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New Enhancer-Gene Map PANTHER16.0 Released.

Analysis Summary: Please report in publication 3

| Analysis Type: PANTHER Enrichment Test (Released 20200728) |
|-----------------------------------------------------------------------------------------------------------------|
| Annotation Version and Release Date: GO Ontology database DOI: 10.5281/zenodo.4437524 Released 2021-01-01 |
| Analyzed List: yorf-lfcmin-all.txt (Saccharomyces cerevisiae) Change |
| Annotation Data Set: GO biological process complete ③ |
| Correction: • Calculate False Discovery Rate Use the Bonferroni correction for multiple testing ② No correction |

Results ?

Analysis details:

Mapped IDs: <u>4678</u> out of 4682

Unmapped IDs: <u>1182</u>
Multiple mapping information: <u>182</u>

Graph selected categories | Export Table | XML with user input ids | JSON with user input ids |

Displaying only results with P<0.05; click here to display all results (Hierarchy NEW! ②)

GO biological process complete

- mRNA polyadenylation (GO:0006378)
- RNA polyadenylation (GO:0043631)

| RNA metabolic process (GO:0016070) |
|------------------------------------------------------------------------------------------------------------------------------------------------------------|
| nucleic acid metabolic process (GO:0090304) |
| nucleobase-containing compound metabolic process (GO:0006139) |
| heterocycle metabolic process (GO:0046483) |
| cellular metabolic process (GO:0044237) |
| metabolic process (GO:0008152) |
| primary metabolic process (GO:0044238) |
| cellular aromatic compound metabolic process (GO:0006725) |
| cellular nitrogen compound metabolic process (GO:0034641) |
| nitrogen compound metabolic process (GO:0006807) |
| organic cyclic compound metabolic process (GO:1901360) |
| organic substance metabolic process (GO:0071704) |
| macromolecule metabolic process (GO:0043170) |
| mRNA 3'-end processing (GO:0031124) |
| □ MRNA processing (GO:0006397) |
| RNA processing (GO:0006396) |
| □ |
| mRNA metabolic process (GO:0016071) |
| RNA 3'-end processing (GO:0031123) |
| endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) (GO:0) |
| maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) (GO:0000462) |
| maturation of SSU-rRNA (GO:0030490) |
| ribosomal small subunit biogenesis (GO:0042274) |
| ribonucleoprotein complex biogenesis (GO:0022613) |

| cellular component biogenesis (GO:0044085) |
|------------------------------------------------------------------------------------------------------------------|
| Cellular component organization or biogenesis (GO:0071840) |
| ribosome biogenesis (GO:0042254) |
| □ |
| ncRNA processing (GO:0034470) |
| ncRNA metabolic process (GO:0034660) |
| rRNA metabolic process (GO:0016072) |
| endonucleolytic cleavage of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) (GO:0000479) |
| endonucleolytic cleavage involved in rRNA processing (GO:0000478) |
| Cleavage involved in rRNA processing (GO:0000469) |
| RNA phosphodiester bond hydrolysis (GO:0090501) |
| nucleic acid phosphodiester bond hydrolysis (GO:0090305) |
| RNA phosphodiester bond hydrolysis, endonucleolytic (GO:0090502) |
| maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) (GO:0000466) |
| maturation of 5.8S rRNA (GO:0000460) |
| pre-mRNA cleavage required for polyadenylation (GO:0098789) |
| □ |
| mRNA cleavage (GO:0006379) |
| endonucleolytic cleavage to generate mature 5'-end of SSU-rRNA from (SSU-rRNA, 5.8S rRNA, LSU-rRNA) (GO:0000472) |
| □ |
| ncRNA 5'-end processing (GO:0034471) |
| RNA 5'-end processing (GO:0000966) |
| endonucleolytic cleavage in 5'-ETS of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) (GO:0000480) |
| translational termination (GO:0006415) |

| Translation (GO:0006412) |
|--------------------------------------------------------------|
| peptide biosynthetic process (GO:0043043) |
| peptide metabolic process (GO:0006518) |
| organonitrogen compound metabolic process (GO:1901564) |
| cellular amide metabolic process (GO:0043603) |
| amide biosynthetic process (GO:0043604) |
| cellular nitrogen compound biosynthetic process (GO:0044271) |
| cellular biosynthetic process (GO:0044249) |
| biosynthetic process (GO:0009058) |
| organonitrogen compound biosynthetic process (GO:1901566) |
| organic substance biosynthetic process (GO:1901576) |
| □ |
| □ |
| macromolecule biosynthetic process (GO:0009059) |
| □ |
| protein metabolic process (GO:0019538) |
| □ |
| protein-containing complex disassembly (GO:0032984) |
| cellular component disassembly (GO:0022411) |
| cellular component organization (GO:0016043) |
| protein-containing complex subunit organization (GO:0043933) |
| vacuolar acidification (GO:0007035) |
| intracellular pH reduction (GO:0051452) |
| □ |

| regulation of pH (GO:0006885) |
|-------------------------------------------------------------------------------------------------------|
| regulation of intracellular pH (GO:0051453) |
| regulation of cellular pH (GO:0030641) |
| maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) (GO:0000463) |
| maturation of LSU-rRNA (GO:0000470) |
| ribosomal large subunit biogenesis (GO:0042273) |
| nuclear-transcribed mRNA catabolic process, 3'-5' exonucleolytic nonsense-mediated decay (GO:0070478) |
| □ huclear-transcribed mRNA catabolic process, nonsense-mediated decay (GO:0000184) |
| cellular macromolecule catabolic process (GO:0044265) |
| macromolecule catabolic process (GO:0009057) |
| nuclear-transcribed mRNA catabolic process, exonucleolytic, 3'-5' (GO:0034427) |
| nuclear-transcribed mRNA catabolic process, exonucleolytic (GO:0000291) |
| nuclear polyadenylation-dependent mRNA catabolic process (GO:0071042) |
| polyadenylation-dependent mRNA catabolic process (GO:0071047) |
| polyadenylation-dependent RNA catabolic process (GO:0043633) |
| modification-dependent macromolecule catabolic process (GO:0043632) |
| proteasomal ubiquitin-independent protein catabolic process (GO:0010499) |
| proteasomal protein catabolic process (GO:0010498) |
| proteolysis involved in cellular protein catabolic process (GO:0051603) |
| cellular protein catabolic process (GO:0044257) |
| protein catabolic process (GO:0030163) |
| polyphosphate metabolic process (GO:0006797) |
| vesicle fusion with Golgi apparatus (GO:0048280) |
| organelle organization (GO:0006996) |

| nuclear polyadenylation-dependent tRNA catabolic process (GO:0071038) |
|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| TRNA catabolic process (GO:0016078) |
| □ Land the transfer of the tr |
| ncRNA catabolic process (GO:0034661) |
| □ uclear polyadenylation-dependent ncRNA catabolic process (GO:0071046) |
| polyadenylation-dependent ncRNA catabolic process (GO:0043634) |
| □ huclear ncRNA surveillance (GO:0071029) |
| nuclear RNA surveillance (GO:0071027) |
| RNA surveillance (GO:0071025) |
| double-strand break repair via break-induced replication (GO:0000727) |
| DNA metabolic process (GO:0006259) |
| polyadenylation-dependent snoRNA 3'-end processing (GO:0071051) |
| □ |
| sno(s)RNA processing (GO:0043144) |
| sno(s)RNA metabolic process (GO:0016074) |
| ncRNA 3'-end processing (GO:0043628) |
| rRNA methylation (GO:0031167) |
| RNA modification (GO:0000154) |
| RNA modification (GO:0009451) |
| RNA methylation (GO:0001510) |
| U4 snRNA 3'-end processing (GO:0034475) |
| snRNA 3'-end processing (GO:0034472) |
| snRNA processing (GO:0016180) |
| snRNA metabolic process (GO:0016073) |

| protein import into nucleus (GO:0006606) |
|------------------------------------------------------|
| protein import (GO:0017038) |
| protein transport (GO:0015031) |
| establishment of protein localization (GO:0045184) |
| protein localization (GO:0008104) |
| macromolecule localization (GO:0033036) |
| peptide transport (GO:0015833) |
| amide transport (GO:0042886) |
| protein localization to nucleus (GO:0034504) |
| protein localization to organelle (GO:0033365) |
| cellular protein localization (GO:0034613) |
| □ |
| cellular localization (GO:0051641) |
| intracellular protein transport (GO:0006886) |
| intracellular transport (GO:0046907) |
| establishment of localization in cell (GO:0051649) |
| □ Laimport into nucleus (GO:0051170) |
| nucleocytoplasmic transport (GO:0006913) |
| nuclear transport (GO:0051169) |
| sulfate transmembrane transport (GO:1902358) |
| inorganic anion transmembrane transport (GO:0098661) |
| inorganic anion transport (GO:0015698) |
| transmembrane transport (GO:0055085) |
| sulfate transport (GO:0008272) |

| □ Sulfur compound transport (GO:0072348) |
|----------------------------------------------------------------------------------------------|
| DNA replication initiation (GO:0006270) |
| DNA-dependent DNA replication (GO:0006261) |
| □ DNA replication (GO:0006260) |
| mitotic sister chromatid segregation (GO:0000070) |
| mitotic nuclear division (GO:0140014) |
| mitotic cell cycle process (GO:1903047) |
| mitotic cell cycle (GO:0000278) |
| □ |
| nuclear division (GO:0000280) |
| organelle fission (GO:0048285) |
| □ |
| nuclear chromosome segregation (GO:0098813) |
| chromosome segregation (GO:0007059) |
| chromosome organization (GO:0051276) |
| protein localization to kinetochore (GO:0034501) |
| protein localization to chromosome, centromeric region (GO:0071459) |
| protein localization to chromosome (GO:0034502) |
| pre-replicative complex assembly involved in nuclear cell cycle DNA replication (GO:0006267) |
| pre-replicative complex assembly involved in cell cycle DNA replication (GO:1902299) |
| pre-replicative complex assembly (GO:0036388) |
| protein-DNA complex assembly (GO:0065004) |
| Cellular protein-containing complex assembly (GO:0034622) |
| protein-containing complex assembly (GO:0065003) |

| cellular component assembly (GO:0022607) |
|--------------------------------------------------------------------------|
| protein-DNA complex subunit organization (GO:0071824) |
| ATP-dependent chromatin remodeling (GO:0043044) |
| □ |
| nuclear polyadenylation-dependent rRNA catabolic process (GO:0071035) |
| □ |
| Arp2/3 complex-mediated actin nucleation (GO:0034314) |
| actin nucleation (GO:0045010) |
| positive regulation of protein-containing complex assembly (GO:0031334) |
| ibosomal small subunit assembly (GO:0000028) |
| ribosome assembly (GO:0042255) |
| organelle assembly (GO:0070925) |
| □ |
| ibonucleoprotein complex subunit organization (GO:0071826) |
| TRNA aminoacylation for protein translation (GO:0006418) |
| nuclear mRNA surveillance (GO:0071028) |
| RNA polymerase II preinitiation complex assembly (GO:0051123) |
| □ transcription initiation from RNA polymerase II promoter (GO:0006367) |
| transcription by RNA polymerase II (GO:0006366) |
| transcription, DNA-templated (GO:0006351) |
| nucleic acid-templated transcription (GO:0097659) |
| RNA biosynthetic process (GO:0032774) |
| nucleobase-containing compound biosynthetic process (GO:0034654) |
| heterocycle biosynthetic process (GO:0018130) |

| □ |
|-----------------------------------------------------------------------------------------------------------------------------------------------|
| aromatic compound biosynthetic process (GO:0019438) |
| □ DNA-templated transcription, initiation (GO:0006352) |
| □ ☐ transcription preinitiation complex assembly (GO:0070897) |
| organic acid transport (GO:0015849) |
| peptidyl-threonine phosphorylation (GO:0018107) |
| peptidyl-threonine modification (GO:0018210) |
| proteasome-mediated ubiquitin-dependent protein catabolic process (GO:0043161) |
| □ |
| modification-dependent protein catabolic process (GO:0019941) |
| exonucleolytic trimming to generate mature 3'-end of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) (GO:0000467) |
| □ |
| □ |
| ribosomal large subunit export from nucleus (GO:0000055) |
| □ |
| ribosome localization (GO:0033750) |
| establishment of organelle localization (GO:0051656) |
| □ |
| ibonucleoprotein complex export from nucleus (GO:0071426) |
| protein export from nucleus (GO:0006611) |
| nuclear export (GO:0051168) |
| ribonucleoprotein complex localization (GO:0071166) |
| RNA export from nucleus (GO:0006405) |
| RNA transport (GO:0050658) |

| □ Lestablishment of RNA localization (GO:0051236) |
|---------------------------------------------------------------------------|
| RNA localization (GO:0006403) |
| nucleic acid transport (GO:0050657) |
| nucleobase-containing compound transport (GO:0015931) |
| protein-containing complex localization (GO:0031503) |
| threonine biosynthetic process (GO:0009088) |
| asparagine catabolic process (GO:0006530) |
| small molecule catabolic process (GO:0044282) |
| □ |
| nucleosome disassembly (GO:0006337) |
| protein-DNA complex disassembly (GO:0032986) |
| □ ucleosome organization (GO:0034728) |
| chromatin disassembly (GO:0031498) |
| positive regulation of mitotic metaphase/anaphase transition (GO:0045842) |
| regulation of mitotic metaphase/anaphase transition (GO:0030071) |
| regulation of metaphase/anaphase transition of cell cycle (GO:1902099) |
| regulation of cell cycle phase transition (GO:1901987) |
| regulation of cell cycle process (GO:0010564) |
| regulation of sister chromatid segregation (GO:0033045) |
| regulation of chromosome organization (GO:0033044) |
| regulation of chromosome segregation (GO:0051983) |
| regulation of mitotic sister chromatid separation (GO:0010965) |
| regulation of chromosome separation (GO:1905818) |
| regulation of mitotic cell cycle phase transition (GO:1901990) |

| positive regulation of cell cycle (GO:0045787) |
|---------------------------------------------------------------------------------|
| positive regulation of metaphase/anaphase transition of cell cycle (GO:1902101) |
| positive regulation of mitotic sister chromatid separation (GO:1901970) |
| positive regulation of chromosome separation (GO:1905820) |
| positive regulation of mitotic nuclear division (GO:0045840) |
| positive regulation of nuclear division (GO:0051785) |
| regulation of nuclear division (GO:0051783) |
| regulation of mitotic nuclear division (GO:0007088) |
| □ rRNA export from nucleus (GO:0006407) |
| ncRNA export from nucleus (GO:0097064) |
| □ |
| ubiquitin-dependent endocytosis (GO:0070086) |
| phosphorylation of RNA polymerase II C-terminal domain (GO:0070816) |
| mitotic spindle assembly checkpoint (GO:0007094) |
| spindle assembly checkpoint (GO:0071173) |
| negative regulation of mitotic metaphase/anaphase transition (GO:0045841) |
| negative regulation of mitotic nuclear division (GO:0045839) |
| negative regulation of metaphase/anaphase transition of cell cycle (GO:1902100) |
| negative regulation of mitotic sister chromatid separation (GO:2000816) |
| negative regulation of chromosome separation (GO:1905819) |
| negative regulation of chromosome segregation (GO:0051985) |
| negative regulation of mitotic sister chromatid segregation (GO:0033048) |
| regulation of mitotic sister chromatid segregation (GO:0033047) |
| negative regulation of sister chromatid segregation (GO:0033046) |

| formation of cytoplasmic translation initiation complex (GO:0001732) |
|----------------------------------------------------------------------|
| cytoplasmic translation (GO:0002181) |
| translational initiation (GO:0006413) |
| □ carbohydrate metabolic process (GO:0005975) |
| response to toxic substance (GO:0009636) |
| response to chemical (GO:0042221) |
| cellular response to oxidative stress (GO:0034599) |
| □ |
| □ tRNA transcription by RNA polymerase III (GO:0042797) |
| TRNA transcription (GO:0009304) |
| ncRNA transcription (GO:0098781) |
| termination of RNA polymerase III transcription (GO:0006386) |
| □ |
| iron-sulfur cluster assembly (GO:0016226) |
| metallo-sulfur cluster assembly (GO:0031163) |
| □ tRNA processing (GO:0008033) |
| transcription, RNA-templated (GO:0001172) |
| DNA unwinding involved in DNA replication (GO:0006268) |
| spliceosomal snRNP assembly (GO:0000387) |
| ribosomal large subunit assembly (GO:0000027) |
| □ fungal-type cell wall organization (GO:0031505) |
| Cell wall organization (GO:0071555) |
| external encapsulating structure organization (GO:0045229) |
| cell adhesion (GO:0007155) |
| biological adhesion (GO:0022610) |

| tRNA gene clustering (GO:0070058) |
|----------------------------------------------------------------------------|
| tRNA transport (GO:0051031) |
| cell division (GO:0051301) |
| poly(A)+ mRNA export from nucleus (GO:0016973) |
| mRNA export from nucleus (GO:0006406) |
| mRNA-containing ribonucleoprotein complex export from nucleus (GO:0071427) |
| mRNA transport (GO:0051028) |
| histidine biosynthetic process (GO:0000105) |
| histidine metabolic process (GO:0006547) |
| leucine metabolic process (GO:0006551) |
| polyol transport (GO:0015791) |
| protein import into mitochondrial matrix (GO:0030150) |
| □ protein targeting to mitochondrion (GO:0006626) |

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