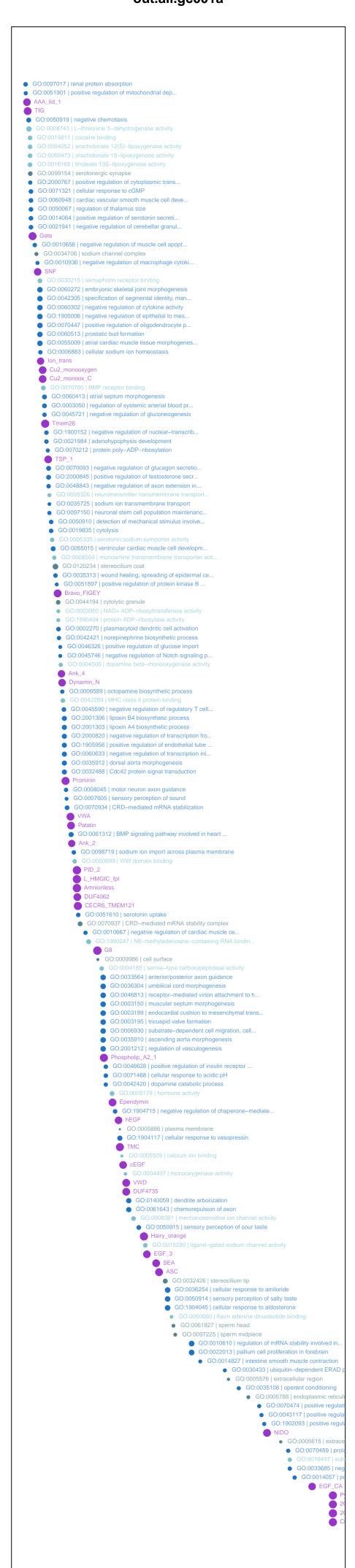
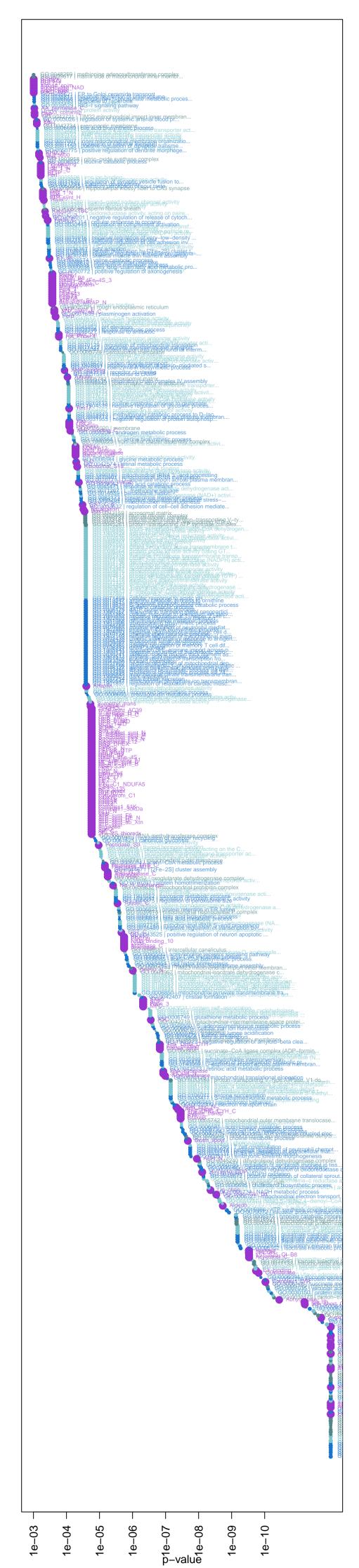
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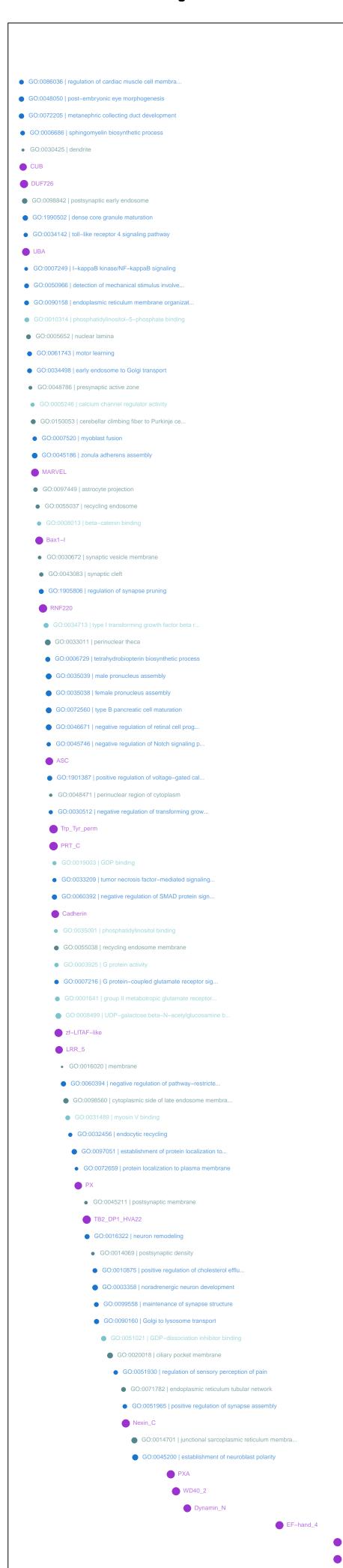


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out.all.gc002b

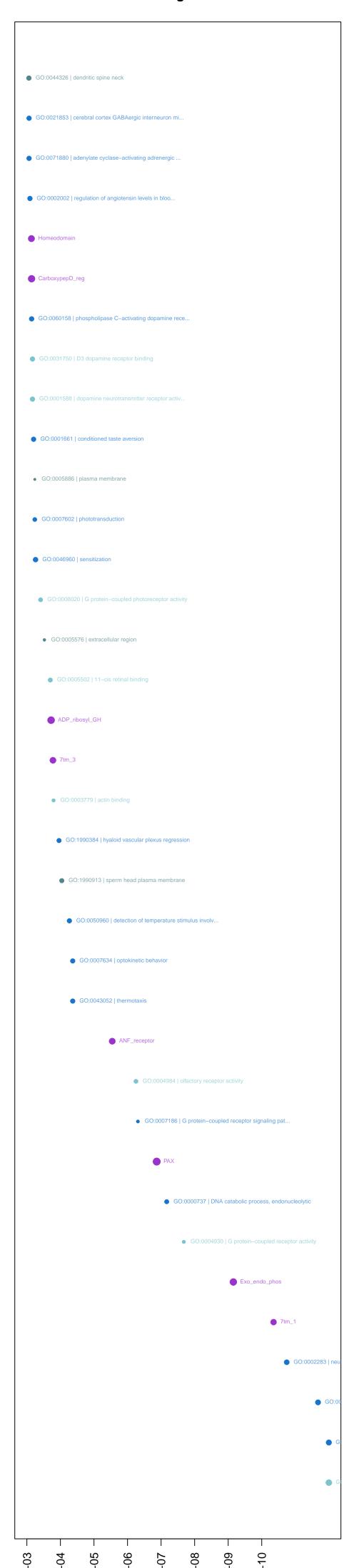


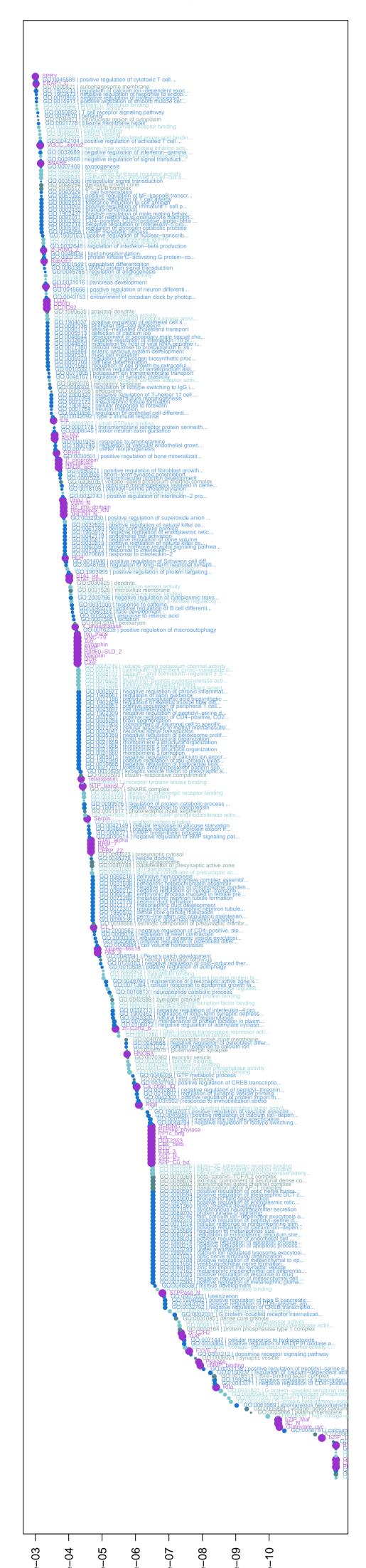
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out.all.gc003a



out.all.gc003b









1e-03 1e-04 1e-05 1e-06 1e-09 1e-09 1e-09

out.all.gc007a

 GO:0006310 | DNA recombination Ribosomal_60s MutS_IV GO:0008097 | 5S rRNA binding Apc13p • GO:1905168 | positive regulation of double-strand bre... GO:0000795 | synaptonemal complex GO:0035861 | site of double-strand break GO:0004364 | glutathione transferase activity SAP GO:0000028 | ribosomal small subunit assembly • GO:0008541 | proteasome regulatory particle, lid subc... GO:0070578 | RISC-loading complex GO:1990726 | Lsm1-7-Pat1 complex GO:0000993 | RNA polymerase II complex binding GO:1901165 | positive regulation of trophoblast cell ... GO:0070922 | small RNA loading onto RISC GO:0045292 | mRNA cis splicing, via spliceosome GO:0007130 | synaptonemal complex assembly Piwi GO:0042138 | meiotic DNA double-strand break formatio... • GO:0048026 | positive regulation of mRNA splicing, vi... GO:0006261 | DNA-dependent DNA replication GST C 2 GO:0031386 | protein tag GO:0043248 | proteasome assembly GO:0003697 | single-stranded DNA binding GO:0005736 | RNA polymerase I complex GO:0005829 | cytosol GO:0007129 | homologous chromosome pairing at meiosis GO:0070181 | small ribosomal subunit rRNA binding GO:0007131 | reciprocal meiotic recombination GO:0006417 | regulation of translation GO:0043596 | nuclear replication fork GO:0008380 | RNA splicing GO:0008250 | oligosaccharyltransferase complex GO:0098808 | mRNA cap binding GO:0003727 | single-stranded RNA binding GO:0043021 | ribonucleoprotein complex binding • GO:0005682 | U5 snRNP GO:0000462 | maturation of SSU-rRNA from tricistronic... GO:0042985 | negative regulation of amyloid precursor... GO:0000027 | ribosomal large subunit assembly GO:0006298 | mismatch repair GO:0060213 | positive regulation of nuclear-transcrib... GO:0071243 | cellular response to arsenic-containing ... GO:0140535 | intracellular protein-containing complex GO:0045947 | negative regulation of translational ini... GO:0017069 | snRNA binding GO:0006413 | translational initiation GO:0035279 | mRNA cleavage involved in gene silencing... GO:0090625 | mRNA cleavage involved in gene silencing... GO:0070551 | endoribonuclease activity, cleaving siRN. GO:0090624 | endoribonuclease activity, cleaving miRN.. GO:0070180 | large ribosomal subunit rRNA binding GO:0060316 | positive regulation of ryanodine-sensiti. GO:0060315 | negative regulation of ryanodine-sensiti... GO:0003684 | damaged DNA binding GO:0030422 | production of siRNA involved in RNA inte... GO:0019774 | proteasome core complex, beta-subunit co... GO:0050610 | methylarsonate reductase activity GO:0045174 | glutathione dehydrogenase (ascorbate) ac.. GO:0000398 | mRNA splicing, via spliceosome GO:0098794 | postsynapse GO:0034719 | SMN-Sm protein complex GO:0003743 | translation initiation factor activity GO:0034715 | plCln-Sm protein complex GO:0000340 | RNA 7-methylguanosine cap binding GO:0005685 | U1 snRNP GO:0019773 | proteasome core complex, alpha-subunit c... GO:0005845 | mRNA cap binding complex GO:0120115 | Lsm2-8 complex GO:0005688 | U6 snRNP GO:0034709 | methylosome GO:0031369 | translation initiation factor binding GO:0071007 | U2-type catalytic step 2 spliceosome GST_N_3 GO:0035278 | miRNA mediated inhibition of translation GO:0000932 | P-body GO:0005689 | U12-type spliceosomal complex GO:0071013 | catalytic step 2 spliceosome Proteasome_A_N GO:0005687 | U4 snRNP GO:0006364 | rRNA processing GO:0005686 | U2 snRNP GO:0140513 | nuclear protein-containing complex • GO:0005844 | polysome GO:0071005 | U2-type precatalytic spliceosome GO:0000387 | spliceosomal snRNP assembly RRM_1 • GO:0005730 | nucleolus GO:0003723 | RNA binding GO:0046540 | U4/U6 x U Proteasom LSM

```
GO:0002039 | p53 binding
GO:0031297 | replication fork processing
GO:0072711 | cellular response to hydroxyurea
GO:1990414 | replication-born double-strand break rep...
GO:0000811 | GINS complex
GO:0002862 | negative regulation of inflammatory resp...
GO:0043137 | DNA replication, removal of RNA primer
GO:0004298 | threonine-type endopeptidase activity
           GO:0001741 | XY body
          Rad60-SLD
eIF-1a
GO:0071208 | histone pre-mRNA DCP binding
Clat_adaptor_s
               Clat_adaptor_s
GO:0003730 | mRNA 3'-UTR binding
GO:1904874 | positive regulation of telomerase RNA lo..
GO:0000502 | proteasome complex
               GO:000502 | proteasome complex
Histone
GO:0077979 | protein K11-linked ubiquitination
GO:0044209 | AMP salvage
GO:0000470 | maturation of LSU-rRNA
GO:0006301 | postreplication repair
GO:0007098 | centrosome cycle
GO:0034501 | protein localization to kinetochore
                      ubiquitin
NOP5NT
EF1_GNE
DEK_C
                         GO:0005852 | eukaryotic translation initiation factor...
GO:0046601 | positive regulation of centriole replica...
PPP1R35_C
GO:0045876 | positive regulation of sister chromatid ...
                         GO:0042273 | ribosomal large subunit biogenesis
GO:0032212 | positive regulation of telomere maintena...
GO:0010621 | negative regulation of transcription by ...
GO:0032556 | pyrimidine deoxyribonucleotide binding
GO:0004019 | adenylosuccinate synthase activity
                               GO:0098894 | extrinsic component of presynaptic endoc...
GO:001824 | blastocyst development
GO:1990825 | sequence–specific mRNA binding
                                  GO:0042274 | ribosomal small subunit biogenesis
DUF1761
GO:0098794 | postsynapse
GO:0043248 | proteasome assembly
                                   GO:0043248 | protects:
E2F_TDP
GO:0001673 | male germ cell nucleus
GO:2000001 | regulation of DNA damage checkpoint
GO:0033597 | mitotic checkpoint complex
GO:0044614 | nuclear pore cytoplasmic filaments
GO:0004523 | RNA_DNA hybrid ribonuclease activity
                                         GO:0004523 | RNA—DNA hybrid ribonuclease activity
GO:0120099 | procentriole replication complex
GO:0071162 | CMG complex
GO:0006401 | RNA catabolic process
GO:0000244 | spliceosomal tri–snRNP complex assembly
Sld5
Prefoldin_2
GO:00704801 | Least 17
                                              GO:0070180 | large ribosomal subunit rRN/
GO:0035861 | site of double–strand break
GO:1901998 | toxin transport
GO:0048478 | replication fork protection
GO:0006284 | base–excision repair
PCI
                                                   Prefoldin
GO:0016605 | PML body
                                                                                                                                                                         randed DNA binding
                                                   GO:0003697 | single-stranded DNA binding
GO:0006406 | mRNA export from nucleus
GO:0010498 | proteasomal protein catabolic process
GO:0000454 | snoRNA guided rRNA pseudouridine synthes...
GO:0030578 | PML body organization
                                                           GO:0000028 | ribosomal small subunit assembly XPG_N
GO:1990062 | RPAP3/R2TP/prefoldin-like complex
                                                               GO:0005829 | cytosol
GO:000800 | lateral element
                                                                   GO:0031369 | translation initiation factor binding
GO:0006334 | nucleosome assembly
GO:0043021 | ribonucleoprotein complex binding
                                                     SIMPL
Mago_nashi
GO:0007004 | telomere maintenance via telomerase
GO:0035145 | exon-exon junction complex
GO:0098631 | postsynaptic endocytic zone cytoplasmic ...
GO:0031439 | positive regulation of mRNA cleavage
GO:2000975 | positive regulation of pro-B cell differ...
XPG_I
DNA_pol_E_B
CSN8_PSD8_EIF3K
GO:0050821 | protein stabilization
GO:0000413 | protein peptidyl-prolyl isomerization
GO:0051168 | nuclear export
HMG_box
                                                                    SIMPL
                                                                       GO:0051168 | nuclear export
HMG_box
GO:1900087 | positive regulation of G1/S transition o...
GO:007339 | binding of sperm to zona pellucida
GO:0008622 | epsilon DNA polymerase complex
GO:0061574 | ASAP complex
GO:0051225 | spindle assembly
GO:0000127 | ribosomal large subunit assembly
GO:0000027 | ribosomal large subunit assembly
GO:0090661 | box H/ACA telomerase RNP complex
GO:031298 | replication fork protection complex
GO:0005854 | nascent polypeptide-associated complex
GO:1990723 | cytoplasmic periphery of the nuclear por...
                                                                                        GO:1990723 | cytoplasmic periphery of the nuclear por..
GO:0070182 | DNA polymerase binding
                                                                           GO:0043111 | replication fork arrest
GO:0034421 | post–translational protein acetylation
Prp19
PAC4
                                                                                              NUDIX 2
                                                                                              Metallophos_2
                                                                                              Clathrin_lg_ch
                                                                                                  GO:0003682 | chromatin binding
GO:00036841 | proteasome regulatory particle, lid subc...
GO:2000622 | regulation of nuclear–transcribed mRNA c
GO:0005813 | centrosome
                                                                                   •
                                                                                                            GO:0005971 | ribonucleoside-diphosphate reductase com..
                                                                                                              GO:0004748 | ribonucleoside—diphosphate reductase act GO:0071006 | U2-type catalytic step 1 spliceosome GO:0005658 | alpha DNA polymerase:primase complex GO:0006269 | DNA replication, synthesis of RNA primer GO:0032040 | small—subunit processome GO:0001650 | fibrillar center GO:0061077 | chaperone—mediated protein folding GO:0005850 | eukaryotic translation initiation factor...
                                                                                                                          NTF2
                                                                                                                          LZ3wCH
GO:0006231 | dTMP biosynthetic process
GO:0006272 | leading strand elongation
GO:1903934 | positive regulation of DNA primase activ..
GO:0000974 | Prp19 complex
GO:0006260 | DNA replication
GO:0031429 | box H/ACA snoRNP complex
GO:0034513 | box H/ACA snoRNA binding
Ribosomal_LZAe
CBFD_NFYB_HMF
GO:0005844 | polysome
GO:0006413 | translational initiation
GO:1990948 | ubiquitin ligase inhibitor activity
                                                                                                               JOSOTING.

JED. NFYB F.I..

O:0005844 | polysus.

O:0005844 | polysus.

O:0005845 | translationa I...

GO:0002183 | cytoplasmic translationa I...

GO:0000586 | SNNA polymerase II...

GO:0005665 | RNA polymerase II...

GO:0001731 | formation of translation preinitiation c...

GO:0001731 | formation of translation preinitiation c...

GO:0001299 | zona pellucida receptor complex

GO:0001299 | zona pellucida receptor complex

GO:0017541 | eukaryotic translation initiation factor...

GO:0017541 | eukaryotic translation initiation factor...

GO:001930 | lower permitted in the previous present in the previous previ
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1e-03 1e-03 1e-05 1e-06 1e-09 1e-09

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GO:0036499 | PERK-mediated unfolded protein response
 Glyco_tran_10_N
GO:1990573 | potassium ion import across plasma membr..
GO:0034663 | endoplasmic reticulum chaperone complex
  Synaptobrevin
   COP-gamma_platf
   Coatomer_g_Cpla
   Coatomer E
   Coatamer_beta_C
Adaptin_N
   V-SNARE C
    GO:0003977 | UDP-N-acetylglucosamine diphosphorylase ...
   GO:0003876 | AMP deaminase activity
GO:0015389 | pyrimidine– and adenine–specific:sodium
   GO:0098989 | NMDA selective glutamate receptor signal...
   GO:0016222 | procollagen-proline 4-dioxygenase comple...
    GO:0010908 | regulation of heparan sulfate proteoglyc.
Clat_adaptor_s
     GO:0006044 | N-acetylglucosamine metabolic process
     GO:1903334 | positive regulation of protein folding GO:0032225 | regulation of synaptic transmission, dop...
      GO:0005789 | endoplasmic reticulum membrane
      GO:0007155 | cell adhesion
      GO:1904749 | regulation of protein localization to nu...
GO:0045662 | negative regulation of myoblast differen.
       E1-E2 ATPase
       GO:0071340 | skeletal muscle acetylcholine-gated chan...
GO:1901621 | negative regulation of smoothened signal...
GO:0060670 | branching involved in labyrinthine layer...
        HLH
         GO:0098696 | regulation of neurotransmitter receptor ..
         O-FucT
         Melibiase_2_C
         GO:0106326 | acetylgalactosaminyl-O-glycosyl-threonyl
         GO:0005388 | P-type calcium transporter activity
GO:0045742 | positive regulation of epidermal growth
         GO:2001256 | regulation of store–operated calcium ent.
GO:0010273 | detoxification of copper ion
         GO:0002426 | immunoglobulin production in mucosal tis...
         GO:0008631 | intrinsic apoptotic signaling pathway in.
         GO:0042998 | positive regulation of Golgi to plasma m..
         GO:0000390 | spliceosomal complex disassembly
GO:0006487 | protein N-linked glycosylation
           AA_permease_2
GO:1903912 | negative regulation of endoplasmic retic...
           GO:0040037 | negative regulation of fibroblast growth...
GO:0006047 | UDP-N-acetylglucosamine metabolic proces..
            GO:0030663 | COPI-coated vesicle membrane
             GO:0032703 | negative regulation of interleukin-2 pro...
             ER_lumen_recept
             GO:1904257 | zinc ion import into Golgi apparatus
GO:1903671 | negative regulation of sprouting angioge...
             GO:0099612 | protein localization to axon
GO:0044316 | cone cell pedicle
GO:0071008 | U2-type post-mRNA release spliceosomal c...
              GO:0070885 | negative regulation of calcineurin-NFAT .
               Bravo_FIGEY

    GO:0003331 | positive regulation of extracellular mat...

                  GO:0045914 | negative regulation of catecholamine met...
                 GO:0032773 | positive regulation of tyrosinase activi..
GO:0051542 | elastin biosynthetic process
                  GO:0033106 | cis-Golgi network membrane
GO:0004653 | polypeptide N-acetylgalactosaminyltransf..
                   GO:1990569 | UDP-N-acetylglucosamine transmembrane tr...
                   GO:1902960 | negative regulation of aspartic–type end. GO:0050714 | positive regulation of protein secretion
                Hydrolase
                     Nuc_sug_transp
                     GO:0033499 | galactose catabolic process via UDP-gala...
                      GO:0046922 | peptide-O-fucosyltransferase activity
                            :0005459 | UDP-galactose transmembrane transporter ...
                     GO:1905069 | allantois development
GO:0019676 | ammonia assimilation cycle
                      GO:1904457 | positive regulation of neuronal action p...
GO:0032472 | Golgi calcium ion transport
                      GO:0032468 | Golgi calcium ion homeostasis
                      EGF_CA

    GO:0006002 | fructose 6-phosphate metabolic process

                     WH1
Rap_GAP
                       Pacifastin_I
                          GO:0032119 | sequestering of zinc ion
                           GO:1990674 | Golgi cis cisterna membrane
                           GDP Man Dehyd
                             GO:0061623 | glycolytic process from galactor
                             GO:1990440 | positive regulation of transcription fro...
GO:0005883 | neurofilament
                               GO:0048280 | vesicle fusion with Golgi apparatus
                                GO:1903078 | positive regulation of protein localizat...
GO:0035251 | UDP-glucosyltransferase activity
                                   Gln-synt_C
                                    GO:0098962 | regulation of postsynaptic neurotransmit.
GO:0030026 | cellular manganese ion homeostasis
                                    GO:0098629 | trans-Golgi network membrane organizatio.
                                     GO:0012507 | ER to Golgi transport vesicle membrane
                                      GO:0050766 | positive regulation of phagocytosis
                                         GO:0018243 | protein O-linked glycosylation via threo.
GO:0006041 | glucosamine metabolic process
GO:0035964 | COPI-coated vesicle budding
                                           EGF_3
                                           SRA1
                                           Rer1
                                           Gln-synt N
                                           GO:0008109 | N-acetyllactosaminide beta-1,6-N-acetylg.
                                           GO:0004356 | glutamate–ammonia ligase activity
GO:0004360 | glutamine–fructose–6–phosphate transamin.
                                           GO:0008456 | alpha-N-acetylgalactosaminidase activity
                                           GO:0021521 | ventral spinal cord interneuron specific...
GO:0090073 | positive regulation of protein homodimer..
                                           GO:0106273 | cytosol to ERGIC protein transport
GO:0106272 | protein localization to ERGIC
                                           GO:0006542 | glutamine biosynthetic process
GO:0005831 | steroid hormone aporeceptor complex
GO:0001967 | suckling behavior
GO:0042589 | zymogen granule membrane
                                                   yos1
Thioredoxin
MFS_1_like
Lectin_lea
Glyce
                                                 Thioredoxin_6
                                                        Lectin_leg-like
                                                        Glyco transf 90
                                                         GO:2000821 | regulation of grooming behavior
GO:1904425 | negative regulation of GTP binding
                                                         GO:1903899 | positive regulation of PERK–mediated unf. GO:1903896 | positive regulation of IRE1–mediated unf...
                                                             GO:0005783 | endoplasmic reticulum
GO:0006621 | protein retention in ER lumen
                                                                     GO:000621 | protein Feteriuon in Ex turnen
GO:0018242 | protein O-linked glycosylation via serin...
GO:0070971 | endoplasmic reticulum exit site
GO:0035256 | G protein-coupled glutamate receptor bin
GO:0004343 | glucosamine 6-phosphate N-acetyltransfe
                                                                                           GO:0060480 | lung goblet cell differentiation
                                                                                           GO:0021858 | GABAergic neuron differentiation in basa. GO:1990792 | cellular response to glial cell derived ...
                                                                                            GO:1903697 | negative regulation of microvillus assem.
                                                                                           GO:1903697 | negative regulation of microvinus asseri...
GO:1904442 | negative regulation of thyroid gland epi...
GO:0005801 | cis=Golgi network
GO:0030137 | COPI-coated vesicle
GO:0034975 | protein folding in endoplas
                                                                                                                           ■ EMP70
                                                                                                                                      GO:0016020 | membrane

• GO:0030127 | COPII
                                                                                                                                              GO:0090110 | COPI
                                                                                                                                                           GO:003031
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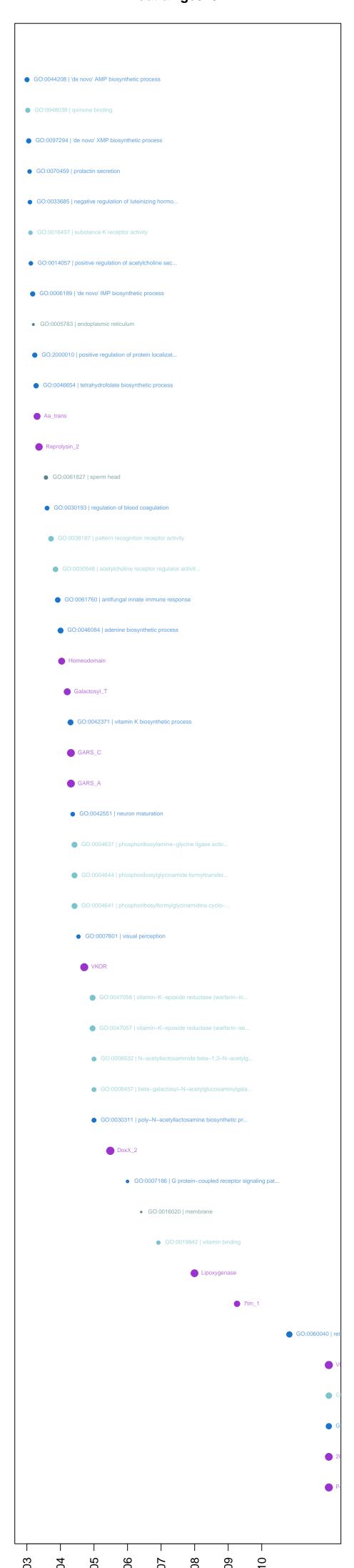
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GO:0006107 | oxaloacetate metabolic process

GO:0006094 | gluconeogenesis

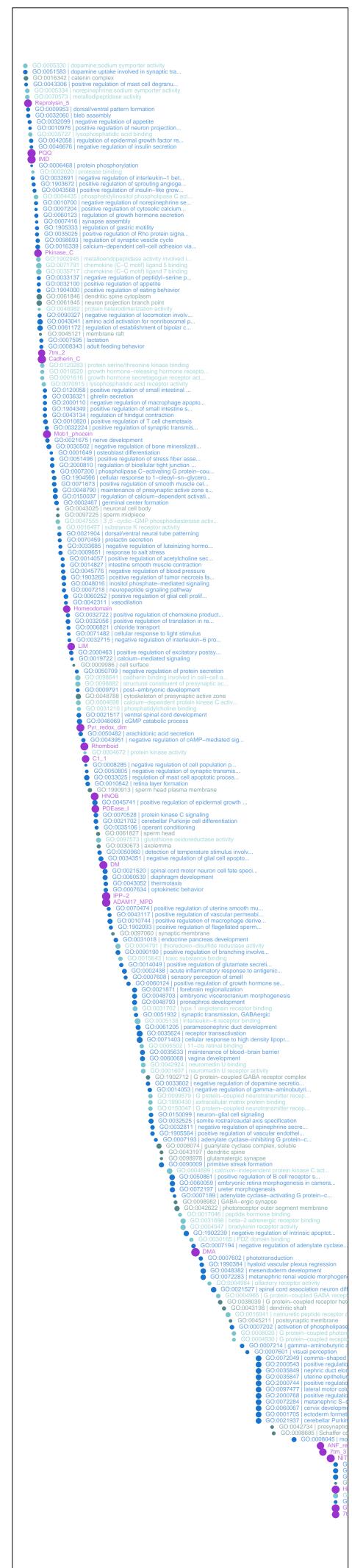
Tcp10_C



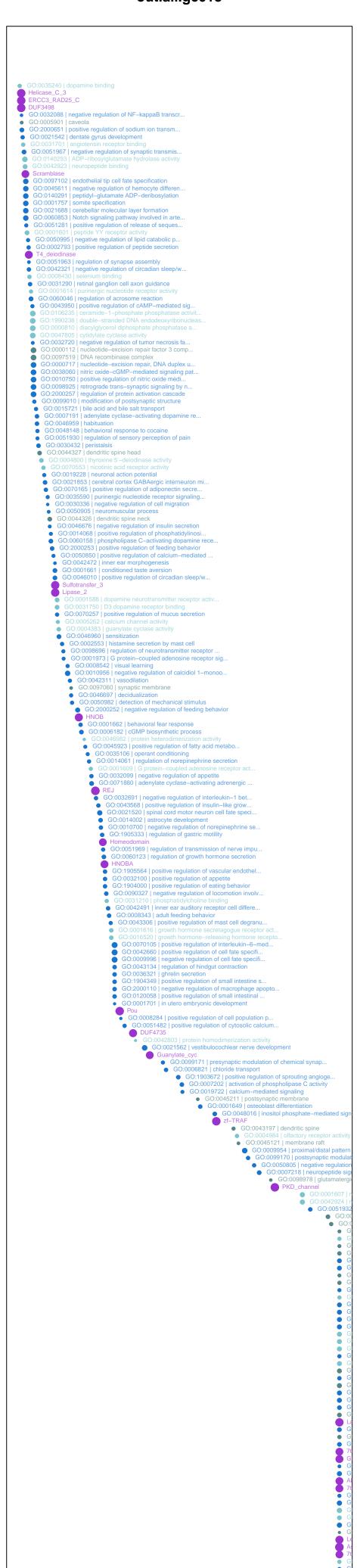
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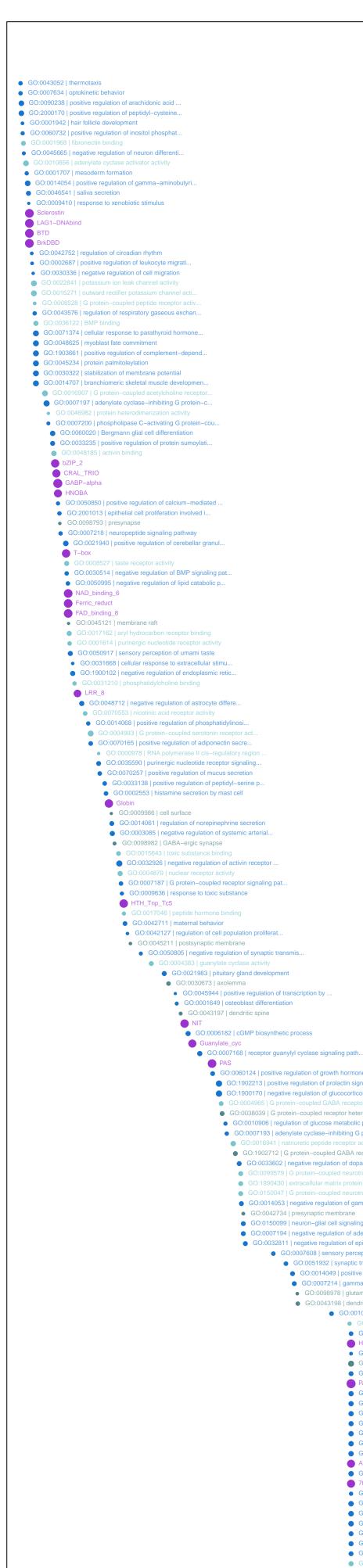


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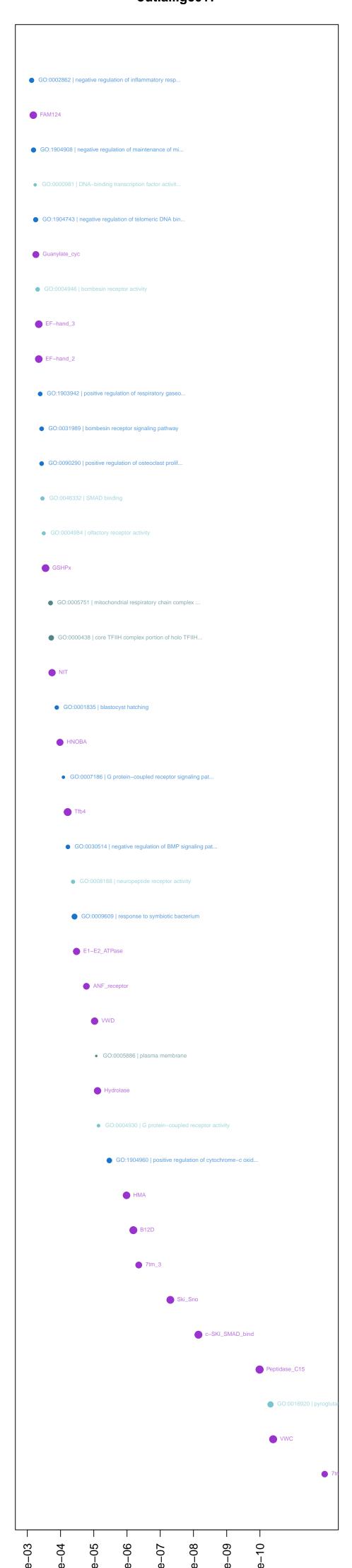
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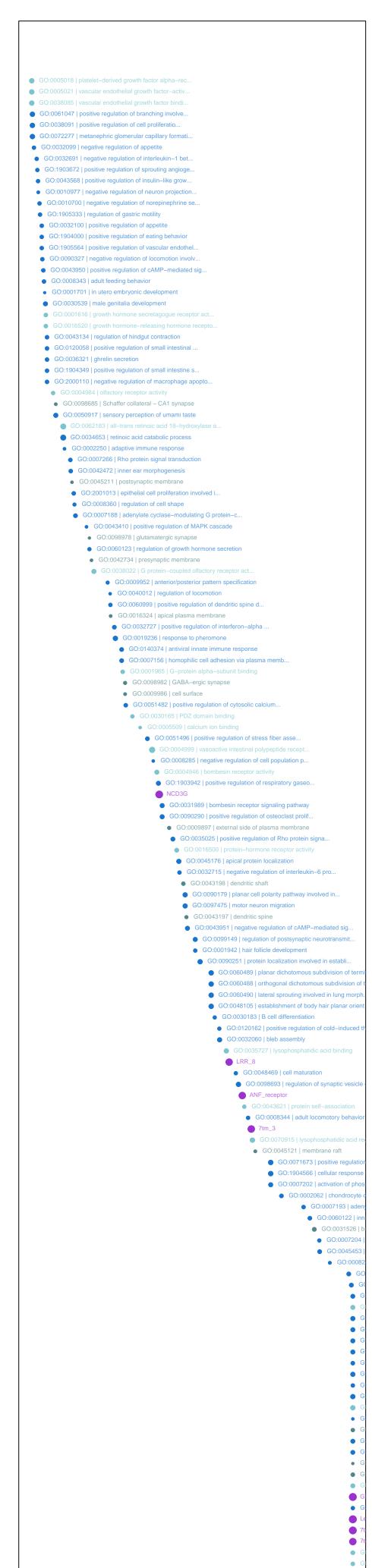
G G

G G G









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GO:0090521 | glomerular visceral epithelial cell migr...
GO:0022027 | interkinetic nuclear migration
GO:0035331 | negative regulation of hippo signaling
GO:0045736 | negative regulation of cyclin-dependent ...
GO:0004776 | chromosome, centromeric region
GO:0045162 | clustering of voltage-gated sodium chann...
GO:0019370 | clustorien biosynthetic process
GO:1905720 | cytoplasmic microtubule bundle
GO:0031870 | thromboxane A2 receptor binding
GO:0140483 | kinetochore adaptor activity
                                                                                                                                                                      kinetochore adaptor activity cortical microtubule hyaluronic acid
                                                                                    votrical microtubule
votrical votrical victor
votrical victor
votrical microtubule
votrical votrical victor
votrical victor
votrical microtubule
votrical victor
votrical v
                                                                                                      61631 | ubiquitin conjugating enzyme activity
HEC
190435 | protein localization to nuclear envelope
090129 | positive regulation of synapse maturatio...
031915 | positive regulation of synaptic plastici...
046602 | regulation of mitotic centrosome separat...
                                                                                                         .
0005829 | cytosol
NAPC11
                                                                                                   _
o_morph_reg
M1
                                                                                                            S1_C
VWSH
4498
(N3
)C144C
                                                                                                               C1440
22 1
A TN
2040020 | regulation of meiotic nuclear division
0007266 | Rho protein signal transduction
1990713 | survivin complex
0098536 | deuterosome
0031552 | negative regulation of brain-derived neu...
                                                                                                                        | Country | Coun
                                                                                                                     O:0019237 | centromeric DNA binding
O:0010800 | positive regulation of peptidyl–threonin...
                                                                                                                                              d3_BUB1_I
IMR_N
                                                                                                      GO:005096 | GTPase activator activity
GO:0051987 | positive regulation of attachment of spi...
GO:0042826 | histone deacetylase binding
                                                                                                                                                                   0010836 | negative regulation of protein ADP-ribos..
0:0007059 | chromosome segregation
0:0032465 | regulation of cytokinesis
-C2HC_2
                                                                                                                                                                                        | GO:0040038 | ciliarly transition zone | Coronador | 
                                                                                                                                                                                                                                                    positive regulation of protein kinase activity 051321 | activation of protein kinase activity 051321 | meiotic cell cycle 042307 | positive regulation of protein import in... 0090063 | positive regulation of microtubule nucle... 0513291 | photoreceptor connecting cilium
                                                                                                                                                                                                                                              con
0000307 | cyclin-dependent protein kinase holoenzy...
prT-like
                                                                                                                                                                                                                                                             T-like
AP
G4_ERG24
                                                                                                                                                                                                                                              north Sciou077099 | centriole replication RhoGEF Sciou077099 | centriole replication RhoGEF Sciou077099 | cestablishment or maintenance of microtub... Go:00030951 | establishment or maintenance of microtub... Go:0003682 | chromatin binding Go:00003682 | chromatin binding Rad52 Rad22 GO:0043203 | axon hillock GO:000120103 | centriolar subdistal appendage GO:0043203 | axon hillock GO:0097726 | CO:0097726 | CO:0097826 | CO:0099726 | CO:0099726 | CO:0099726 | CO:0099726 | CO:0099026 | CO:00990273 | co:00990726 | CO:0099026 | CO:0099026 | CO:0099026 | CO:00990273 | co:00990726 | CO:00990273 | co:00990726 | CO:0099026 | CO:009026 | CO:0099026 | CO:0099026 | CO:009026 | CO:009026 | CO:009026 
                                                                                                                                                                                                                                                                0:0007099 | centriole replication
                                                                                                                                                                                                                                                                                                                                                                                                                  PX2

DPRIM_C
ACC_C

sindle_Spc25

P1_bind
OLO_box
KLP1_Arf_bdg
ito_fiss_reg

IIP
                                                                                                                                                                                                                                                                                                                                                                                                                                       rotub_bind
P65_ASE1
ENP_ARK-bind
MR_C
SET_N
54485
                                                                                                                                                                                                                                                                                                                                                                                                                                                         _N
                                                                                                                                                                                                                                                                                                                                                                                                                                    MS_motif
                                                                                                                                                                                                                                                                                                                                                                                                                                             P
:0005634 | nucleus
:1990757 | ubiquitin ligase activator activity
O:0051010 | microtubule plus-end binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1081 | nuclear membrane disassembly

17088 | regulation of mitotic nuclear division

1000070 | mitotic sister chromatid segregation

1008022 | protein C-terminus binding

1007084 | mitotic nuclear membrane reassembly

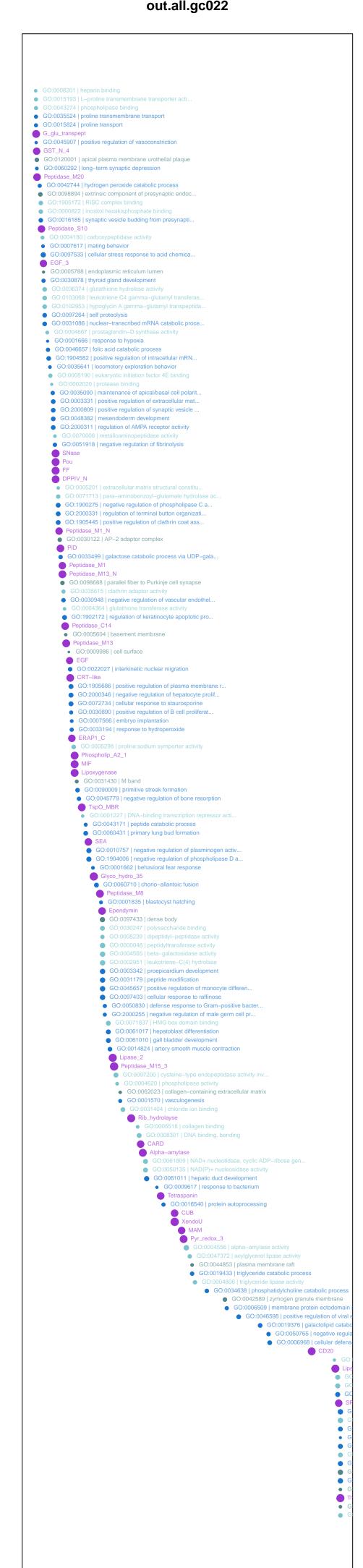
10031536 | positive regulation of exit from mitosis

100005815 | microtubule organizing center

100007091 | metaphase/anaphase transition of mitotic...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16321 | female meiosis chromosome segregation
097539 | ciliary transition fiber
0008608 | attachment of spindle microtubules to ki...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D070194 | synaptonemal complex disassembly
2 hinge:
0005721 | pericentric heterochromatin:
0005524 | ATP binding:
0010369 | controlled |

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0070194 | synaptonemal complex disassembly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      031616 | spindle pole centrosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6538 | cyclin-dependent protein seri
19901 | protein kinase binding
901673 | regulation of mitotic spindle
900086 | G2/M transition of mitotic ce
032154 | cleavage furrow
0060236 | regulation of mitotic spindle
1005038 | regulation of attachment
Cyclin V
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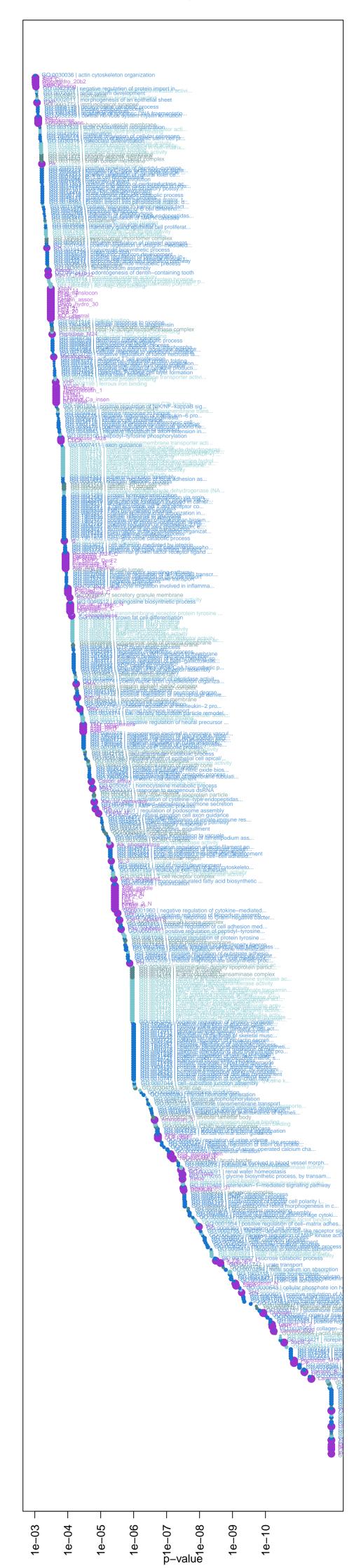
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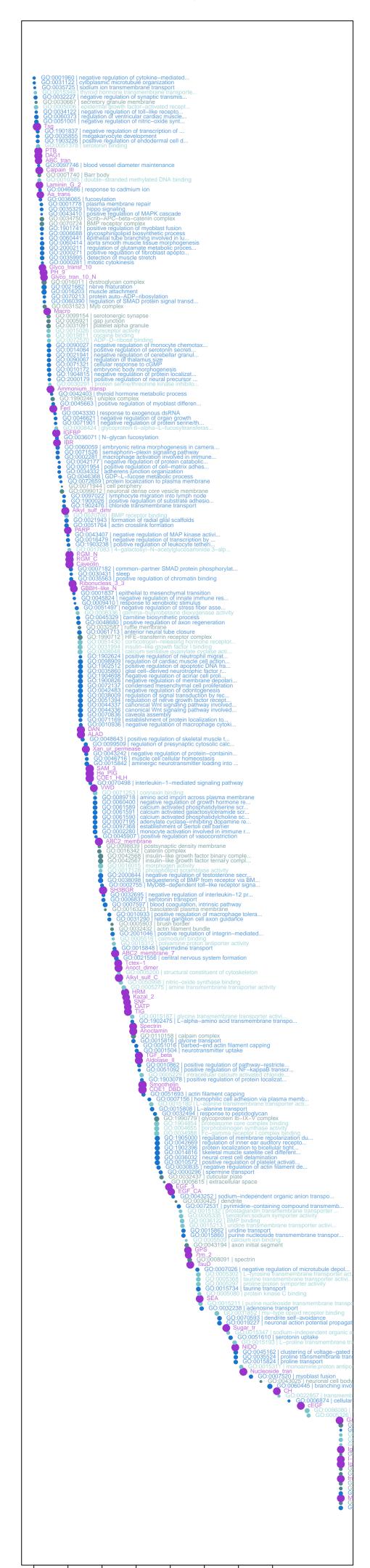


- out.all.gc023 GO:0001784 | phosphotyrosine residue binding GO:0001661 | conditioned taste aversion GO:0060134 | prepulse inhibition GO:0035136 | forelimb morphogenesis GO:0045110 | intermediate filament bundle assembly GO:0042311 | vasodilation GO:0001588 | dopamine neurotransmitter receptor activ... GO:0017166 | vinculin binding GO:0031750 | D3 dopamine receptor binding GO:0046960 | sensitization GO:0090136 | epithelial cell-cell adhesion GO:0031701 | angiotensin receptor binding GO:0001662 | behavioral fear response GO:0055075 | potassium ion homeostasis GO:0071801 | regulation of podosome assembly GO:0004879 | nuclear receptor activity GO:0098978 | glutamatergic synapse GO:0016342 | catenin complex GO:0008360 | regulation of cell shape GAF DMAP_binding GO:0046715 | active borate transmembrane transporter ■ GO:0033678 | 5'-3' DNA/RNA helicase activity GO:0046713 | borate transport GO:0005796 | Golgi lumen GO:0050796 | regulation of insulin secretion GO:2001241 | positive regulation of extrinsic apoptot... ● GO:0021670 | lateral ventricle development GO:0032211 | negative regulation of telomere maintena... GO:0035137 | hindlimb morphogenesis GO:0001938 | positive regulation of endothelial cell ... GO:0007406 | negative regulation of neuroblast prolif... GO:0055078 | sodium ion homeostasis GO:0106162 | mRNA N-acetyltransferase activity GO:1990883 | rRNA cytidine N-acetyltransferase activi... GO:0050379 | UDP-glucuronate 5'-epimerase act GO:0047464 | heparosan-N-sulfate-glucuronate 5-epimer.. GO:1904812 | rRNA acetylation involved in maturation .. GO:0072513 | positive regulation of secondary heart f.. GO:0070563 | negative regulation of vitamin D recepto. GO:0021849 | neuroblast division in subventricular zo... tRNA_bind_2 Helicase_RecD GNAT_acetyltr_2 **GDWWSH** Endosulfine DUF1726 C5-epim_C GO:0048745 | smooth muscle tissue development ■ GO:0060292 | long-term synaptic depression GO:0072044 | collecting duct development ● GO:0072017 | distal tubule development SAM_2 PSI GO:0008074 | guanylate cyclase complex, soluble GO:0003091 | renal water homeostasis PIF1 GO:0045295 | gamma-catenin binding GO:0021853 | cerebral cortex GABAergic interneuron mi... GO:0042622 | photoreceptor outer segment membrane GO:0051022 | Rho GDP-dissociation inhibitor binding DUF4205 DUF1736 GO:0071681 | cellular response to indole-3-methanol GO:0001669 | acrosomal vesicle GO:0010593 | negative regulation of lamellipodium ass... GO:0072210 | metanephric nephron development GO:0005901 | caveola GO:2001045 | negative regulation of integrin-mediated... GO:0010960 | magnesium ion homeostasis GO:0021542 | dentate gyrus development GO:0035909 | aorta morphogenesis GO:0017154 | semaphorin receptor activity Plexin_cytopl GO:0002116 | semaphorin receptor complex GO:1902287 | semaphorin-plexin signaling pathway invo... GO:0035269 | protein O-linked mannosylation GO:0008285 | negative regulation of cell population p... ● GO:0097070 | ductus arteriosus closure TIG_2 GO:0016264 | gap junction assembly GO:0001228 | DNA-binding transcription activator acti. GO:0035810 | positive regulation of urine volume SAM_1 GO:0045296 | cadherin binding GO:0060404 | axonemal microtubule depolymerization GO:0070462 | plus-end specific microtubule depolymeri... ■ GO:0005915 | zonula adherens GO:0048172 | regulation of short-term neuronal synapt... GO:2001240 | negative regulation of extrinsic apoptot... GO:0004169 | dolichyl-phosphate-mannose-protein manno. ● GO:0048485 | sympathetic nervous system development GO:0098831 | presynaptic active zone cytoplasmic comp... GO:0016081 | synaptic vesicle docking zf-C3HC4_4
 - 1e-03 1e-04 1e-05 1e-06 1e-09 1e-10 1e-09 1e-10

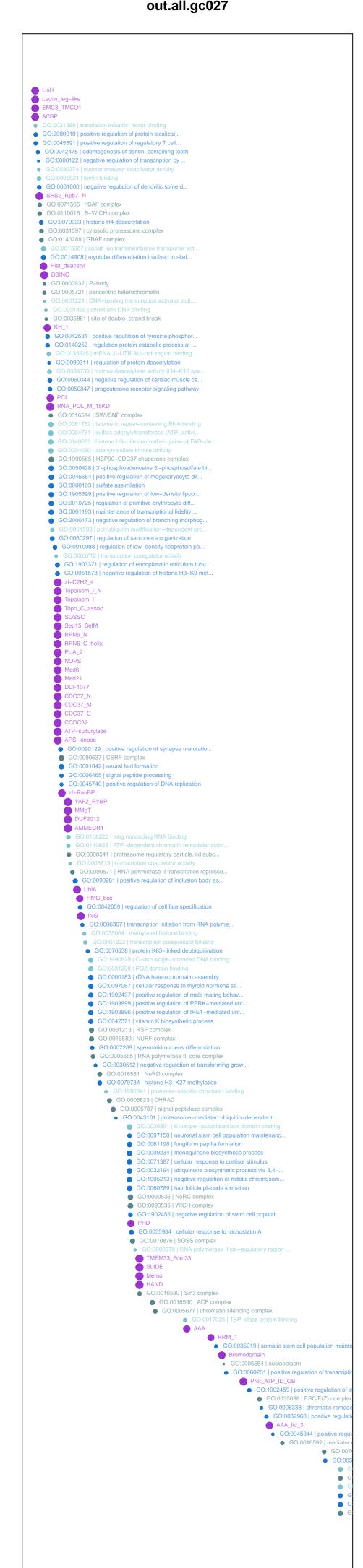
GO:0097275 | cellular ammonium homeosta
 GO:0097277 | cellular urea homeostasis
 GO:0097276 | cellular creatinine homeostas

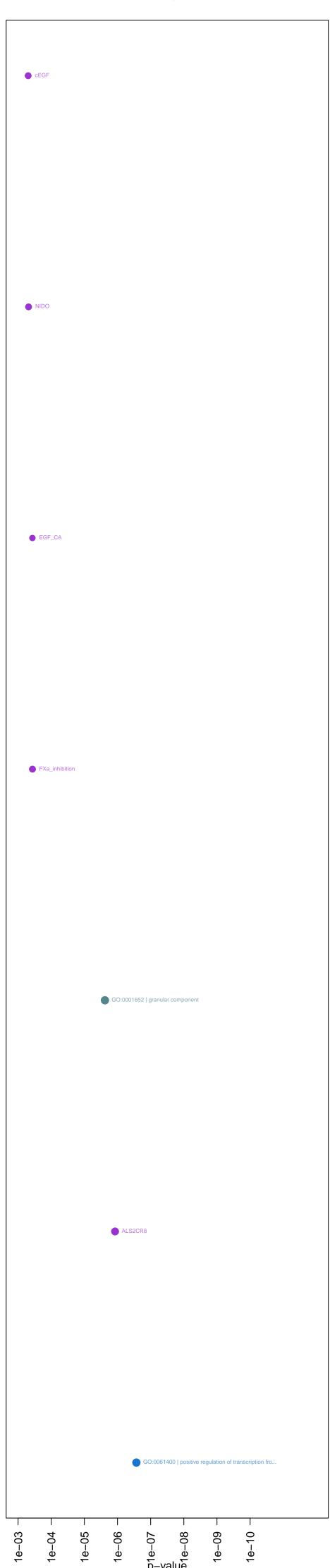
● GO:0098875 |





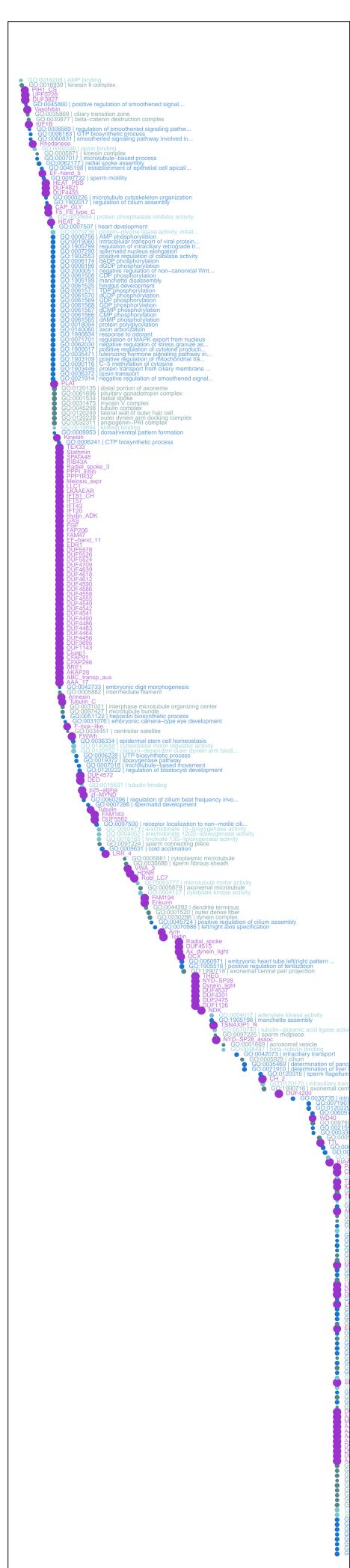








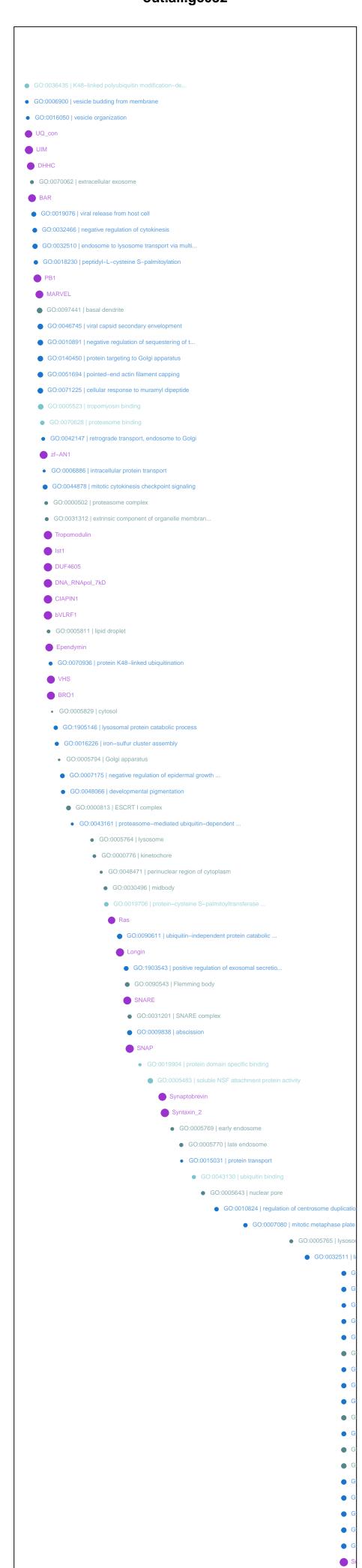
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1e-10

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