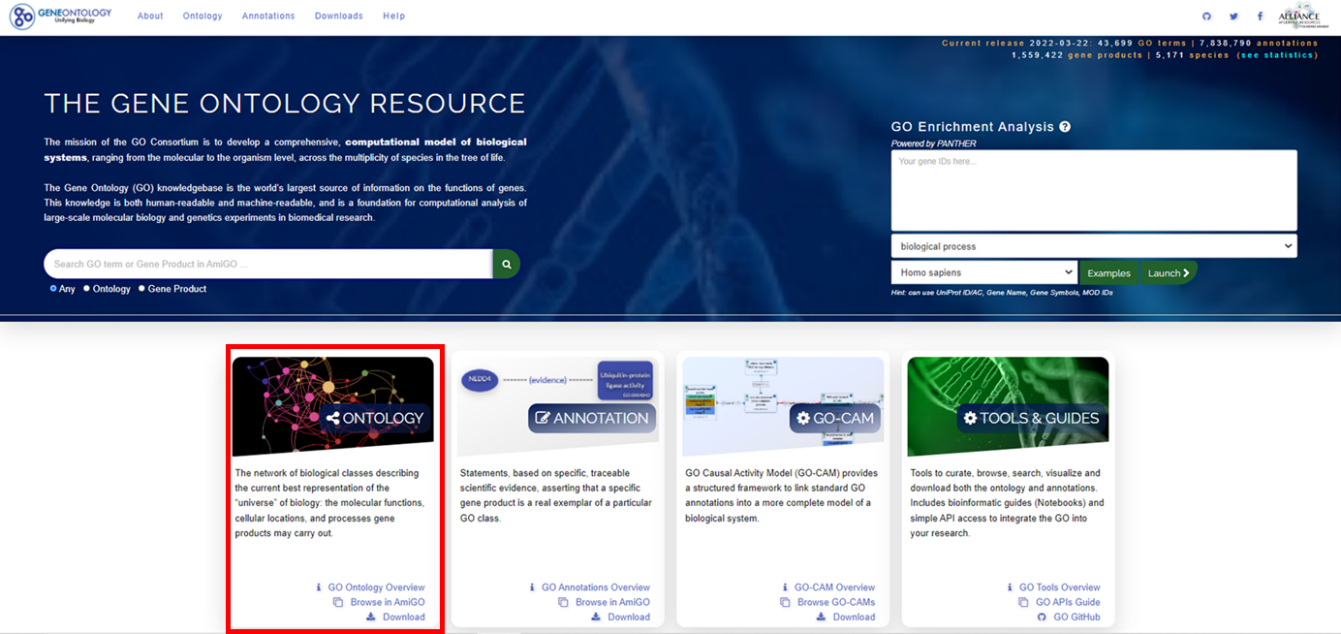
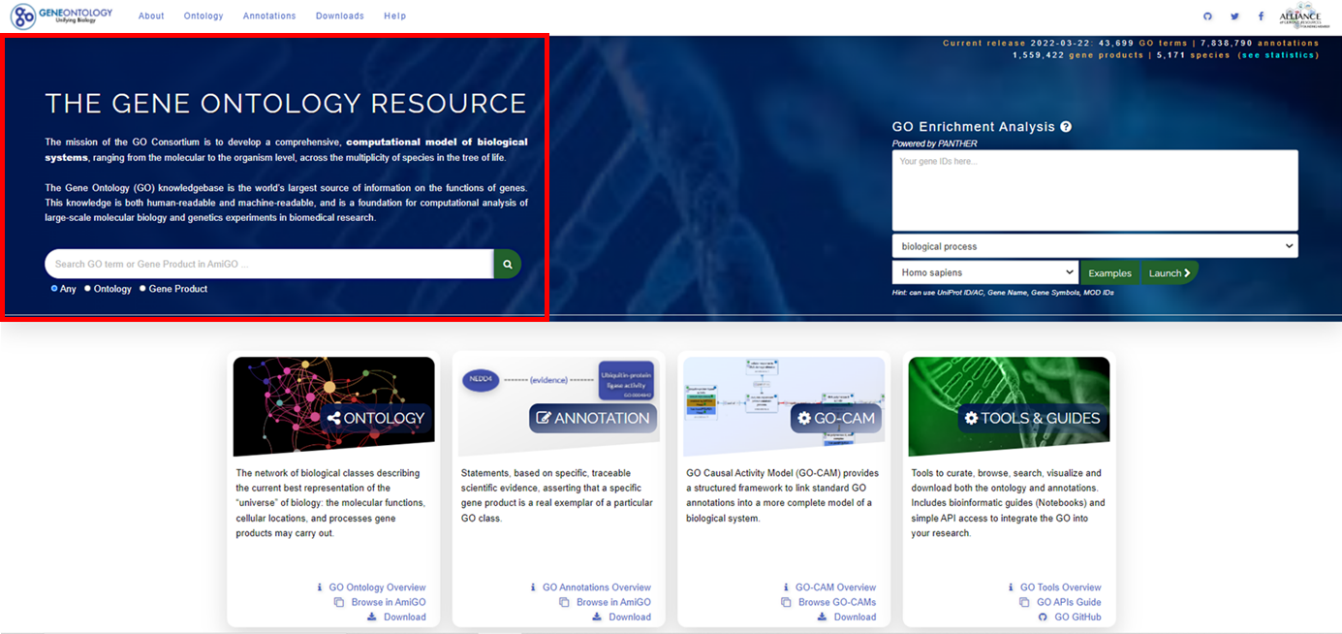
**A ontologia GO e algumas das suas aplicações**

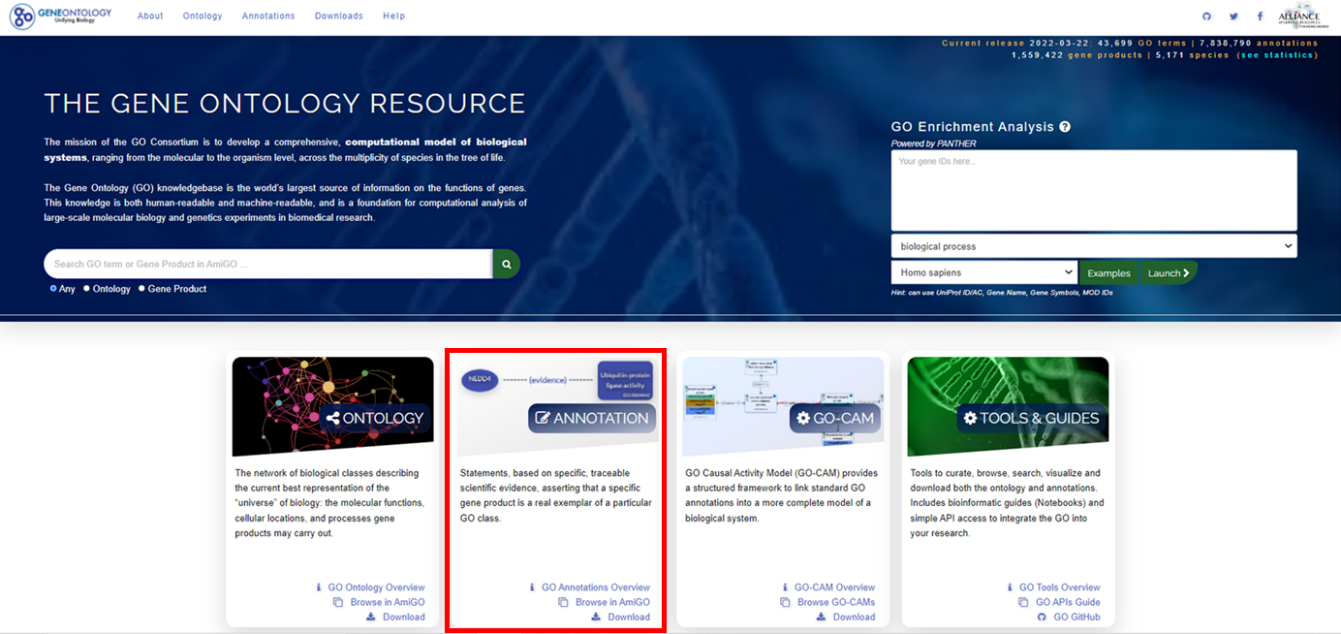
1. Explore a página <http://geneontology.org/>
   * 1. Em baixo, no primeiro painel, encontram uma visão global sobre o que é a ontologia GO ([Gene Ontology overview](http://geneontology.org/docs/ontology-documentation/)). Explorem e tentem esclarecer alguma dúvida com que tenham ficado da apresentação inicial.
     2. Utilizem a seguinte ligação [AmiGO 2: Drill-down Browser (geneontology.org)](http://amigo.geneontology.org/amigo/dd_browse) para ter uma visão da estrutura da ontologia GO.



* 1. No canto superior esquerdo, procurem por produtos génicos, ontologia ou ambos (experimentem por exemplo “**metabolism**”, “**SOD2**” ou outro palavra do vosso interesse). Observem o resultado de cada pesquisa. Para cada pesquisa qual é o número de resultados? Que informação está associada a:
     1. Termos GO (Termos GO, definição, ontologia, …)
     2. Genes/productos génicos (genes/produtos génicos, nome, organismo, …)
     3. Anotações (genes/produtos génicos, qualificador da anotação, …)



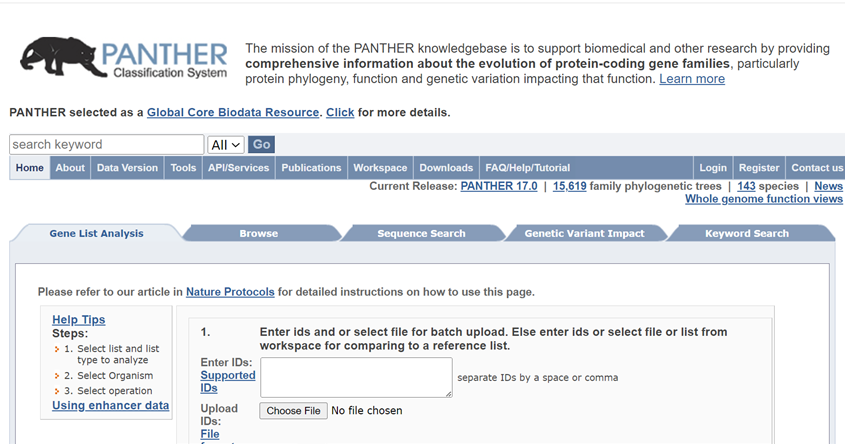
* 1. Em baixo, no segundo painel, encontram informação sobre como anotar genes/produto génicos (<http://geneontology.org/docs/go-annotations/>). Quantos tipos de categorias gerais de códigos de evidência GO existem?



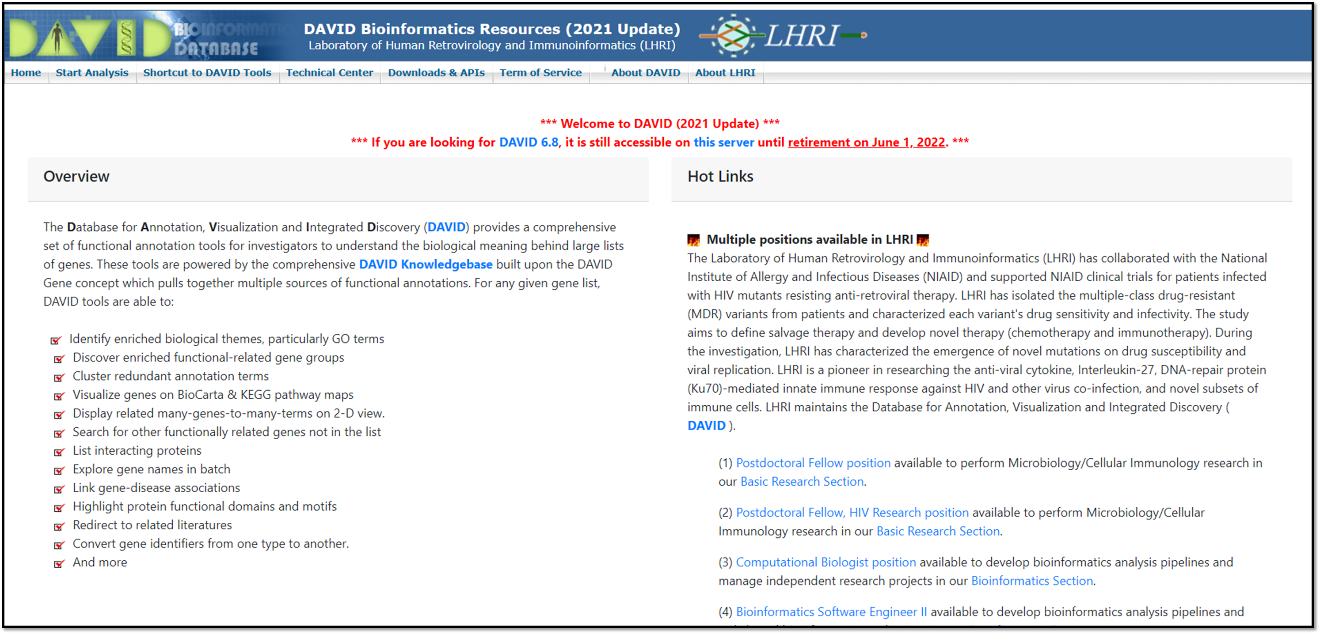
1. Pesquisem utilizando QuickGO (<https://www.ebi.ac.uk/QuickGO/>) por:
   1. os termos GO “hydrolase activity”, “cellular response to antibiotic” e “biofilm matrix” e identifiquem:
      1. a que ontologia GO pertencem
      2. a qual nível da respective ontologia estão
      3. quantos termos GO ancestrais directos têm
      4. quantos termos GO descendentes directos têm
   2. os genes/produtos génicos GSY2, TRX2, CTT1 e identifiquem:
      1. se há diferentes organismos com o mesmo gene/produto génico e se têm o mesmo de número de anotações.
2. Procedam à anotação GO, justificando a(s) anotação(ões), do gene *FPS1* da levedura *Saccharomyces cerevisae*. Este procedimento deve ser feito exclusivamente a partir da informação contida no sequinte resumo:

A metabolomic analysis using high resolution 1H NMR spectroscopy coupled with multivariate statistical analysis was used to characterize the alterations in the endo- and exo-metabolome of S. cerevisiae BY4741 during the exponential phase of growth in minimal medium supplemented with different ethanol concentrations (0, 2, 4 and 6% v/v). This study provides evidence that supports the notion that ethanol stress induces reductive stress in yeast cells, which, in turn, appears to be counteracted by the increase in the rate of NAD+ regenerating bioreactions. Metabolomics data also shows increased intra- and extra-cellular accumulation of most amino acids and TCA cycle intermediates in yeast cells growing under ethanol stress suggesting a state of overflow metabolism in turn of the pyruvate branch-point. Given its previous implication in ethanol stress resistance in yeast, this study also focused on the effect of the expression of the aquaglyceroporin encoded by *FPS1* in the yeast metabolome, in the absence or presence of ethanol stress. The metabolomics data collected herein shows that the deletion of the *FPS1* gene in the absence of ethanol stress partially mimics the effect of ethanol stress in the parental strain. Moreover, the results obtained suggest that the reported action of Fps1 in mediating the passive diffusion of glycerol is a key factor in the maintenance of redox balance, an important feature for ethanol stress resistance, and may interfere with the ability of the yeast cell to accumulate trehalose. Overall, the obtained results corroborate the idea that metabolomic approaches may be crucial tools to understand the function and/or the effect of membrane transporters/porins, such as Fps1, and may be an important tool for the clear-cut design of improved process conditions and more robust yeast strains aiming to optimize industrial fermentation performance.

1. Procedam à interpretação biológica de um conjunto de dados resultante de uma experiência de RNA-seq (Anexo A).
   1. Utilize a ferramenta PANTHER knowledgebase (<http://www.pantherdb.org/>) para fazer essa análise. No quadro ***Gene List Analysis***: **1.** Coloque a lista de genes (Anexo A); **2.** Selecione o organismo (*S. cerevisiae*). **3.** Utilize *Functional classification viewed in gene list*, *Functional classification viewed in graphic charts* e *Statistical overrepresentation test*. Com base nos resultados façam uma análise dos dados providenciados.



* 1. Explore a página *Database for Annotation, Visualization and Integrated Discovery* (DAVID) (<https://david.ncifcrf.gov/>). **1.** *Start Analysis*; **2.** Coloque a lista de genes (Anexo A); **3.** Utilize *Functional Annotation Table* e *Functional Annotation Chart*. Com base nos resultados façam uma análise dos dados providenciados.



**Anexo A**

YDR534C

YOR382W

YJR005C-A

YLR237W

YIR019C

YLR004C

YOR383C

YHL047C

YLR411W

YBR092C

YHR094C

YPR124W

YBR032W

YCR020C

YOL055C

YBR240C

YLR214W

YNL141W

YLL053C

YDL049C

YLL052C

YGR159C

YDL184C

YOR294W

YJL122W

YAL059W

YNL112W

YBR034C

YIL064W

YLR073C

YGR035C

YOR381W

YDL205C

YOL080C

YDL133C-A

YDL039C

YIL096C

YFR055W

YLR068W

YPL211W

YKL043W

YPR035W

YGL029W

YBR267W

YLR257W

YOR252W

YKL172W

YKR081C

YLR074C

YBL028C

YJR063W

YDL213C

YPR143W

YNL024C

YDR034C-A

YGR063C

YCL058C

YFR001W

YKR024C

YML056C

YCR087C-A

YLR435W

YPL093W

YDR101C

YIL127C

YOR306C

YNR053C

YOR004W

YGR280C

YLR009W

YOL077C

YLR363W-A

YPL266W

YGR271C-A

YNL175C

YNR015W

YHR216W

YML080W

YPL043W

YBL039C

YML108W

YNL110C

YPL146C

YKL078W

YHR089C

YHR143W-A

YMR319C

YCR047C

YDR465C

YER174C

YHR072W-A

YNL113W

YCL054W

YKL186C

YER137C

YJR010C-A

YKL021C

YMR269W

YMR290C

YOR145C

YLR051C

YAL025C

YNL259C

YPR016C

YBL024W

YHR128W

YIL019W

YLL018C-A

YDR087C

YDR299W

YER126C

YOR272W

YDR399W

YGL099W

YKL009W

YLR196W

YOR101W

YGR103W

YGR123C

YGR245C

YPL245W

YDL208W

YHR052W

YKR060W

YMR014W

YOL124C

YPL012W

YGL078C

YGR145W

YIL008W

YLR186W

YCL059C

YDL153C

YDR365C

YJL033W

YCR024C-A

YDR496C

YER127W

YDR045C

YER145C-A

YHR085W

YNL151C

YDL014W

YHR148W

YJR148W

YLL011W

YNL182C

YCR016W

YDR083W

YIR012W

YNL244C

YDR043C

YDR184C

YDR345C

YER002W

YIR026C

YLR264C-A

YOR021C

YOR095C

YPR069C

YCR051W

YHR191C

YKL099C

YBL054W

YBR088C

YDL201W

YHR081W

YOR224C

YGR187C

YLR017W

YBR191W

YDR514C

YPL193W

YBR252W

YHR169W

YOR182C

YOR253W

YBR142W

YDL031W

YDR021W

YKL082C

YKL096W-A

YDL051W

YNL065W

YNL308C

YPL037C

YPL217C

YPR112C

YCR072C

YDR382W

YLR449W

YER006W

YGR251W

YJR070C

YKL143W

YLR197W

YLR325C

YMR217W

YPR187W

YHR170W

YJL148W

YJR056C

YNL132W

YOR159C

YOR293W

YPL239W

YDR441C

YBR271W

YKL056C

YKL191W

YLR172C

YLR175W

YLR262C-A

YML024W

YBR061C

YHL020C

YHR197W

YKL024C

YOR056C

YAL033W

YGL211W

YMR229C

YEL003W

YFL017W-A

YHR040W

YJL125C

YLR146C

YMR260C

YOL144W

YOR276W

YDL060W

YDL166C

YHR088W

YML022W

YMR131C

YMR239C

YNR024W

YOL125W

YOR143C