

# An Insight into the Functional Annotation of *Kaupichthys*

## *hyproroides*

Kenneth Rosario, Heba Shaaban, and Shaadi Mehr

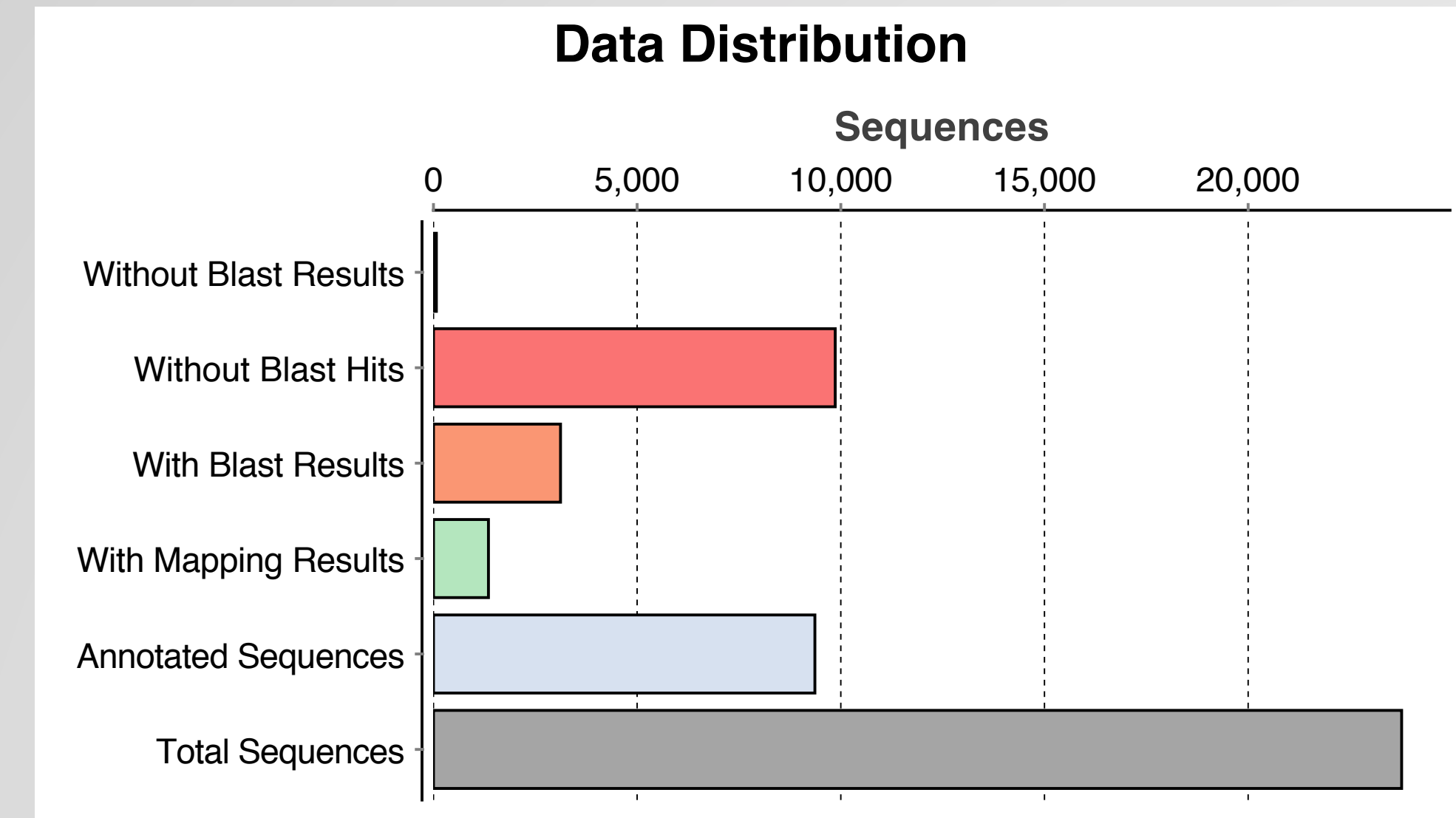
### Abstract

The false moray eel, categorized under the family of *Chlopsidae*, order *Anguilliformes*, is one of the most well-known eels, with over 100 species occupying tropical oceans worldwide. The sample of this study was collected from the Cayman Islands. The application of the Next Generation Sequencing (NGS) method in generating the genomic sequences has led to a great expansion of genomic resources in NCBI. These resources are very useful tools in population genetic, phylogenetics, and novel transcript and protein identification. The present study reports, for the first time, the annotated transcriptome of *Kaupichthys hyproroides*. Our functional annotation analysis led to annotation of 9,000 sequences. Regulation, Integral to membrane, and ATP-binding were the most frequent observed functions. This annotated data will increase the protein content of NCBI for *Kaupichthys hyproroides* by a factor of 21,153% (from 52 proteins to 11,000 proteins).

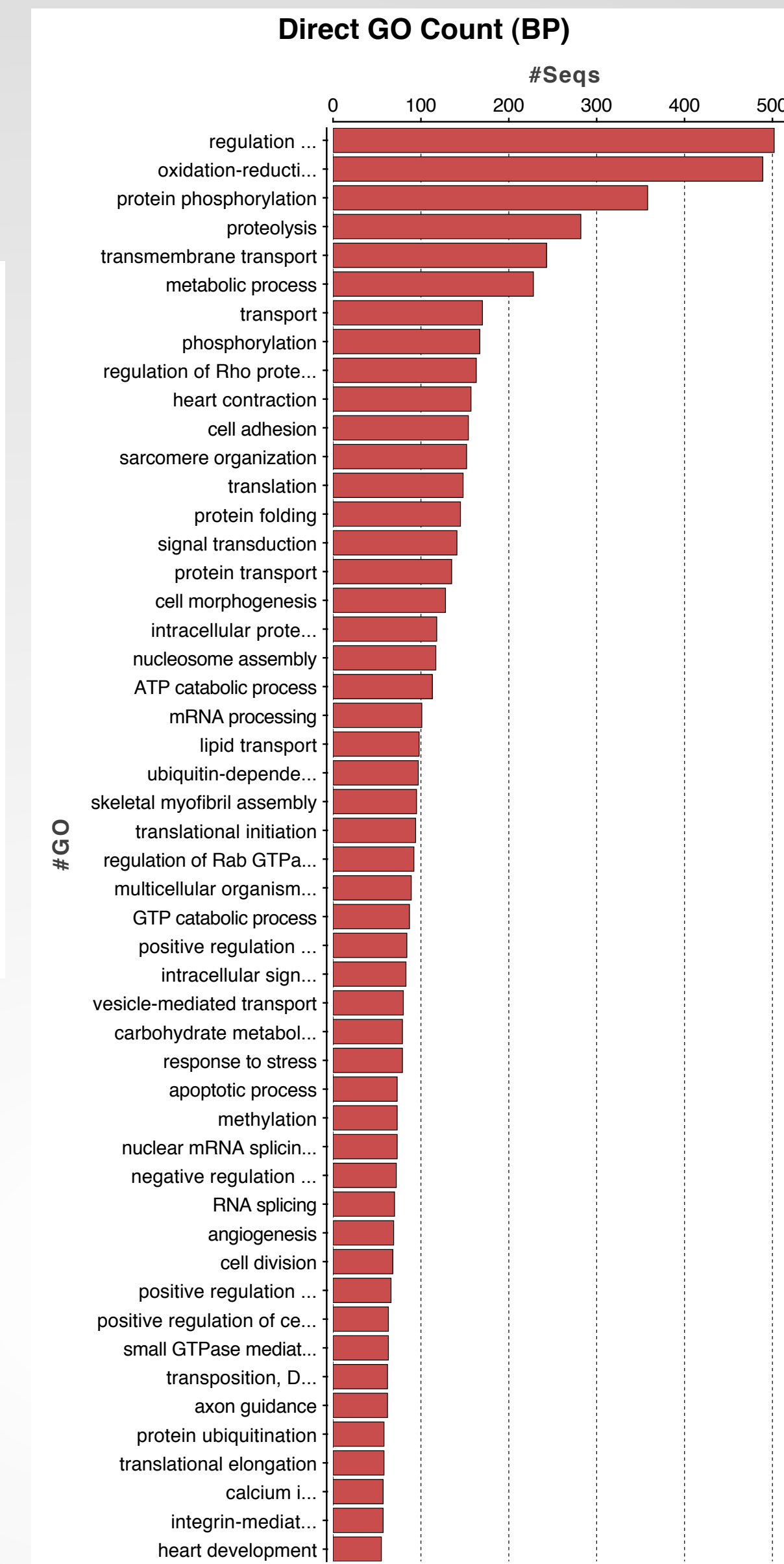
### Methods

- 1) Sample collection and RNA preparation
- 2) Illumina sequencing and quality control
- 3) De Novo Assembly
- 4) Similarity search and functional annotation were done by comparing the transcriptome sequences to all protein databank in NCBI, using BLAST2GO program.

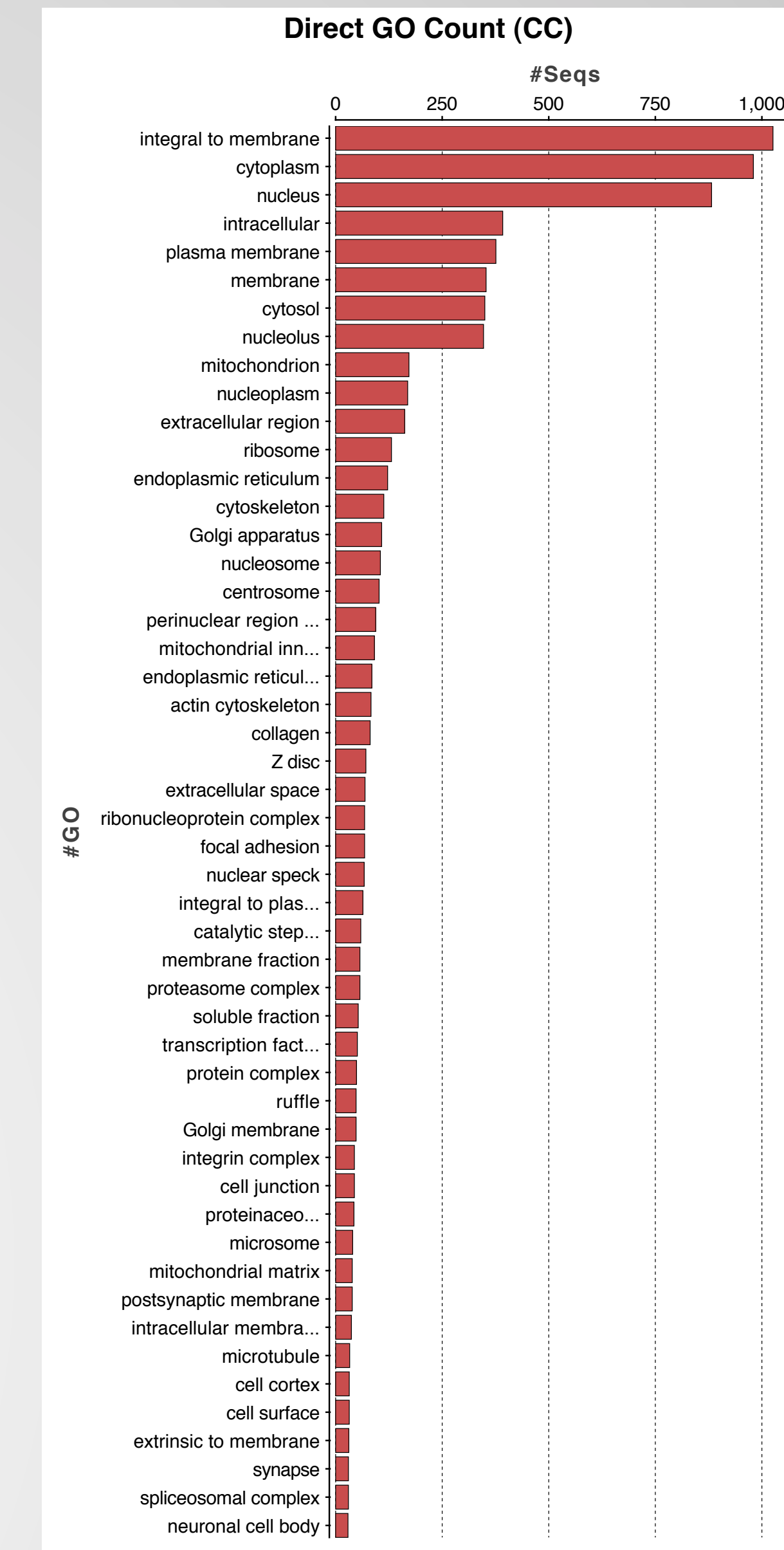
### Results



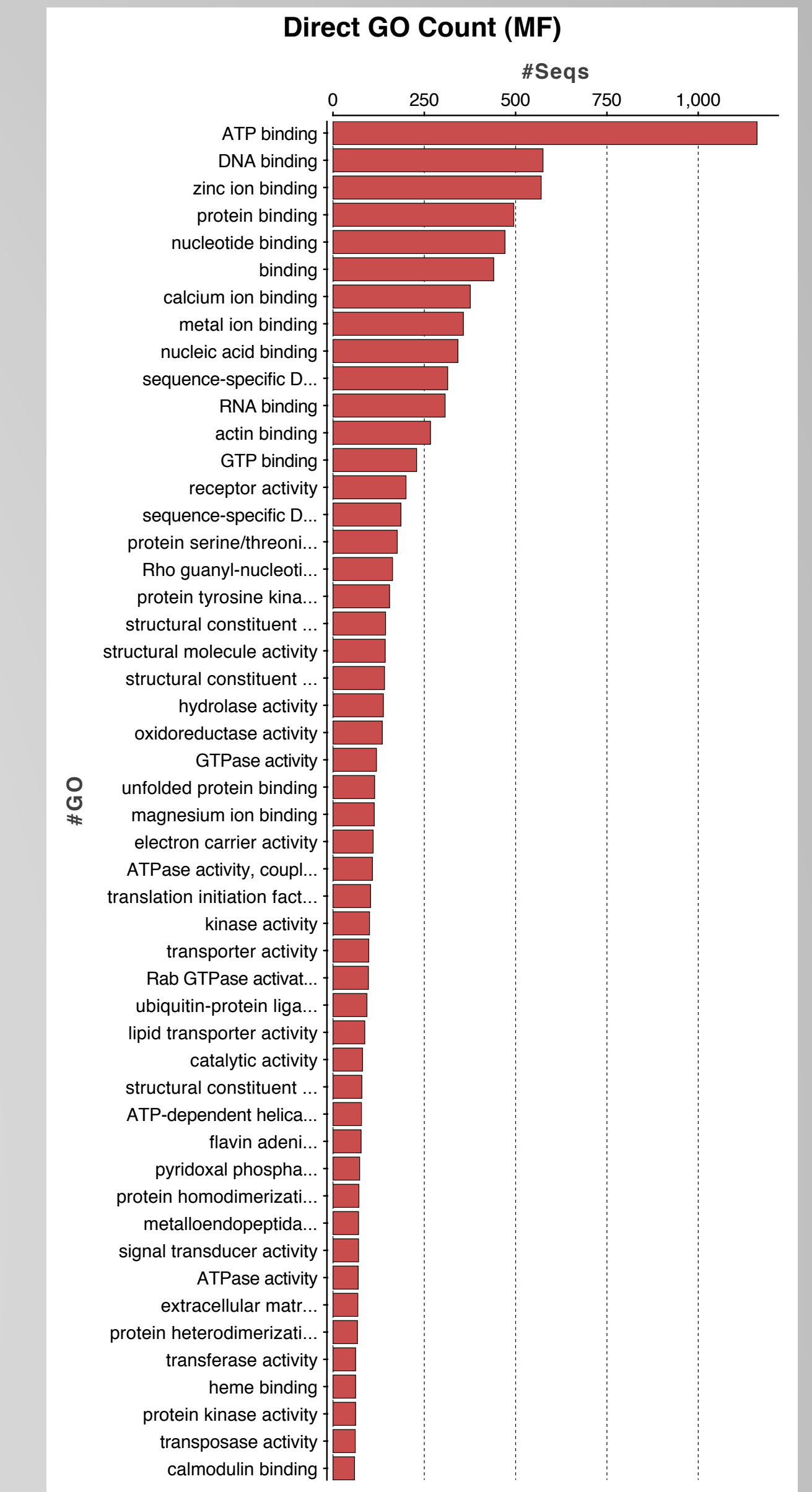
Out of a total of about 23,000 sequences, about 9,000 were functionally annotated.



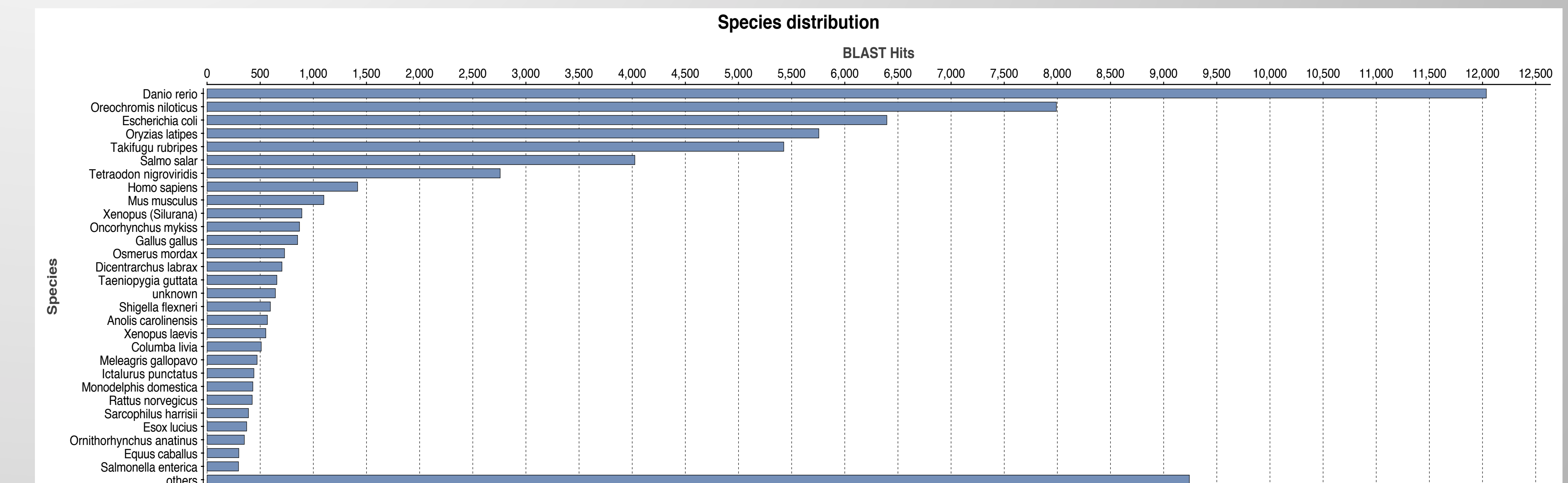
Among all biological processes and cell activities in GO categories, the frequency of regulation and oxidation-reduction was the highest with about 500 sequences.



Among the most frequent cellular components in GO categories, near 1000 sequences were annotated as integral to membrane, and less than 1000 sequences with cytoplasmic function.



Among molecular functions in Go categories the most frequently observed function was ATP-binding with 1,100 sequences.



According to the BLAST Hits, the *Danio rerio* fish has about 12,000 similar sequences with *Kaupichthys hyproroides*.

### Acknowledgements

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