? Help Center

*Quick tips to get the most out of Root Omics:*

### Filter Data

Enter text in any search field and click [Search](#).

### Reset Filters

Click [Reset](#) to clear all fields.

### Explore Links

Click any [Pathway](#) or [GO term](#) to jump to the external detail page.

### Download Data

Head to the [Download](#) tab to export your filtered results as CSV or Excel.

### Need More Help?

Use the [Contact](#) tab to send us your questions or suggestions.

**Thank You!!!**