

## Input Types

Two searches are possible: 1) a name/text based search that can include protein name, and taxon, protein family (PFAM) number or description, or other community id 2) a sequence based search where the user pastes their protein or peptide sequence into the search box.

## Results

### Where is my protein in the oceans?

Searches can be filtered by geography, time, depth, or cruise, and the results are presented in map and tabular form.

### Who does my protein belong to?

Taxonomic assignments of peptides can be determined using existing software capabilities of METATRYP. A standalone web application for METATRYP is also now being developed based on workshop feedback and interest.

### How much is Present?

The user can select specific peptide components of a protein of interest to determine the number of stations with this protein and the total protein spectral counts.

### 1. Name/Text

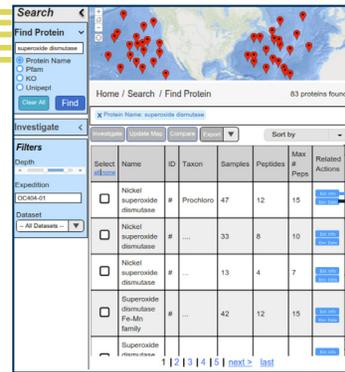
Protein Name, EC, KC, PFAM, Unipeptide

Protein ID #



### Filters

- Geography
- Depth
- Time
- Cruise



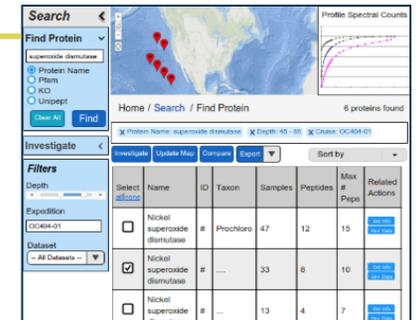
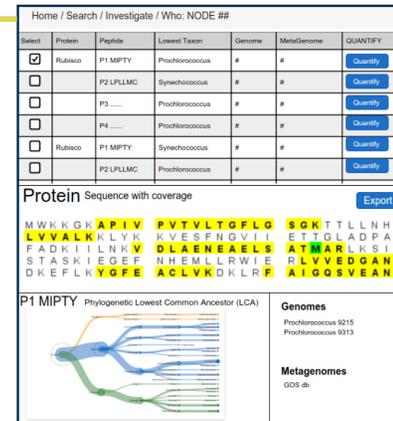
Because many organisms contain similar proteins, the user can select from the tabular results to narrow the number of proteins by examining its peptide constituents (unit of measurement).

### 2. Sequence

Protein Sequence

Peptide Sequence

Digest proteins



External links are provided from protein results such as 3D structure (Protein Bank) and related environmental datasets (BCO-DMO).



This work is funded by the National Science Foundation Award 1639714