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.

**Input Types**
- **1. Name/Text**
  - Protein Name, EC, KC, PFAM, Unipeptide
  - Protein ID #

- **2. Sequence**
  - Protein Sequence
  - Peptide Sequence

**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.

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).

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

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