Incorporating Community Annotation Interfaces into the CIPRO2.5 Database with Comprehensible Sketches to Support Quick Annotations of Proteome Data.

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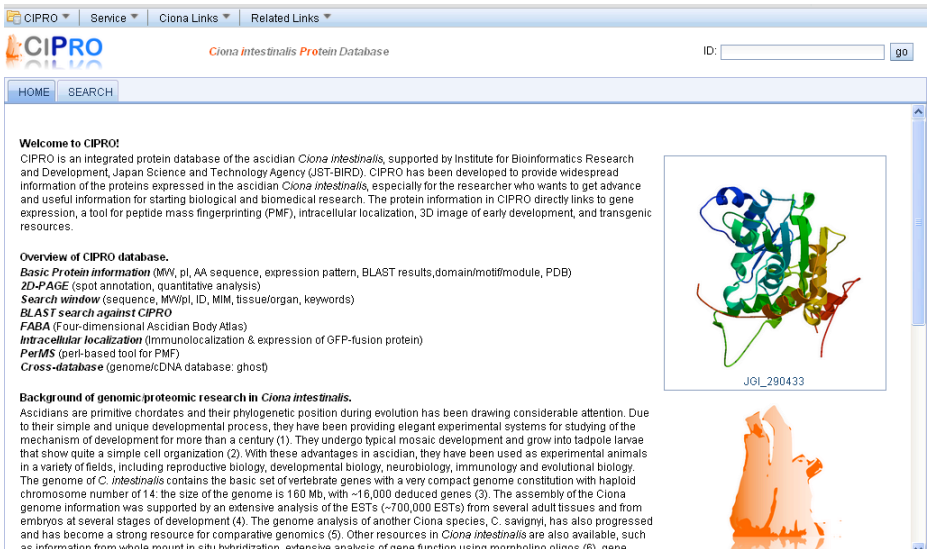
The system for wet laboratory workers is the goal of *Ciona intestinalis* protein database (CIPRO)

- To improve usability for experimental ascidian researchers
- To give feedback to the ascidian researchers
- To facilitate interactions with other researchers concerned with developmental biology, evolutionary biology and human diseases



Biological database requires several basic functionalities

- To evaluate reliability, to keep quality, and to provide timely information
- To reduce redundancy and to synchronize cross-references
- To lead toward desired information by using retrieval systems and providing reticulated links rather than ordinary hierarchical links

Community websites & community annotation become the next standard for data resources?

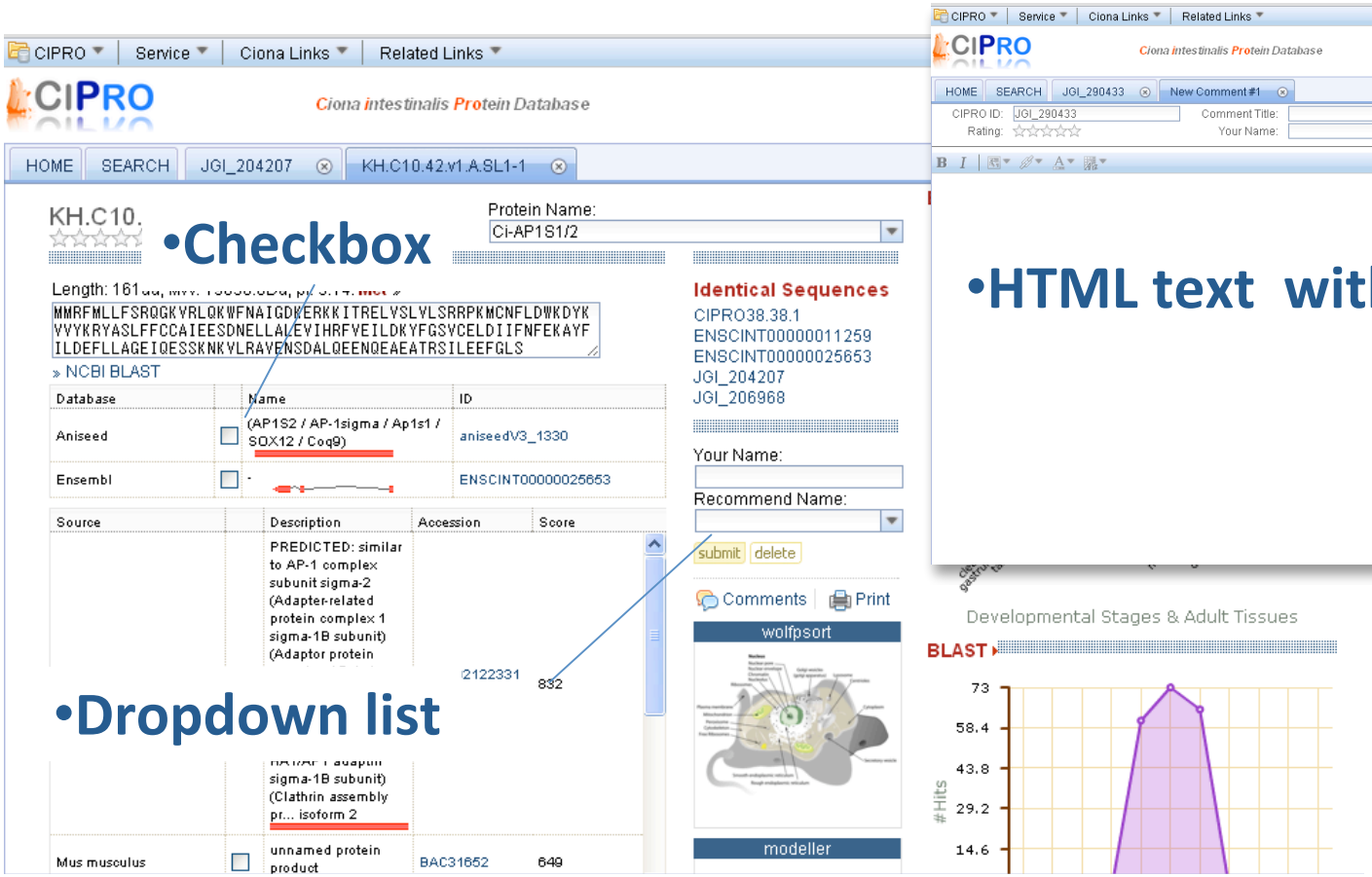
- Social network sites have grown in importance globally
- Wikipedia is also a successful example. However, the reliability of descriptions is controversial
- The community annotation among experts is ideal

Incorporating three new functions into CIPRO2.5 database

- Formatted web forms & a free comment editor
- Comprehensible sketches
- Retrieval systems including combined fields

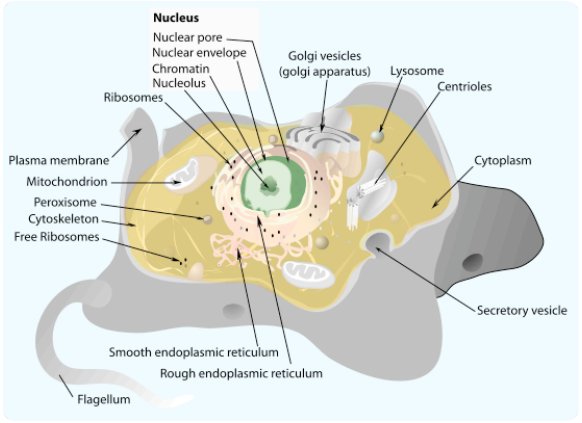
Two types of annotation interfaces make up for each other's deficiencies

- Web form
- Comment editor

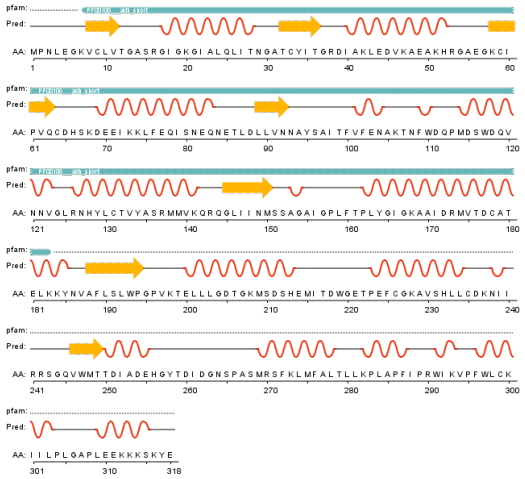


Comprehensible sketches were designed to be compact for quickly understandable overview

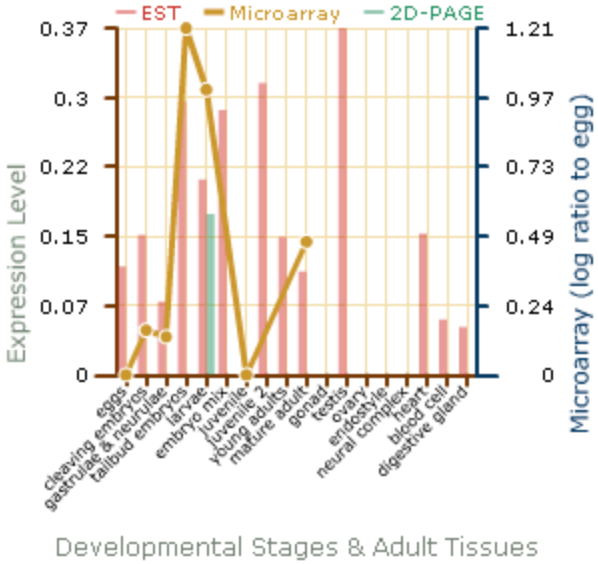
Cytolocalization



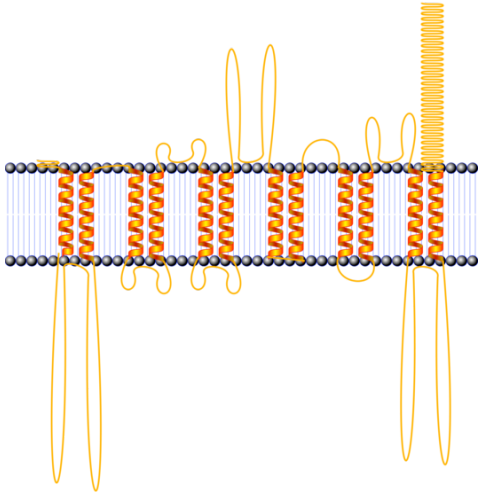
Sequence & motifs



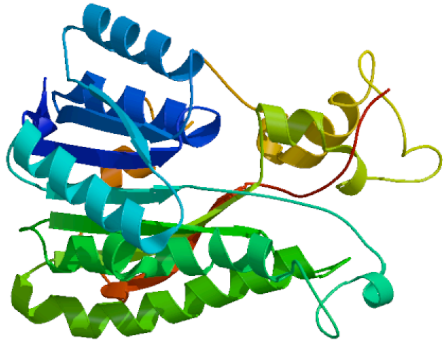
Expression data



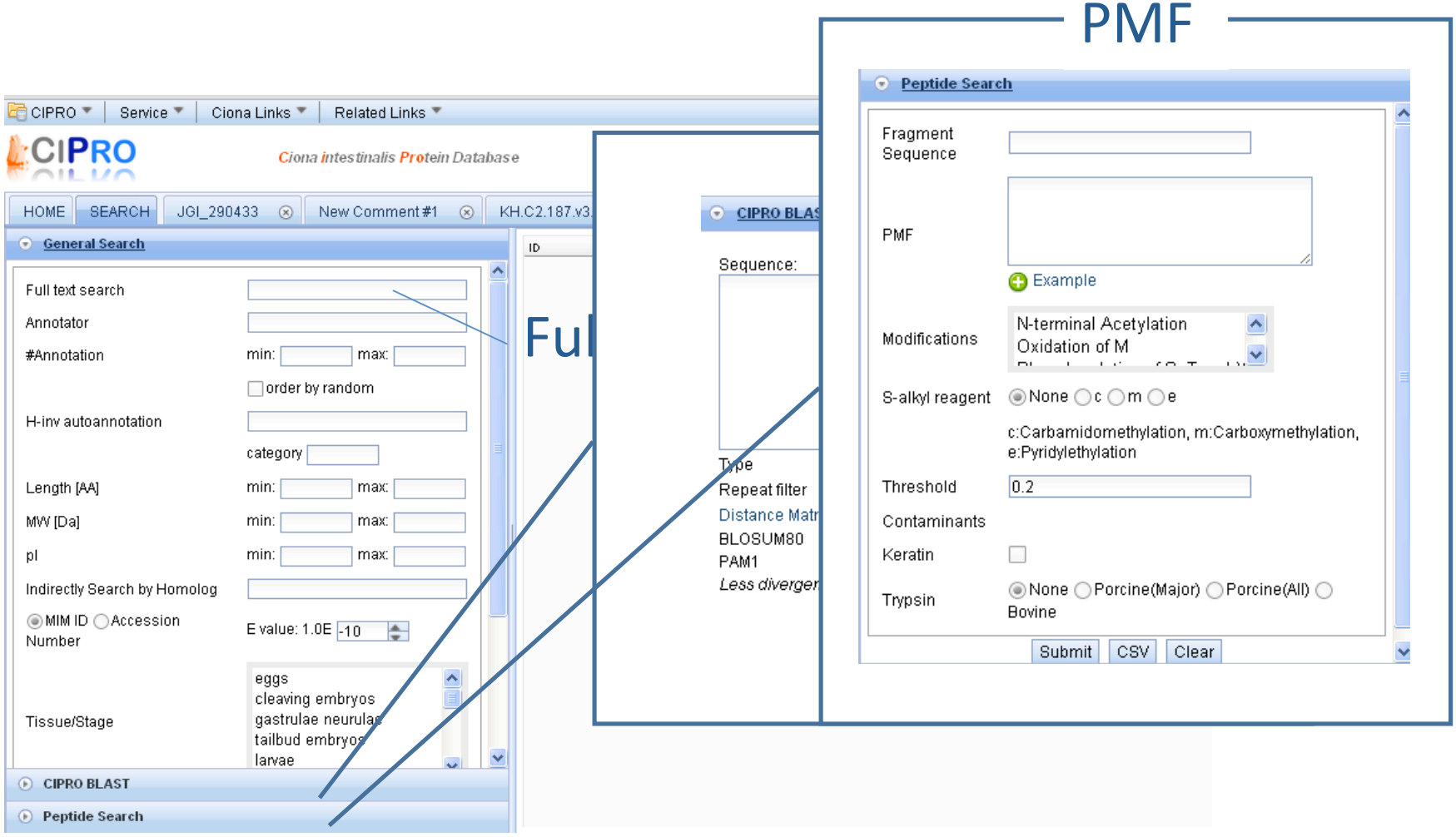
TM prediction



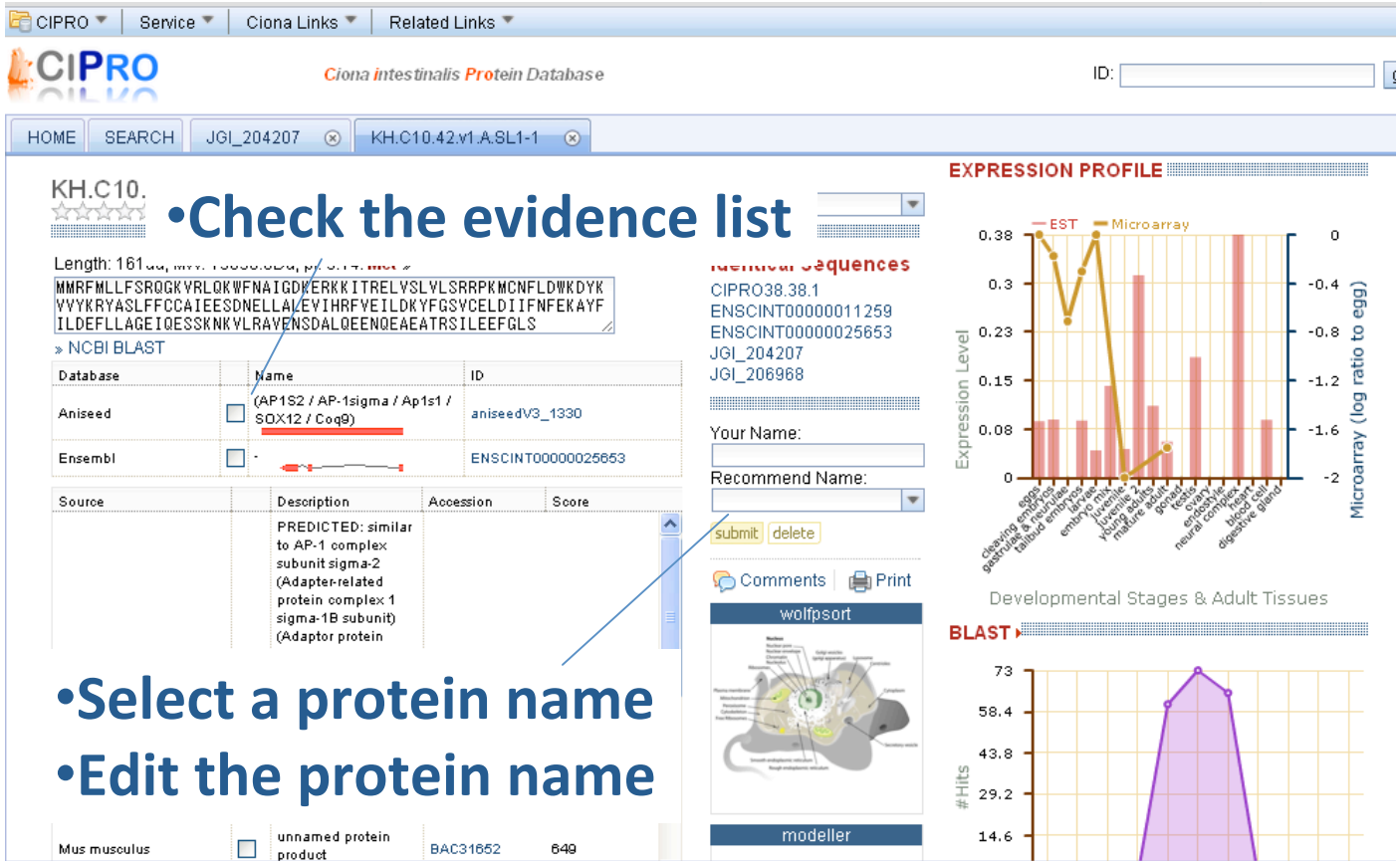
Homology model



Retrieval system with combined fields is useful for searching a familiar protein and its neighbors



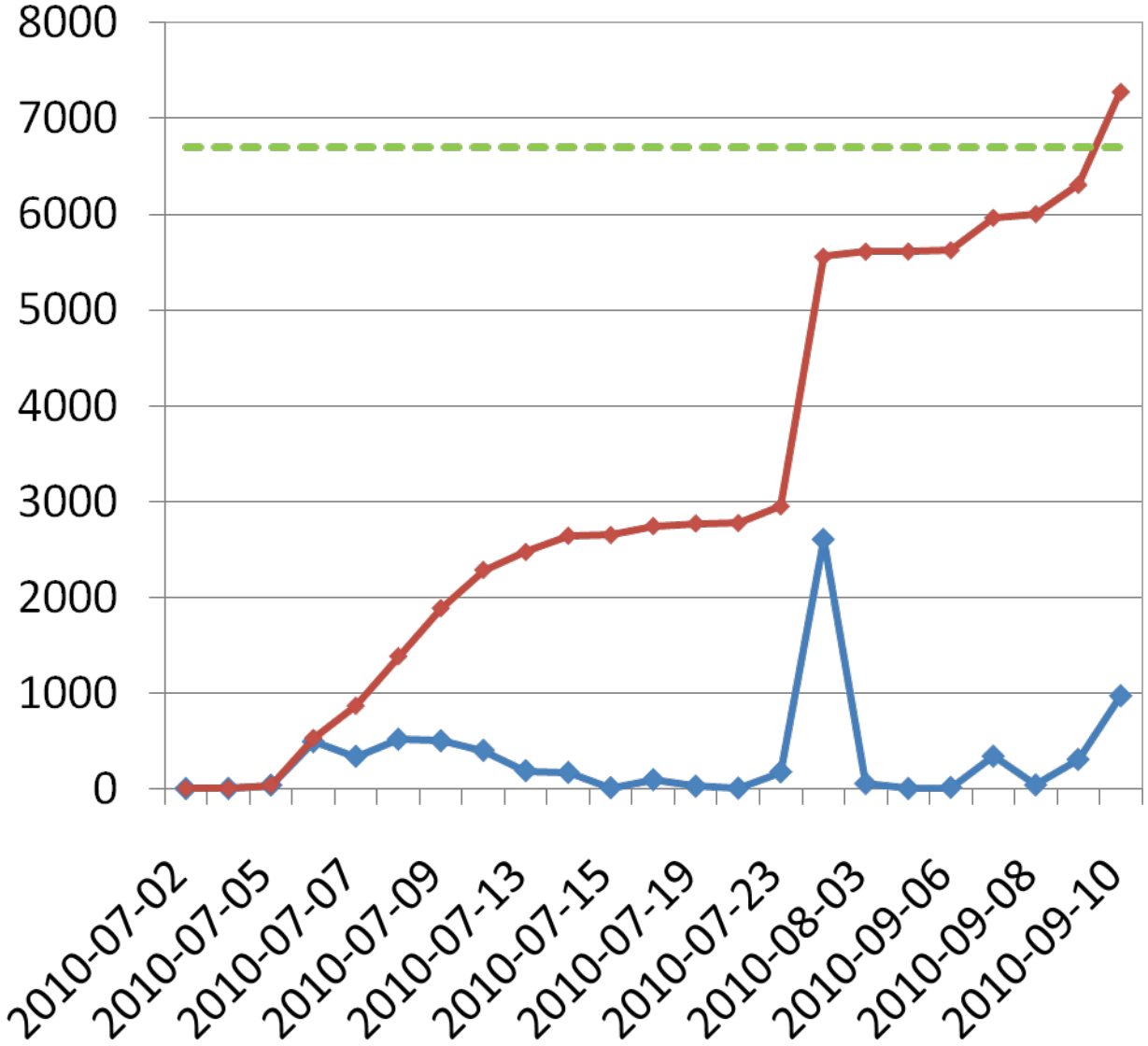
Case study: annotation of protein names by using web forms



How to decide explicit formalism against implicit criteria

- **Class I**: ≥50% identity, ≥ 50% coverage
  - HOMOLOGOUS TO
- **Class II**: ≥ 25% identity
  - SIMILAR TO
- **Class III**: Found a motif or domain in databases
  - XXX domain containing proteins
- **Class IV**: Predicted proteins with evolutionary conservation
  - Conserved hypothetical proteins
- **Class V**: Predicted proteins longer than or equal to 80 aa
  - Hypothetical proteins
- **Class VI**: Predicted proteins shorter than 80 aa
  - Hypothetical short proteins

Results: Comparison of the annotation of protein names with previous annotation



This time

- ~ 10 days
- ~ 10 people
- Total #7,282

Previous annotation

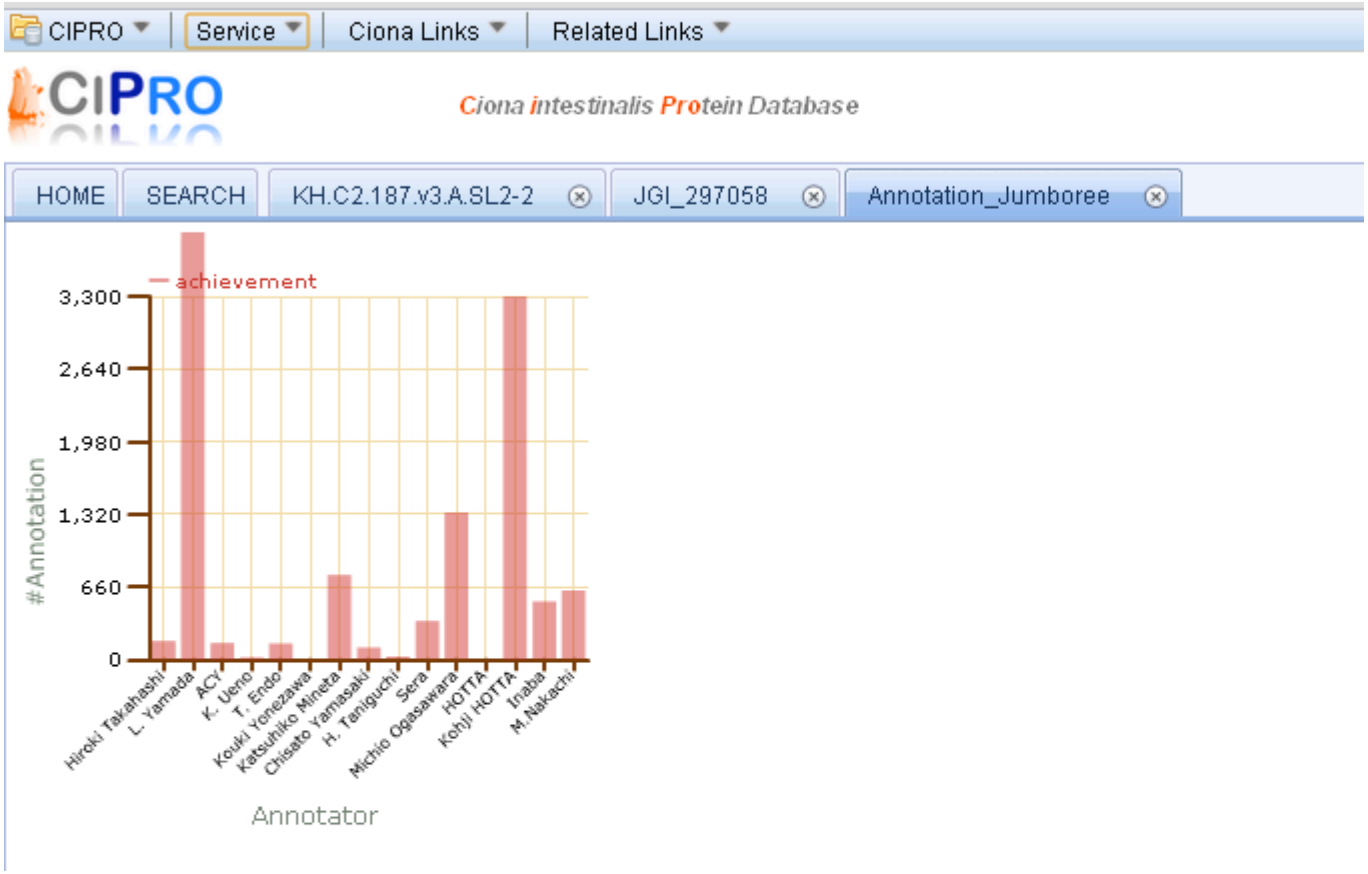
- 1 year ~
- 1 person
- Total #6,697

Flexible descriptions were essentially inescapable

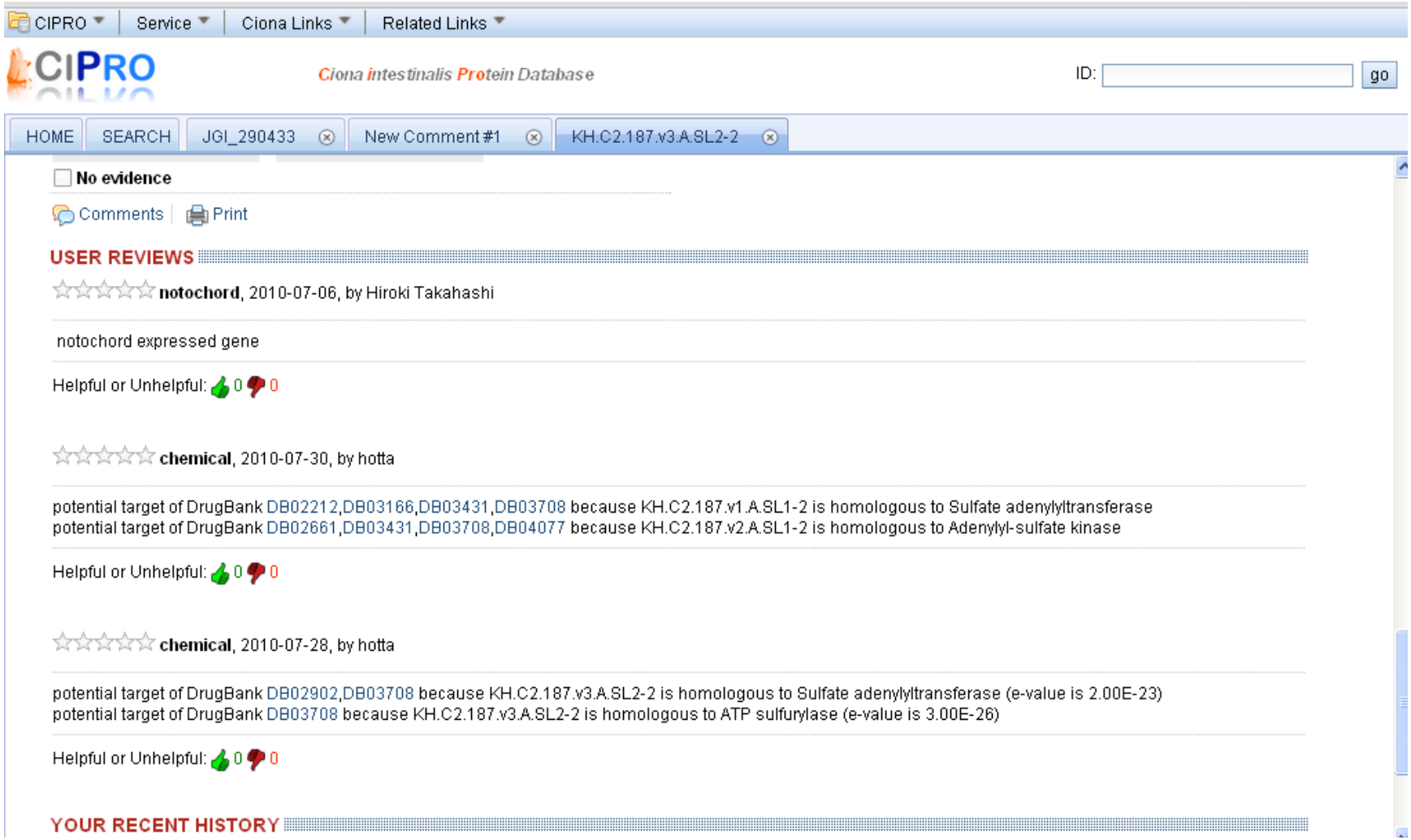
- poly(A)
- poly-A
- polyadenylation

- Dehydrogenase/reductase SDR family member, short-chain dehydrogenase/reductase
- Dehydrogenase-reductase SDR family member 11

Simple chart provided an incentive



An example of useful comments by using the comment editor



Summary

- The annotation of protein names were assisted by using formatted web forms .
- Additional information such as chemical targets were also provided by using the user comment editor.
- These annotated data are freely accessible at the CIPRO2.5 web site

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