

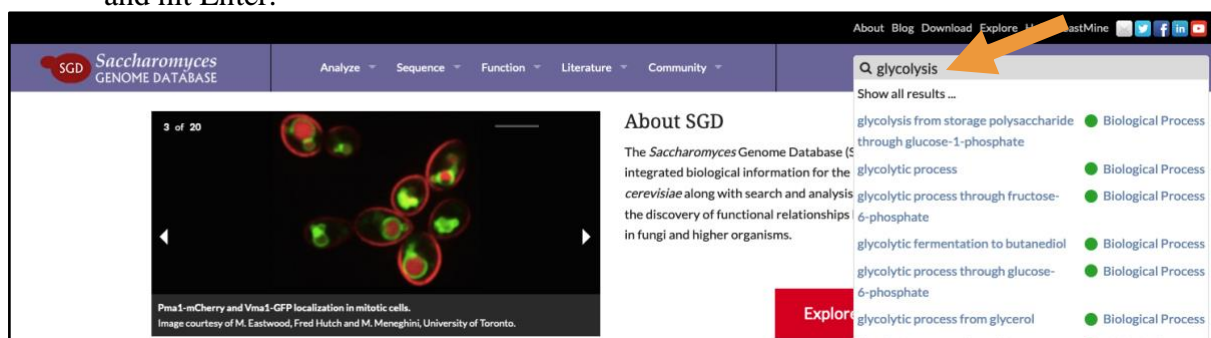
# Using SPELL to Analyze Expression Datasets & Co-expressed Genes at SGD

SPELL (Serial Pattern of Expression Levels Locator) is a query-driven search engine for large gene expression microarray compendia. Given a small set of query genes, SPELL identifies which datasets are most informative for these genes, then within those datasets additional genes are identified with expression profiles most similar to the query set.

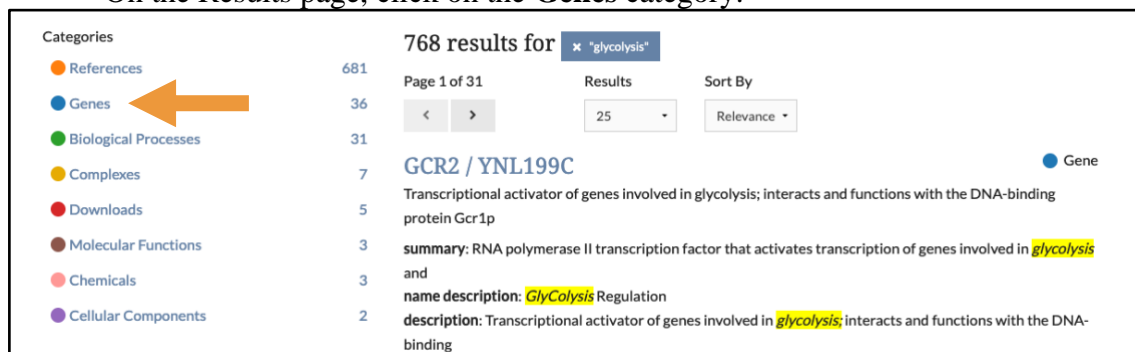
Use SPELL to find out which genes are co-expressed with genes involved in glycolysis.

## Compile a list of genes involved in glycolysis.

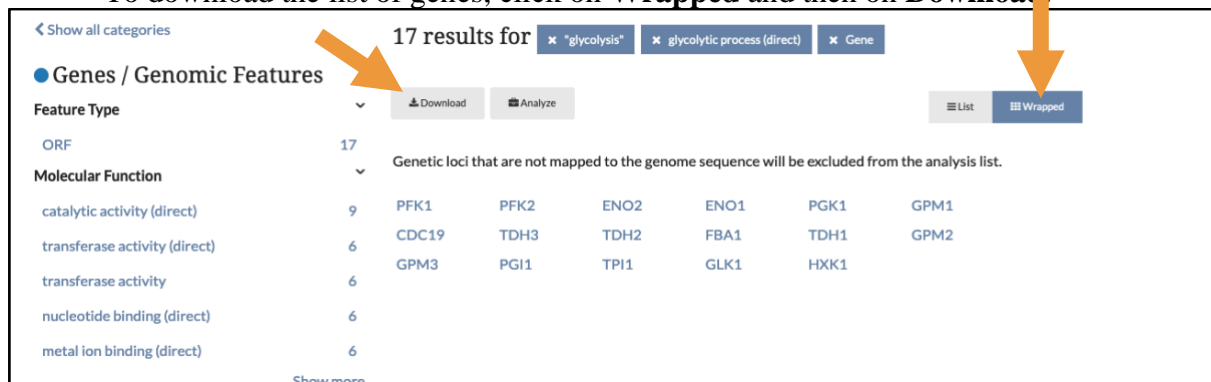
- On the SGD home page ([www.yeastgenome.org](http://www.yeastgenome.org)), enter glycolysis into the search box and hit Enter.



- On the Results page, click on the **Genes** category.



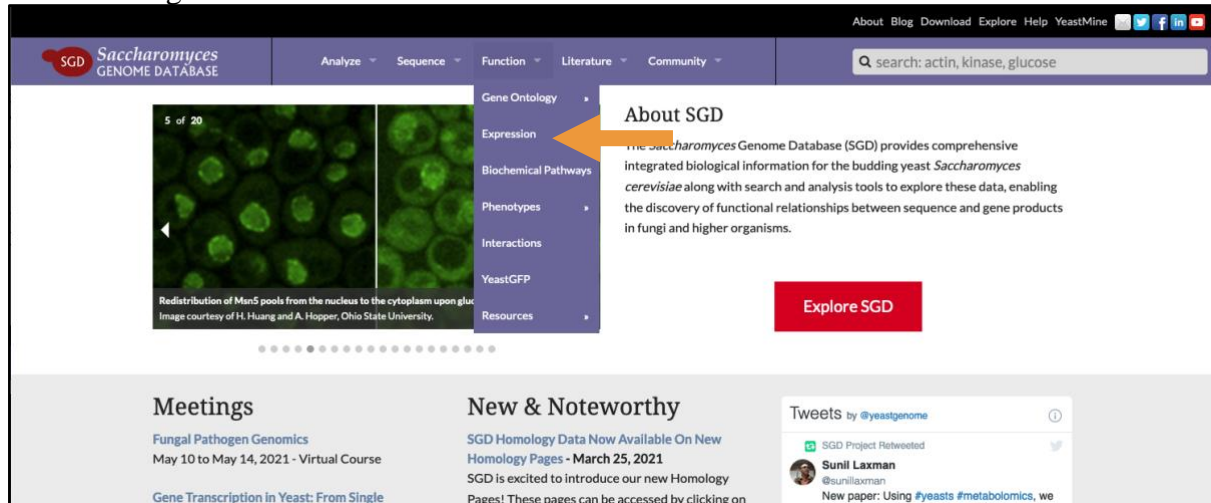
- Scroll down the page and find the **Biological Process** category on the left hand menu. Hit Show more and select **glycolytic process (direct)**.
- To download the list of genes, click on **Wrapped** and then on **Download**.



- The **Analyze** button, directly to the right of Download, enables you to import your search results directly into SPELL (among other tools at SGD). However, for the sake of demonstration, in this exercise we are instead going to enter our gene list into SPELL manually.

### Import your gene list into SPELL and run a query:

- To access SPELL, go to the SGD home page at [www.yeastgenome.org](http://www.yeastgenome.org), open the **Function** tab on top of the page and click on **Expression**. Or, if you are already on a Locus Summary page, open the Expression tab and click on the SPELL link under the histogram.



- On the SPELL page, copy and paste the list of glycolysis genes you downloaded in step 1 into the Gene Name(s) box. For the sake of demonstration, remove **FBA1** from your list before hitting Search. This is to test if SPELL can properly identify missing members of glycolysis based on coexpression.

### SPELL - *S. cerevisiae*

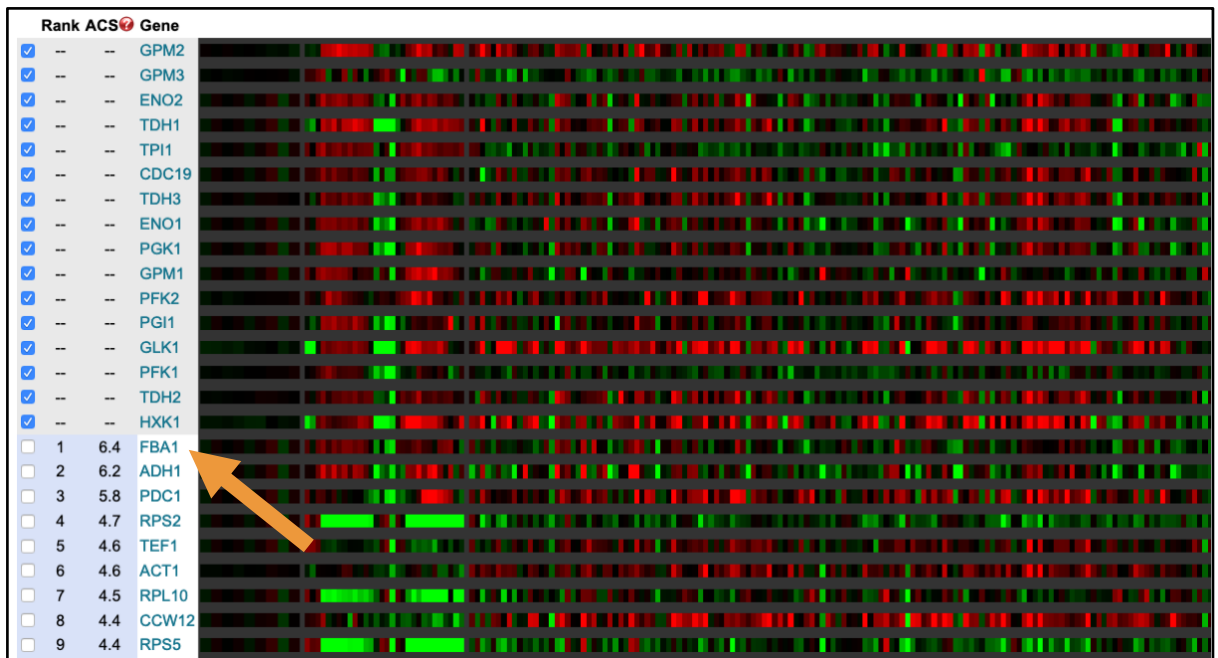
SPELL (Yeast)

Gene Name(s): GPM1 PGK1 PFK1 PFK2 ENO2 ENO1 CDC
Search

# Results:
20

[+ Options for Filtering Results by Dataset Tags<sup>FB</sup>](#)

- Scroll down the list of genes on the left. Genes with checked boxes are from our query; the remaining genes are "hits", ordered from top to bottom according to their ranks. The rank reflects the correlation of expression of that gene with the query gene(s), given the relevance weight of that expression dataset. Thus, genes that show the highest degree of coexpression with the query genes in the most relevant datasets receive the highest rank.



- Notice that the glycolysis gene we deleted earlier, FBA1, is indeed the highest-ranking gene!
- Examine other genes enriched for this query set. You can click on their names to be taken to their respective summary pages at SGD. Does it make sense for any of these genes to be highly co-expressed with members of glycolysis?
- Click on + **Additional Display Options** to change the default mapping method and color scheme to blue/yellow. Directly above this section are options to change the number of genes and datasets shown in your results.

# of Result Genes to Show: 20
Datasets to view: From 1 to 10

+ Additional Display Options

Mapping method

Color scheme

For single channel data: Per-gene log2 fold change

For dual channel data: Reported log2 fold change

- To select only datasets with particular tags, click on + **Options** for Filtering Results.

Dataset Tags

Select: all none previous query toggle

☐ amino acid metabolism
☐ amino acid utilization
☐ carbon utilization
☐ cell aging
☐ cell cycle regulation
☐ cell morphogenesis
☐ cell wall organization
☐ cellular ion homeostasis
☐ chemical stimulus
☐ chromatin organization
☐ cofactor metabolism
☐ diauxic shift
☐ disease
☐ DNA damage stimulus
☐ DNA replication, recombination and repair
☐ environmental-sensing

☐ evolution
☐ fermentation
☐ filamentous growth
☐ flocculation
☐ genetic interaction
☐ genome variation
☐ heat shock
☐ histone modification
☐ lipid metabolism
☐ mating
☐ metabolism
☐ metal or metalloid ion stress
☐ mitotic cell cycle
☐ mRNA processing
☐ nitrogen utilization
☐ nutrient utilization

☐ organelles, biogenesis, structure, and function
☐ osmotic stress
☐ oxidative stress
☐ oxygen level alteration
☐ phosphorus utilization
☐ ploidy
☐ protein dephosphorylation
☐ protein glycosylation
☐ protein modification
☐ protein phosphorylation
☐ protein trafficking, localization and degradation
☐ proteolysis
☐ QTLs
☐ radiation
☐ respiration
☐ response to unfolded protein

☐ RNA catabolism
☐ signaling
☐ sporulation
☐ starvation
☐ stationary phase entry
☐ stationary phase maintenance
☐ stress
☐ sulfur utilization
☐ synthetic biology
☐ transcription
☐ transcriptional regulation
☐ translational regulation
☐ ubiquitin or ULP modification

- Rank ACSF Gene**

✓	--	ENO2
✓	--	TDH1
✓	--	TPH1
✓	--	TDH3
✓	--	ENO1
✓	--	CDC19
✓	--	PGK1
✓	--	GPM1
✓	--	PFK2
✓	--	TDH2
✓	--	PGI1
✓	--	PFK1
✓	--	GLK1
✓	--	HXK2
✓	--	HXK1
1	6.5	FBA1
2	6.3	ADH1
3	5.9	PDC1
4	5.0	TEP1

**Citation** Hu Z, *et al.* Genetic reconstruction of a functional transcriptional regulatory network. *Nature genetics*, 2007.

**Short Description** Genetic reconstruction of a functional transcriptional regulatory network.

ylr098c ybi054w yki062w yer051w ylr176c yki032c yjl176c yjr060w ypr008w yhl009c ypl001w ymr273c yol028c ykd028c ygi062w ygl001w ygl002w ygl003w ygl004w ygl005w ygl006w ygl007w ygl008w ygl009w ygl010w ygl011w ygl012w ygl013w ygl014w ygl015w ygl016w ygl017w ygl018w ygl019w ygl020w ygl021w ygl022w ygl023w ygl024w ygl025w ygl026w ygl027w ygl028w ygl029w ygl030w ygl031w ygl032w ygl033w ygl034w ygl035w ygl036w ygl037w ygl038w ygl039w ygl040w ygl041w ygl042w ygl043w ygl044w ygl045w ygl046w ygl047w ygl048w ygl049w ygl050w ygl051w ygl052w ygl053w ygl054w ygl055w ygl056w ygl057w ygl058w ygl059w ygl060w ygl061w ygl062w ygl063w ygl064w ygl065w ygl066w ygl067w ygl068w ygl069w ygl070w ygl071w ygl072w ygl073w ygl074w ygl075w ygl076w ygl077w ygl078w ygl079w ygl080w ygl081w ygl082w ygl083w ygl084w ygl085w ygl086w ygl087w ygl088w ygl089w ygl090w ygl091w ygl092w ygl093w ygl094w ygl095w ygl096w ygl097w ygl098w ygl099w ygl100w ygl101w ygl102w ygl103w ygl104w ygl105w ygl106w ygl107w ygl108w ygl109w ygl110w ygl111w ygl112w ygl113w ygl114w ygl115w ygl116w ygl117w ygl118w ygl119w ygl120w ygl121w ygl122w ygl123w ygl124w ygl125w ygl126w ygl127w ygl128w ygl129w ygl130w ygl131w ygl132w ygl133w ygl134w ygl135w ygl136w ygl137w ygl138w ygl139w ygl140w ygl141w ygl142w ygl143w ygl144w ygl145w ygl146w ygl147w ygl148w ygl149w ygl150w ygl151w ygl152w ygl153w ygl154w ygl155w ygl156w ygl157w ygl158w ygl159w ygl160w ygl161w ygl162w ygl163w ygl164w ygl165w ygl166w ygl167w ygl168w ygl169w ygl170w ygl171w ygl172w ygl173w ygl174w ygl175w ygl176w ygl177w ygl178w ygl179w ygl180w ygl181w ygl182w ygl183w ygl184w ygl185w ygl186w ygl187w ygl188w ygl189w ygl190w ygl191w ygl192w ygl193w ygl194w ygl195w ygl196w ygl197w ygl198w ygl199w ygl200w ygl201w ygl202w ygl203w ygl204w ygl205w ygl206w ygl207w ygl208w ygl209w ygl210w ygl211w ygl212w ygl213w ygl214w ygl215w ygl216w ygl217w ygl218w ygl219w ygl220w ygl221w ygl222w ygl223w ygl224w ygl225w ygl226w ygl227w ygl228w ygl229w ygl230w ygl231w ygl232w ygl233w ygl234w ygl235w ygl236w ygl237w ygl238w ygl239w ygl240w ygl241w ygl242w ygl243w ygl244w ygl245w ygl246w ygl247w ygl248w ygl249w ygl250w ygl251w ygl252w ygl253w ygl254w ygl255w ygl256w ygl257w ygl258w ygl259w ygl260w ygl261w ygl262w ygl263w ygl264w ygl265w ygl266w ygl267w ygl268w ygl269w ygl270w ygl271w ygl272w ygl273w ygl274w ygl275w ygl276w ygl277w ygl278w ygl279w ygl280w ygl281w ygl282w ygl283w ygl284w ygl285w ygl286w ygl287w ygl288w ygl289w ygl290w ygl291w ygl292w ygl293w ygl294w ygl295w ygl296w ygl297w ygl298w ygl299w ygl300w ygl301w ygl302w ygl303w ygl304w ygl305w ygl306w ygl307w ygl308w ygl309w ygl310w ygl311w ygl312w ygl313w ygl314w ygl315w ygl316w ygl317w ygl318w ygl319w ygl320w ygl321w ygl322w ygl323w ygl324w ygl325w ygl326w ygl327w ygl328w ygl329w ygl330w ygl331w ygl332w ygl333w ygl334w ygl335w ygl336w ygl337w ygl338w ygl339w ygl340w ygl341w ygl342w ygl343w ygl344w ygl345w ygl346w ygl347w ygl348w ygl349w ygl350w ygl351w ygl352w ygl353w ygl354w ygl355w ygl356w ygl357w ygl358w ygl359w ygl360w ygl361w ygl362w ygl363w ygl364w ygl365w ygl366w ygl367w ygl368w ygl369w ygl370w ygl371w ygl372w ygl373w ygl374w ygl375w ygl376w ygl377w ygl378w ygl379w ygl380w ygl381w ygl382w ygl383w ygl384w ygl385w ygl386w ygl387w ygl388w ygl389w ygl390w ygl391w ygl392w ygl393w ygl394w ygl395w ygl396w ygl397w ygl398w ygl399w ygl400w ygl401w ygl402w ygl403w ygl404w ygl405w ygl406w ygl407w ygl408w ygl409w ygl410w ygl411w ygl412w ygl413w ygl414w ygl415w ygl416w ygl417w ygl418w ygl419w ygl420w ygl421w ygl422w ygl423w ygl424w ygl425w ygl426w ygl427w ygl428w ygl429w ygl430w ygl431w ygl432w ygl433w ygl434w ygl435w ygl436w ygl437w ygl438w ygl439w ygl440w ygl441w ygl442w ygl443w ygl444w ygl445w ygl446w ygl447w ygl448w ygl449w ygl450w ygl451w ygl452w ygl453w ygl454w ygl455w ygl456w ygl457w ygl458w ygl459w ygl460w ygl461w ygl462w ygl463w ygl464w ygl465w ygl466w ygl467w ygl468w ygl469w ygl470w ygl471w ygl472w ygl473w ygl474w ygl475w ygl476w ygl477w ygl478w ygl479w ygl480w ygl481w ygl482w ygl483w ygl484w ygl485w ygl486w ygl487w ygl488w ygl489w ygl490w ygl491w ygl492w ygl493w ygl494w ygl495w ygl496w ygl497w ygl498w ygl499w ygl500w ygl501w ygl502w ygl503w ygl504w ygl505w ygl506w ygl507w ygl508w ygl509w ygl510w ygl511w ygl512w ygl513w ygl514w ygl515w ygl516w ygl517w ygl518w ygl519w ygl520w ygl521w ygl522w ygl523w ygl524w ygl525w ygl526w ygl527w ygl528w ygl529w ygl530w ygl531w ygl532w ygl533w ygl534w ygl535w ygl536w ygl537w ygl538w ygl539w ygl540w ygl541w ygl542w ygl543w ygl544w ygl545w ygl546w ygl547w ygl548w ygl549w ygl550w ygl551w ygl552w ygl553w ygl554w ygl555w ygl556w ygl557w ygl558w ygl559w ygl560w ygl561w ygl562w ygl563w ygl564w ygl565w ygl566w ygl567w ygl568w ygl569w

- | GO Term  | P-val    | % query  | % genome   | Annotated Genes  |
|--|----------|----------|------------|--|
| <a href="#">pyruvate metabolic process</a> (biological_process)  | 1.50e-32 | 19 of 36 | 38 of 6381 | <a href="#">PGI1</a> , <a href="#">TDH2</a> , <a href="#">CDC19</a> , <a href="#">GPM1</a> , <a href="#">TDH1</a> , <a href="#">PFK1</a> , <a href="#">HXXK1</a> , <a href="#">PFK2</a> , <a href="#">ENO1</a> , <a href="#">TDH3</a> , <a href="#">GPM3</a> , <a href="#">PGK1</a> , <a href="#">GPM2</a> , <a href="#">TPI1</a> , <a href="#">FBA1</a> , <a href="#">ENO2</a> , <a href="#">PDC5</a> , <a href="#">GLK1</a> , <a href="#">PDC1</a> |
| <a href="#">glycolytic process</a> (biological_process)  | 2.65e-30 | 17 of 36 | 29 of 6381 | <a href="#">PGI1</a> , <a href="#">TDH2</a> , <a href="#">CDC19</a> , <a href="#">GPM1</a> , <a href="#">TDH1</a> , <a href="#">PFK1</a> , <a href="#">HXXK1</a> , <a href="#">PFK2</a> , <a href="#">ENO1</a> , <a href="#">TDH3</a> , <a href="#">GPM3</a> , <a href="#">PGK1</a> , <a href="#">GPM2</a> , <a href="#">TPI1</a> , <a href="#">FBA1</a> , <a href="#">ENO2</a> , <a href="#">GLK1</a>   |
| <a href="#">phosphopyruvate hydratase activity</a> (molecular_function)  | 2.65e-30 | 17 of 36 | 29 of 6381 | <a href="#">PGI1</a> , <a href="#">TDH2</a> , <a href="#">CDC19</a> , <a href="#">GPM1</a> , <a href="#">TDH1</a> , <a href="#">PFK1</a> , <a href="#">HXXK1</a> , <a href="#">PFK2</a> , <a href="#">ENO1</a> , <a href="#">TDH3</a> , <a href="#">GPM3</a> , <a href="#">PGK1</a> , <a href="#">GPM2</a> , <a href="#">TPI1</a> , <a href="#">FBA1</a> , <a href="#">ENO2</a> , <a href="#">GLK1</a>   |
| <a href="#">ATP generation from ADP</a> (biological_process)   | 2.65e-30 | 17 of 36 | 29 of 6381 | <a href="#">PGI1</a> , <a href="#">TDH2</a> , <a href="#">CDC19</a> , <a href="#">GPM1</a> , <a href="#">TDH1</a> , <a href="#">PFK1</a> , <a href="#">HXXK1</a> , <a href="#">PFK2</a> , <a href="#">ENO1</a> , <a href="#">TDH3</a> , <a href="#">GPM3</a> , <a href="#">PGK1</a> , <a href="#">GPM2</a> , <a href="#">TPI1</a> , <a href="#">FBA1</a> , <a href="#">ENO2</a> , <a href="#">GLK1</a>   |
| <a href="#">phosphoglycerate mutase activity</a> (molecular_function)  | 2.65e-30 | 17 of 36 | 29 of 6381 | <a href="#">PGI1</a> , <a href="#">TDH2</a> , <a href="#">CDC19</a> , <a href="#">GPM1</a> , <a href="#">TDH1</a> , <a href="#">PFK1</a> , <a href="#">HXXK1</a> , <a href="#">PFK2</a> , <a href="#">ENO1</a> , <a href="#">TDH3</a> , <a href="#">GPM3</a> , <a href="#">PGK1</a> , <a href="#">GPM2</a> , <a href="#">TPI1</a> , <a href="#">FBA1</a> , <a href="#">ENO2</a> , <a href="#">GLK1</a>   |
| <a href="#">glyceraldehyde-3-phosphate dehydrogenase (NAD(P)+.phosphorylating) activity</a> (molecular_function) | 2.65e-30 | 17 of 36 | 29 of 6381 | <a href="#">PGI1</a> , <a href="#">TDH2</a> , <a href="#">CDC19</a> , <a href="#">GPM1</a> , <a href="#">TDH1</a> , <a href="#">PFK1</a> , <a href="#">HXXK1</a> , <a href="#">PFK2</a> , <a href="#">ENO1</a> , <a href="#">TDH3</a> , <a href="#">GPM3</a> , <a href="#">PGK1</a> , <a href="#">GPM2</a> , <a href="#">TPI1</a> , <a href="#">FBA1</a> , <a href="#">ENO2</a> , <a href="#">GLK1</a>   |
| <a href="#">phosphoglycerate kinase activity</a> (molecular_function)  | 2.65e-30 | 17 of 36 | 29 of 6381 | <a href="#">PGI1</a> , <a href="#">TDH2</a> , <a href="#">CDC19</a> , <a href="#">GPM1</a> , <a href="#">TDH1</a> , <a href="#">PFK1</a> , <a href="#">HXXK1</a> , <a href="#">PFK2</a> , <a href="#">ENO1</a> , <a href="#">TDH3</a> , <a href="#">GPM3</a> , <a href="#">PGK1</a> , <a href="#">GPM2</a> , <a href="#">TPI1</a> , <a href="#">FBA1</a> , <a href="#">ENO2</a> , <a href="#">GLK1</a>   |
| <a href="#">ADP metabolic process</a> (biological_process)   | 6.10e-30 | 17 of 36 | 30 of 6381 | <a href="#">PGI1</a> , <a href="#">TDH2</a> , <a href="#">CDC19</a> , <a href="#">GPM1</a> , <a href="#">TDH1</a> , <a href="#">PFK1</a> , <a href="#">HXXK1</a> , <a href="#">PFK2</a> , <a href="#">ENO1</a> , <a href="#">TDH3</a> , <a href="#">GPM3</a> , <a href="#">PGK1</a> , <a href="#">GPM2</a> , <a href="#">TPI1</a> , <a href="#">FBA1</a> , <a href="#">ENO2</a> , <a href="#">GLK1</a>   |
| <a href="#">nucleoside diphosphate phosphorylation</a> (biological_process)                                      | 6.10e-30 | 17 of 36 | 30 of 6381 | <a href="#">PGI1</a> , <a href="#">TDH2</a> , <a href="#">CDC19</a> , <a href="#">GPM1</a> , <a href="#">TDH1</a> , <a href="#">PFK1</a> , <a href="#">HXXK1</a> , <a href="#">PFK2</a> , <a href="#">ENO1</a> , <a href="#">TDH3</a> , <a href="#">GPM3</a> , <a href="#">PGK1</a> , <a href="#">GPM2</a> , <a href="#">TPI1</a> , <a href="#">FBA1</a> , <a href="#">ENO2</a> , <a href="#">GLK1</a>   |
| <a href="#">purine ribonucleoside diphosphate metabolic process</a> (biological_process)                         | 1.35e-29 | 17 of 36 | 31 of 6381 | <a href="#">PGI1</a> , <a href="#">TDH2</a> , <a href="#">CDC19</a> , <a href="#">GPM1</a> , <a href="#">TDH1</a> , <a href="#">PFK1</a> , <a href="#">HXXK1</a> , <a href="#">PFK2</a> , <a href="#">ENO1</a> , <a href="#">TDH3</a> , <a href="#">GPM3</a> , <a href="#">PGK1</a> , <a href="#">GPM2</a> , <a href="#">TPI1</a> , <a href="#">FBA1</a> , <a href="#">ENO2</a> , <a href="#">GLK1</a>   |
| <a href="#">ribonucleoside diphosphate metabolic process</a> (biological_process)                                | 1.35e-29 | 17 of 36 | 31 of 6381 | <a href="#">PGI1</a> , <a href="#">TDH2</a> , <a href="#">CDC19</a> , <a href="#">GPM1</a> , <a href="#">TDH1</a> , <a href="#">PFK1</a> , <a href="#">HXXK1</a> , <a href="#">PFK2</a> , <a href="#">ENO1</a> , <a href="#">TDH3</a> , <a href="#">GPM3</a> , <a href="#">PGK1</a> , <a href="#">GPM2</a> , <a href="#">TPI1</a> , <a href="#">FBA1</a> , <a href="#">ENO2</a> , <a href="#">GLK1</a>   |
| <a href="#">purine nucleoside diphosphate metabolic process</a> (biological_process)                             | 1.35e-29 | 17 of 36 | 31 of 6381 | <a href="#">PGI1</a> , <a href="#">TDH2</a> , <a href="#">CDC19</a> , <a href="#">GPM1</a> , <a href="#">TDH1</a> , <a href="#">PFK1</a> , <a href="#">HXXK1</a> , <a href="#">PFK2</a> , <a href="#">ENO1</a> , <a href="#">TDH3</a> , <a href="#">GPM3</a> , <a href="#">PGK1</a> , <a href="#">GPM2</a> , <a href="#">TPI1</a> , <a href="#">FBA1</a> , <a href="#">ENO2</a> , <a href="#">GLK1</a>   |
| <a href="#">nucleotide phosphorylation</a> (biological_process)  | 5.90e-29 | 17 of 36 | 33 of 6381 | <a href="#">PGI1</a> , <a href="#">TDH2</a> , <a href="#">CDC19</a> , <a href="#">GPM1</a> , <a href="#">TDH1</a> , <a href="#">PFK1</a> , <a href="#">HXXK1</a> , <a href="#">PFK2</a> , <a href="#">ENO1</a> , <a href="#">TDH3</a> , <a href="#">GPM3</a> , <a href="#">PGK1</a> , <a href="#">GPM2</a> , <a href="#">TPI1</a> , <a href="#">FBA1</a> , <a href="#">ENO2</a> , <a href="#">GLK1</a>   |
| <a href="#">phosphotransferase activity, carboxyl group as acceptor</a> (molecular_function)                     | 5.90e-29 | 17 of 36 | 33 of 6381 | <a href="#">PGI1</a> , <a href="#">TDH2</a> , <a href="#">CDC19</a> , <a href="#">GPM1</a> , <a href="#">TDH1</a> , <a href="#">PFK1</a> , <a href="#">HXXK1</a> , <a href="#">PFK2</a> , <a href="#">ENO1</a> , <a href="#">TDH3</a> , <a href="#">GPM3</a> , <a href="#">PGK1</a> , <a href="#">GPM2</a> , <a href="#">TPI1</a> , <a href="#">FBA1</a> , <a href="#">ENO2</a> , <a href="#">GLK1</a>   |