BURNHAM INSTITUTE for MEDICAL RESEARCH

From Research, the Power to Cure

JAFA

a protein function prediction meta-server

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FH BINGEN

Life Sciences and Engineering

Start a new session

To start a new JAFA Session, enter a protein sequence in the text field below. The following servers will be queried using default values. To change these values, click on the **[+]** sign next to the server you want to change values. Have fun.

☑ Include **GOblet** using user defined values **[+]** < 5 min

☑ Include **GOfigure** using default values **[+]** < 5 min

☑ Include **GOtcha** using default values **[+]** < 5 min

☑ Include **InterProScan** using default values **[+]** < 5 min

☐ Include **Phydbac** using default values *(Sorry, nothing to configure here)* 5-15 min

Common:
* Email:
Title:
* Sequence (FASTA format, or sequence only): Only protein sequences for now
Upload FASTA File: Durchsuchen...
* mandatory

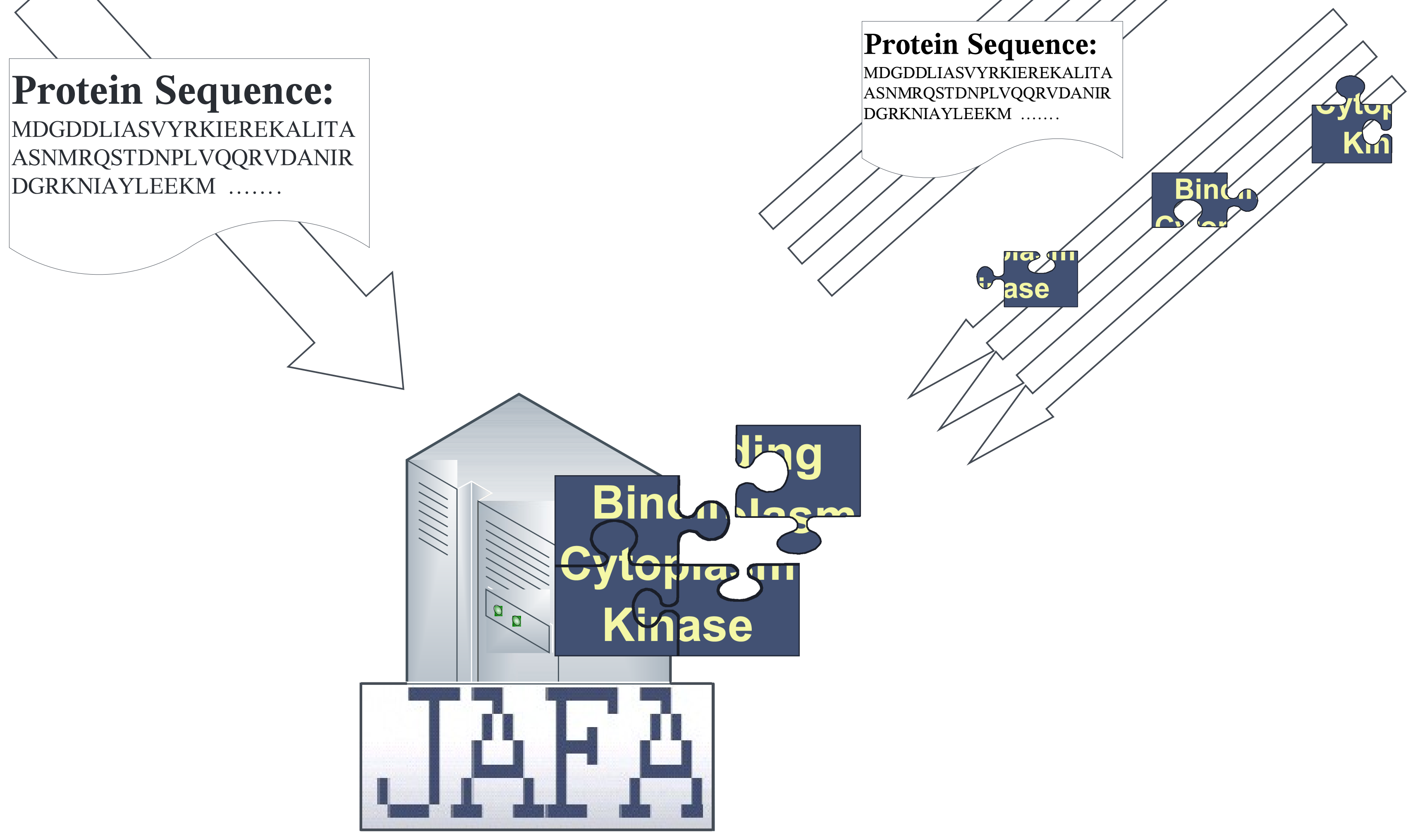
reset form | send request

JAFA Input:

- Enter a query sequence
- All parameters can be adjusted to the query

JAFA Run

- Query remote servers, wait for them to finish, receive results.
- Interim result are available, as soon as they are received
- Currently queried servers: Gotcha[3], Goblet[4], GoFigure[5], InterproScan[6], Phydbac[7]



Protein Sequence:
MDGDDLIASVYRKIEREKALITA
ASNMRQSTDNPLVQQRVDANIR
DGRKNIAYLEEKM …….

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Function Prediction is difficult …

- Biological function has different aspects: what happens, where in the cell, which process does this function belong to.
- Each method / program has it own strengths in predicting one or the other.

… but many different pieces build a picture.

- Combining the prediction of different methods / programs can provide a better understanding of the proteins function.
- Differences in each prediction lead to a broader over all picture
- Similar or identical predictions by different programs increase prediction confidence

Future Plans:

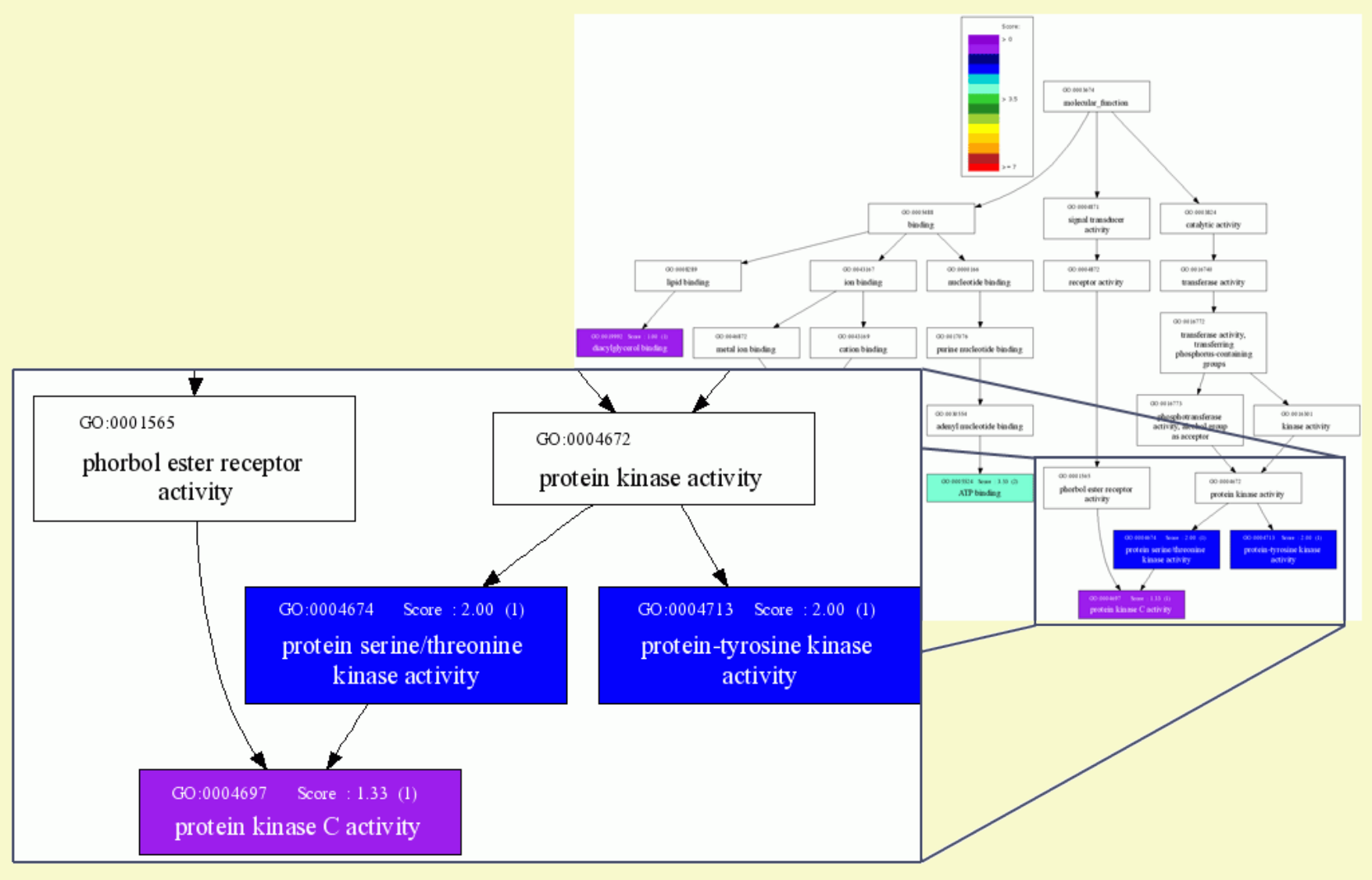
- A standalone version of JAFA, for use in high throughput research
- Create a standardized XML protocol for reporting function predictions
- Analysis of the different prediction programs capabilities will lead us to better overall predictions
- Improve scoring function to weight different programs based on known strengths and weaknesses

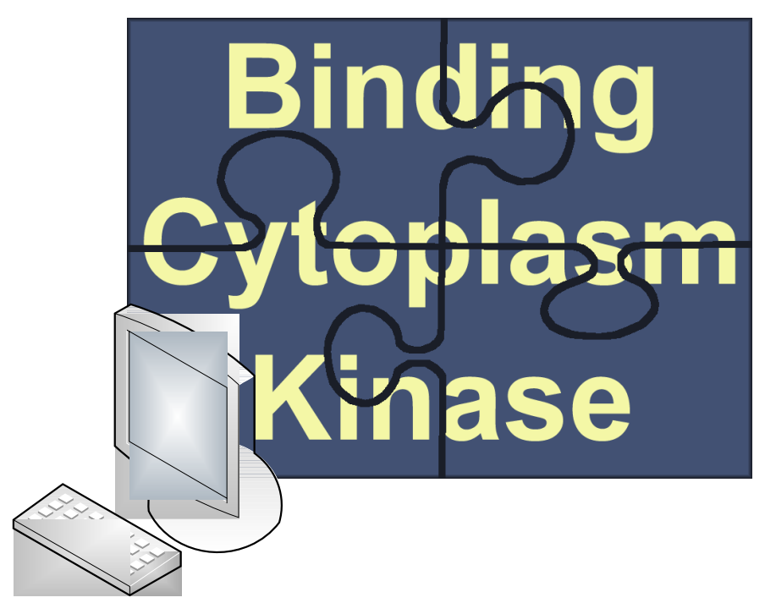
Gene Ontology (GO):

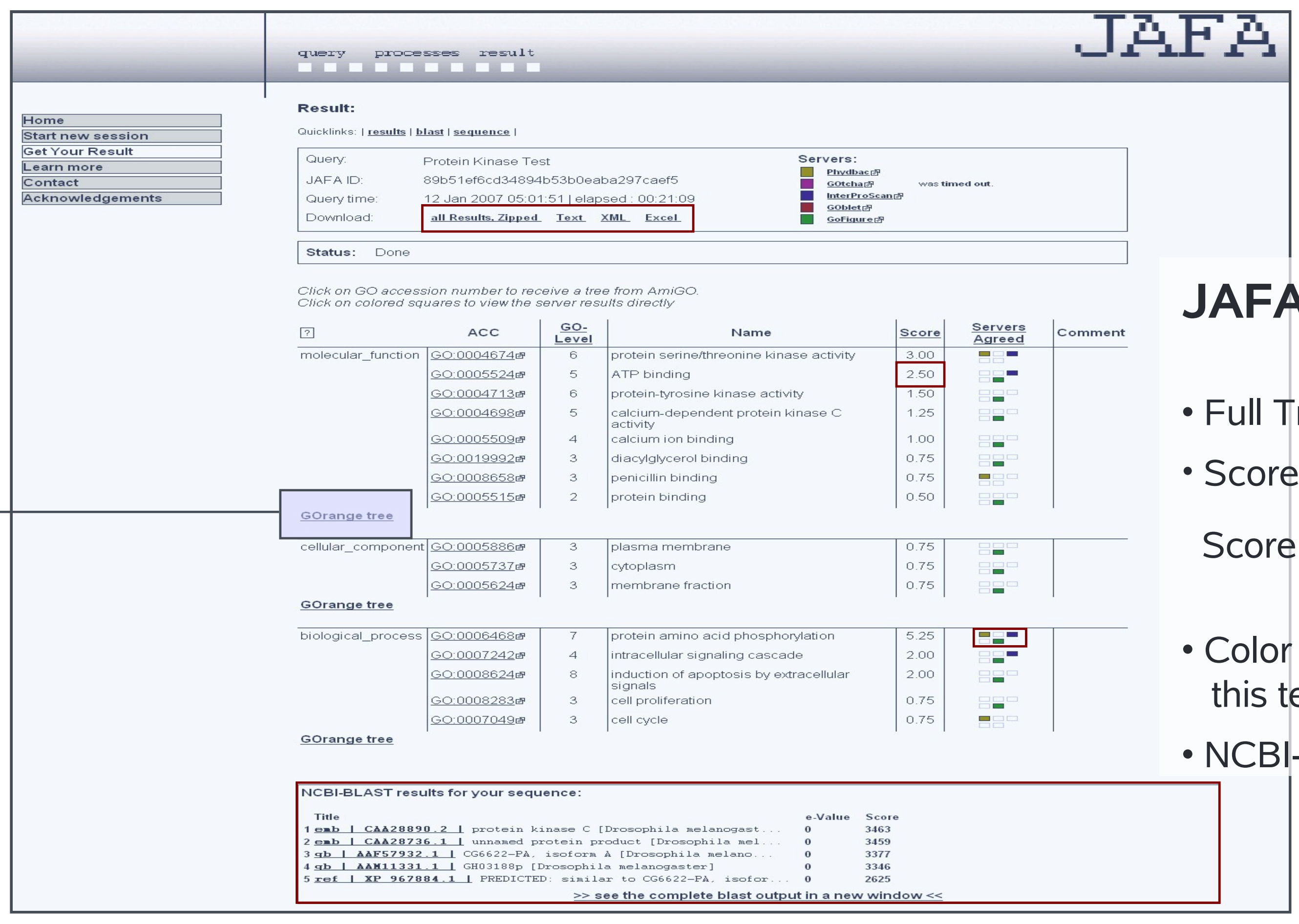
- Controlled vocabulary for the description of genes and gene product attributes
- Hierarchical: general to specific
- Different functional aspects: Biological Process, Molecular Function and Cellular Component
- http://www.geneontology.org [2]

JAFA - GOrange Tree:

- Predicted GO terms displayed hierarchically. Prediction confidence is color coded







Result:

Quicklinks: | results | blast | sequence |

Query: Protein Kinase Test
JAFA ID: 89b51ef6cd34894b53b0eaba297caef5
Query time: 12 Jan 2007 05:01:51 | elapsed : 00:21:09
Download: all Results, Zipped Text XML Excel

Servers:
🟨 Phydbac
🟪 GOtcha was timed out.
🟦 InterProScan
🟥 GOblet
🟩 GoFigure

Status: Done

Click on GO accession number to receive a tree from AmiGO.
Click on colored squares to view the server results directly

?	ACC	GO-Level	Name	Score	Servers Agreed	Comment
molecular_function	GO:0004674	6	protein serine/threonine kinase activity	3.00		
	GO:0005524	5	ATP binding	2.50		
	GO:0004713	6	protein-tyrosine kinase activity	1.50		
	GO:0004698	5	calcium-dependent protein kinase C activity	1.25		
	GO:0005509	4	calcium ion binding	1.00		
	GO:0019992	3	diacylglycerol binding	0.75		
	GO:0008658	3	penicillin binding	0.75		
	GO:0005515	2	protein binding	0.50		
cellular_component	GO:0005886	3	plasma membrane	0.75		
	GO:0005737	3	cytoplasm	0.75		
	GO:0005624	3	membrane fraction	0.75		
biological_process	GO:0006468	7	protein amino acid phosphorylation	5.25		
	GO:0007242	4	intracellular signaling cascade	2.00		
	GO:0008624	8	induction of apoptosis by extracellular signals	2.00		
	GO:0008283	3	cell proliferation	0.75		
	GO:0007049	3	cell cycle	0.75		

NCBI-BLAST results for your sequence:

```
  Title                                                          e-Value  Score
1 emb | CAA28890.2 |  protein kinase C [Drosophila melanogast...   0       3463
2 emb | CAA28736.1 |  unnamed protein product [Drosophila mel...  0       3459
3 gb | AAF57932.1 |  CG6622-PA, isoform A [Drosophila melano...    0       3377
4 gb | AAM11331.1 |  GH03188p [Drosophila melanogaster]           0       3346
5 ref | XP 967884.1 |  PREDICTED: similar to CG6622-PA, isofor... 0       2625
```

>> see the complete blast output in a new window <<

JAFA Results

- Full Traceback Information downloadable
- Scored GO Terms

$$\text{Score} = \frac{\text{number of predicting programs} \times \text{GO level}}{\text{total number of programs}}$$

- Color indication which server predicted this term
- NCBI-Blast [8] Run Results

Online:

JAFA is available online at **http://jafa.burnham.org**
Contact: **jafateam@gmail.com**

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ISCB INTERNATIONAL SOCIETY FOR COMPUTATIONAL BIOLOGY

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http://jafa.burnham.org