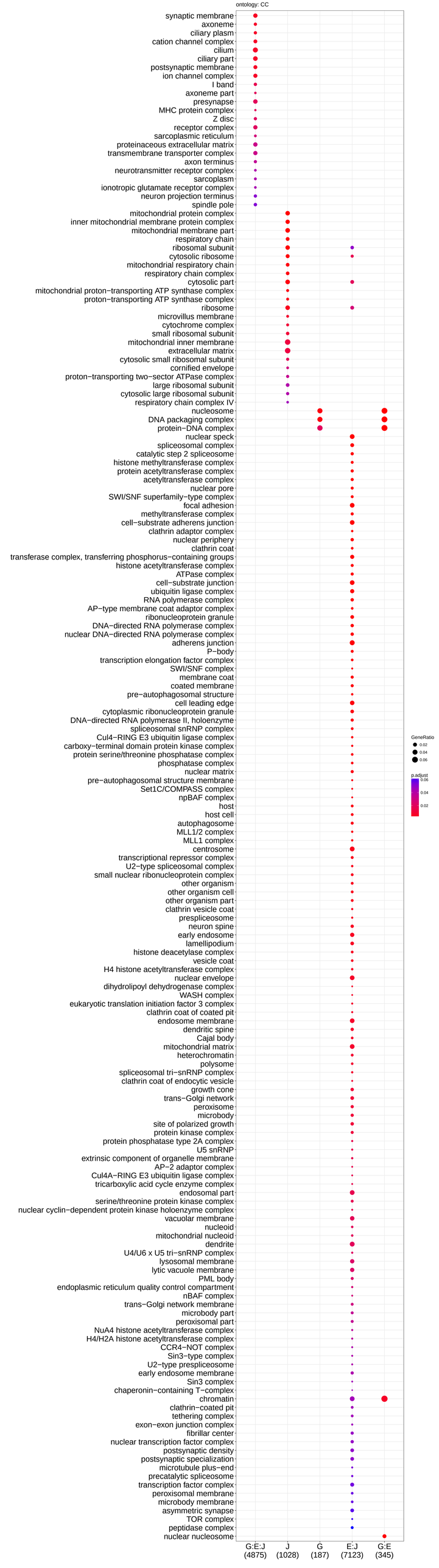
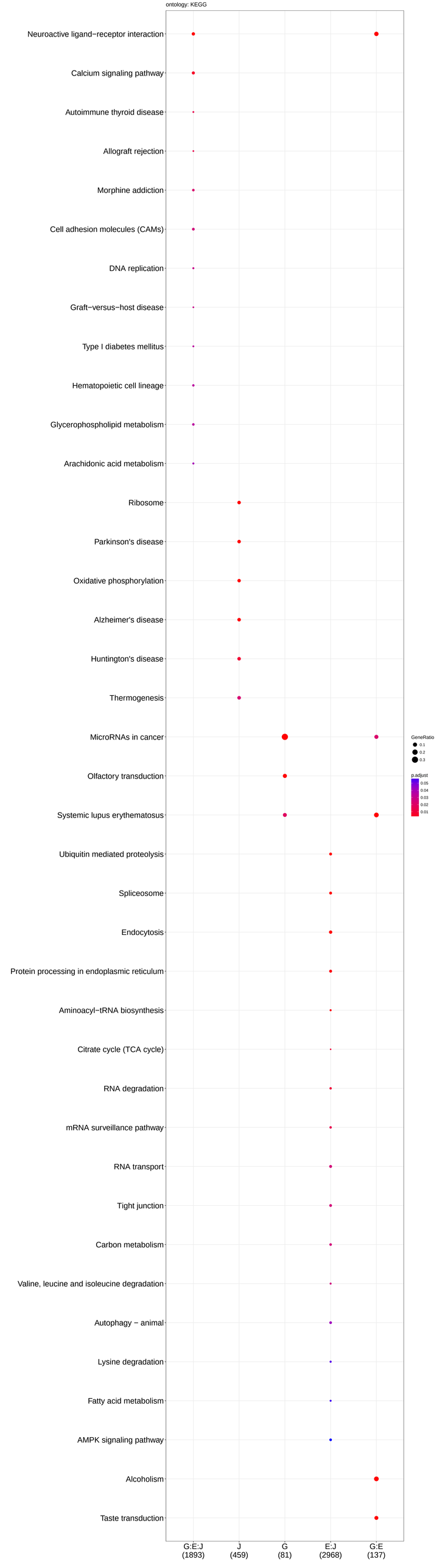

ontology: BP
protein targeting to ER
establishment of protein localization to endoplasmic reticulum
nucleoside monophosphate metabolic process
ribonucleoside monophosphate metabolic process
ATP metabolic process
ATP synthesis coupled electron transport
SRP−dependent cotranslational protein targeting to membrane
oxidative phosphorylation
cotranslational protein targeting to membrane
purine ribonucleoside monophosphate metabolic process
ribonucleoside triphosphate metabolic process
purine nucleoside triphosphate metabolic process
mitochondrial ATP synthesis coupled electron transport
purine ribonucleoside triphosphate metabolic process
respiratory electron transport chain
protein targeting to membrane
protein localization to endoplasmic reticulum
nucleoside triphosphate metabolic process
purine nucleoside triphosphate metabolic process
establishment of protein localization to membrane
cristae formation
nuclear−transcribed mRNA catabolic process, nonsense−mediated decay
protein targeting
inner mitochondrial membrane organization
cornification
mitochondrial membrane organization
ATP biosynthetic process
cellular response to tumor necrosis factor
keratinization
ribonucleoside monophosphate biosynthetic process
electron transport chain
response to tumor necrosis factor
regulation of receptor activity
hydrogen ion transmembrane transport
viral transcription
translational initiation
mitochondrial ATP synthesis coupled proton transport
ribonucleoside triphosphate biosynthetic process
nucleoside monophosphate biosynthetic process
linoleic acid metabolic process
nucleoside triphosphate biosynthetic process
purine ribonucleoside triphosphate biosynthetic process
gene silencing by miRNA
posttranscriptional gene silencing by RNA
posttranscriptional gene silencing
gene silencing
gene silencing by RNA
regulation of gene expression, epigenetic
negative regulation of translation
negative regulation of cellular amide metabolic process
regulation of translation
detection of chemical stimulus involved in sensory perception of smell
detection of chemical stimulus involved in sensory perception
sensory perception of smell
sensory perception of chemical stimulus
detection of stimulus involved in sensory perception
detection of chemical stimulus
miRNA mediated inhibition of translation
negative regulation of translation, ncRNA−mediated
regulation of translation, ncRNA−mediated
detection of stimulus
sensory perception
homophilic cell adhesion via plasma membrane adhesion molecules
mRNA processing
RNA splicing
RNA splicing, via transesterification reactions
RNA splicing, via transesterification reactions with bulged adenosine as nucleophile
mRNA splicing, via spliceosome
spliceosomal complex assembly
ribonucleoprotein complex biogenesis
histone modification
regulation of RNA splicing
RNA localization
ribonucleoprotein complex assembly
ribonucleoprotein complex export from nucleus
regulation of mRNA processing
ribonucleoprotein complex localization
regulation of mRNA metabolic process
ribonucleoprotein complex subunit organization
establishment of RNA localization
RNA catabolic process
mRNA transport
nucleic acid transport
RNA transport
RNA export from nucleus
nuclear−transcribed mRNA catabolic process
histone methylation
mRNA export from nucleus
mRNA−containing ribonucleoprotein complex export from nucleus
regulation of mRNA splicing, via spliceosome
mRNA catabolic process
peptidyl−lysine modification
RNA 3'−end processing
mRNA splice site selection
macromolecule methylation
mRNA 3'−end processing
proteasomal protein catabolic process
nucleobase−containing compound transport
methylation
protein export from nucleus
protein methylation
protein alkylation
negative regulation of mRNA metabolic process
multi−organism transport
multi−organism localization
histone lysine methylation
nuclear export
DNA−templated transcription, elongation
ncRNA processing
proteasome−mediated ubiquitin−dependent protein catabolic process
transport of virus
viral gene expression
negative regulation of mRNA processing
nucleobase−containing compound catabolic process
tricarboxylic acid cycle
Golgi vesicle transport
cytosolic transport
protein polyubiquitination
negative regulation of RNA splicing
RNA polyadenylation
nuclear transport
transcription elongation from RNA polymerase II promoter
protein sumoylation
intracellular transport of virus
nucleocytoplasmic transport
endomembrane system organization
peptidyl−lysine methylation
endosomal transport
DNA−templated transcription, termination
mRNA polyadenylation
protein deubiquitination
citrate metabolic process
protein modification by small protein removal
positive regulation of DNA−templated transcription, elongation
rRNA metabolic process
clathrin−dependent endocytosis
ribosome biogenesis
termination of RNA polymerase II transcription
regulation of chromosome organization
positive regulation of chromosome organization
protein localization to membrane
autophagy
process utilizing autophagic mechanism
positive regulation of transcription elongation from RNA polymerase II promoter
macroautophagy
post−Golgi vesicle−mediated transport
regulation of transcription elongation from RNA polymerase II promoter
tRNA metabolic process
protein deglycosylation
alternative mRNA splicing, via spliceosome
nuclear−transcribed mRNA catabolic process, deadenylation−dependent decay
regulation of telomere maintenance
tricarboxylic acid metabolic process
histone H3−K4 methylation
cellular response to nerve growth factor stimulus
response to endoplasmic reticulum stress
negative regulation of mRNA splicing, via spliceosome
protein folding
nucleus organization
protein dephosphorylation
regulation of DNA−templated transcription, elongation
activation of protein kinase activity
positive regulation of RNA splicing
regulation of chromatin organization
cofactor metabolic process
regulation of autophagy
vacuole organization
regulation of histone methylation
ncRNA transcription
neuron projection organization
rRNA processing
positive regulation of dendritic spine development
regulation of ATPase activity
dendritic spine organization
endoplasmic reticulum organization
nuclear−transcribed mRNA catabolic process, exonucleolytic
cytoplasmic pattern recognition receptor signaling pathway
membrane disassembly
nuclear envelope disassembly
coenzyme metabolic process
vesicle−mediated transport between endosomal compartments
global genome nucleotide−excision repair
Ras protein signal transduction
protein ubiquitination involved in ubiquitin−dependent protein catabolic process
chaperone−mediated protein folding
regulation of cellular protein catabolic process
RNA modification
hippo signaling
early endosome to late endosome transport
dephosphorylation
regulation of receptor biosynthetic process
response to nerve growth factor
macromolecular complex disassembly
'de novo' protein folding
tRNA transport
branched−chain amino acid catabolic process
nuclear−transcribed mRNA poly(A) tail shortening
regulation of alternative mRNA splicing, via spliceosome
Golgi organization
autophagosome organization
regulation of histone modification
ER to Golgi vesicle−mediated transport
chromatin remodeling
histone deacetylation
tRNA export from nucleus
exonucleolytic nuclear−transcribed mRNA catabolic process involved in deadenylation−dependent decay
tRNA−containing ribonucleoprotein complex export from nucleus
developmental cell growth
ERAD pathway
nucleotide−excision repair, DNA duplex unwinding
mitotic sister chromatid cohesion
autophagosome assembly
activation of MAPKKK activity
positive regulation of mRNA splicing, via spliceosome
phosphorylation of RNA polymerase II C−terminal domain
dendritic spine maintenance
nucleosome assembly
chromatin assembly
nucleosome organization
chromatin assembly or disassembly
DNA packaging
chromatin silencing
chromatin silencing at rDNA
protein−DNA complex assembly
negative regulation of gene expression, epigenetic
detection of chemical stimulus involved in sensory perception of bitter taste
DNA replication−dependent nucleosome assembly
DNA replication−dependent nucleosome organization
protein−DNA complex subunit organization
detection of chemical stimulus involved in sensory perception of taste
G−protein coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger
sensory perception of bitter taste
adenylate cyclase−modulating G−protein coupled receptor signaling pathway
DNA conformation change
protein heterotetramerization
regulation of myeloid cell differentiation
serotonin receptor signaling pathway
G−protein coupled serotonin receptor signaling pathway
regulation of megakaryocyte differentiation
sensory perception of taste
positive regulation of gene expression, epigenetic
adenylate cyclase−inhibiting G−protein coupled receptor signaling pathway
megakaryocyte differentiation
p.adjust
0.05
0.04
0.03
0.02
0.01
GeneRatio
0.05
0.10
0.15
0.20


ontology: MF
gated channel activity
cation channel activity
potassium channel activity
voltage−gated ion channel activity
voltage−gated channel activity
substrate−specific channel activity
ion channel activity
passive transmembrane transporter activity
channel activity
voltage−gated cation channel activity
voltage−gated potassium channel activity
sodium channel activity
potassium ion transmembrane transporter activity
metal ion transmembrane transporter activity
peptide antigen binding
hormone activity
phosphotransferase activity, nitrogenous group as acceptor
receptor ligand activity
ligand−gated ion channel activity
ligand−gated channel activity
extracellular ligand−gated ion channel activity
structural constituent of ribosome
pattern binding
polysaccharide binding
receptor regulator activity
oxidoreductase activity, acting on NAD(P)H
hydrogen ion transmembrane transporter activity
mRNA binding involved in posttranscriptional gene silencing
mRNA binding
G−protein coupled receptor activity
olfactory receptor activity
neuropeptide binding
S−adenosylmethionine−dependent methyltransferase activity
protein serine/threonine kinase activity
modification−dependent protein binding
ligase activity
ubiquitin−like protein transferase activity
transferase activity, transferring one−carbon groups
histone methyltransferase activity
methyltransferase activity
ubiquitin−like protein ligase activity
translation initiation factor activity
translation factor activity, RNA binding
protein methyltransferase activity
catalytic activity, acting on RNA
ubiquitin−protein transferase activity
protein C−terminus binding
ubiquitin protein ligase activity
histone−lysine N−methyltransferase activity
helicase activity
N−methyltransferase activity
pre−mRNA binding
protein transporter activity
ubiquitin−like protein binding
ubiquitinyl hydrolase activity
N−acyltransferase activity
N−acetyltransferase activity
thiol−dependent ubiquitinyl hydrolase activity
transcription cofactor activity
methylated histone binding
methylation−dependent protein binding
ubiquitin−like protein ligase binding
signal sequence binding
ubiquitin protein ligase binding
peptide N−acetyltransferase activity
single−stranded RNA binding
tRNA binding
histone methyltransferase activity (H3−K4 specific)
ubiquitin−like protein−specific protease activity
peptide transporter activity
acetyltransferase activity
small GTPase binding
Ras GTPase binding
ATPase activator activity
lysine N−methyltransferase activity
cadherin binding
U6 snRNA binding
clathrin adaptor activity
endocytic adaptor activity
translation initiation factor binding
SUMO transferase activity
protein−lysine N−methyltransferase activity
transcription coactivator activity
nuclear localization sequence binding
aminoacyl−tRNA ligase activity
Rab GTPase binding
protein kinase A catalytic subunit binding
ATPase activity
transcription corepressor activity
phosphatase binding
thiol−dependent ubiquitin−specific protease activity
protein phosphatase 1 binding
ATP−dependent helicase activity
purine NTP−dependent helicase activity
transferase activity, transferring acyl groups other than amino−acyl groups
cell adhesion molecule binding
transcription factor binding
SH3 domain binding
transferase activity, transferring acyl groups
protein phosphatase binding
protein disulfide isomerase activity
intramolecular oxidoreductase activity, transposing S−S bonds
nucleoside−triphosphatase regulator activity
histone acetyltransferase activity
peptide−lysine−N−acetyltransferase activity
poly−pyrimidine tract binding
ubiquitin binding
p53 binding
cysteine−type peptidase activity
catalytic activity, acting on a tRNA
phosphoprotein phosphatase activity
ribonucleoprotein complex binding
protein complex scaffold activity
histone deacetylase activity
protein serine/threonine phosphatase activity
protein heterodimerization activity
G−protein coupled amine receptor activity
bitter taste receptor activity
taste receptor activity
amine binding
serotonin binding
G−protein coupled serotonin receptor activity
neurotransmitter receptor activity
serotonin receptor activity
nucleosomal DNA binding
catecholamine binding
G:E:J (4597)
J (973)
G (157)
E:J (6881)
G:E (310)
p.adjust
0.05
0.04
0.03
0.02
0.01
GeneRatio
0.04
0.08
0.12
0.16


ontology: CC
synaptic membrane
axoneme
ciliary plasm
cation channel complex
cilium
ciliary part
postsynaptic membrane
ion channel complex
I band
axoneme part
presynapse
MHC protein complex
Z disc
receptor complex
sarcoplasmic reticulum
proteinaceous extracellular matrix
transmembrane transporter complex
axon terminus
neurotransmitter receptor complex
sarcoplasm
ionotropic glutamate receptor complex
neuron projection terminus
spindle pole
mitochondrial protein complex
inner mitochondrial membrane protein complex
mitochondrial membrane part
respiratory chain
ribosomal subunit
cytosolic ribosome
mitochondrial respiratory chain
respiratory chain complex
cytosolic part
mitochondrial proton−transporting ATP synthase complex
proton−transporting ATP synthase complex
ribosome
microvillus membrane
cytochrome complex
small ribosomal subunit
mitochondrial inner membrane
extracellular matrix
cytosolic small ribosomal subunit
cornified envelope
proton−transporting two−sector ATPase complex
large ribosomal subunit
cytosolic large ribosomal subunit
respiratory chain complex IV
nucleosome
DNA packaging complex
protein−DNA complex
nuclear speck
spliceosomal complex
catalytic step 2 spliceosome
histone methyltransferase complex
protein acetyltransferase complex
acetyltransferase complex
nuclear pore
SWI/SNF superfamily−type complex
focal adhesion
methyltransferase complex
cell−substrate adherens junction
clathrin adaptor complex
nuclear periphery
clathrin coat
transferase complex, transferring phosphorus−containing groups
histone acetyltransferase complex
ATPase complex
cell−substrate junction
ubiquitin ligase complex
RNA polymerase complex
AP−type membrane coat adaptor complex
ribonucleoprotein granule
DNA−directed RNA polymerase complex
nuclear DNA−directed RNA polymerase complex
adherens junction
P−body
transcription elongation factor complex
SWI/SNF complex
membrane coat
coated membrane
pre−autophagosomal structure
cell leading edge
cytoplasmic ribonucleoprotein granule
DNA−directed RNA polymerase II, holoenzyme
spliceosomal snRNP complex
Cul4−RING E3 ubiquitin ligase complex
carboxy−terminal domain protein kinase complex
protein serine/threonine phosphatase complex
phosphatase complex
nuclear matrix
pre−autophagosomal structure membrane
Set1C/COMPASS complex
npBAF complex
host
host cell
autophagosome
MLL1/2 complex
MLL1 complex
centrosome
transcriptional repressor complex
U2−type spliceosomal complex
small nuclear ribonucleoprotein complex
other organism
other organism cell
other organism part
clathrin vesicle coat
prespliceosome
neuron spine
early endosome
lamellipodium
histone deacetylase complex
vesicle coat
H4 histone acetyltransferase complex
nuclear envelope
dihydrolipoyl dehydrogenase complex
WASH complex
eukaryotic translation initiation factor 3 complex
clathrin coat of coated pit
endosome membrane
dendritic spine
Cajal body
mitochondrial matrix
heterochromatin
polysome
spliceosomal tri−snRNP complex
clathrin coat of endocytic vesicle
growth cone
trans−Golgi network
peroxisome
microbody
site of polarized growth
protein kinase complex
protein phosphatase type 2A complex
U5 snRNP
extrinsic component of organelle membrane
AP−2 adaptor complex
Cul4A−RING E3 ubiquitin ligase complex
tricarboxylic acid cycle enzyme complex
endosomal part
serine/threonine protein kinase complex
nuclear cyclin−dependent protein kinase holoenzyme complex
vacuolar membrane
nucleoid
mitochondrial nucleoid
dendrite
U4/U6 x U5 tri−snRNP complex
lysosomal membrane
lytic vacuole membrane
PML body
endoplasmic reticulum quality control compartment
nBAF complex
trans−Golgi network membrane
microbody part
peroxisomal part
NuA4 histone acetyltransferase complex
H4/H2A histone acetyltransferase complex
CCR4−NOT complex
Sin3−type complex
U2−type prespliceosome
early endosome membrane
Sin3 complex
chaperonin−containing T−complex
chromatin
clathrin−coated pit
tethering complex
exon−exon junction complex
fibrillar center
nuclear transcription factor complex
postsynaptic density
postsynaptic specialization
microtubule plus−end
precatalytic spliceosome
transcription factor complex
peroxisomal membrane
microbody membrane
asymmetric synapse
TOR complex
peptidase complex
nuclear nucleosome
G:E:J (4875)
J (1028)
G (187)
E:J (7123)
G:E (345)
GeneRatio
0.02
0.04
0.06
p.adjust
0.06
0.04
0.02


ontology: KEGG
Neuroactive ligand−receptor interaction
Calcium signaling pathway
Autoimmune thyroid disease
Allograft rejection
Morphine addiction
Cell adhesion molecules (CAMs)
DNA replication
Graft−versus−host disease
Type I diabetes mellitus
Hematopoietic cell lineage
Glycerophospholipid metabolism
Arachidonic acid metabolism
Ribosome
Parkinson's disease
Oxidative phosphorylation
Alzheimer's disease
Huntington's disease
Thermogenesis
MicroRNAs in cancer
Olfactory transduction
Systemic lupus erythematosus
Ubiquitin mediated proteolysis
Spliceosome
Endocytosis
Protein processing in endoplasmic reticulum
Aminoacyl−tRNA biosynthesis
Citrate cycle (TCA cycle)
RNA degradation
mRNA surveillance pathway
RNA transport
Tight junction
Carbon metabolism
Valine, leucine and isoleucine degradation
Autophagy − animal
Lysine degradation
Fatty acid metabolism
AMPK signaling pathway
Alcoholism
Taste transduction
G:E:J
(1893)
J
(459)
G
(81)
E:J
(2968)
G:E
(137)
GeneRatio
0.1
0.2
0.3
p.adjust
0.05
0.04
0.03
0.02
0.01