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BIOL3014 – Advanced Bioinformatics
Practical 2

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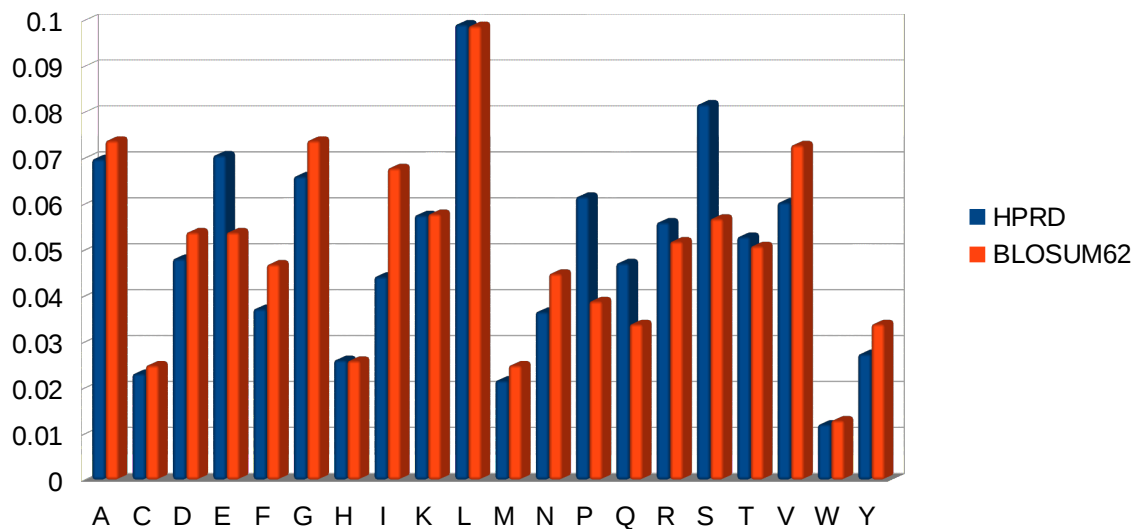
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Exercise 1B

HPRD background distribution has been created from the set of sequences found the HPRD.fasta file. Distribution was created by the `get_distrib_from_fasta` function shown in code listing below.

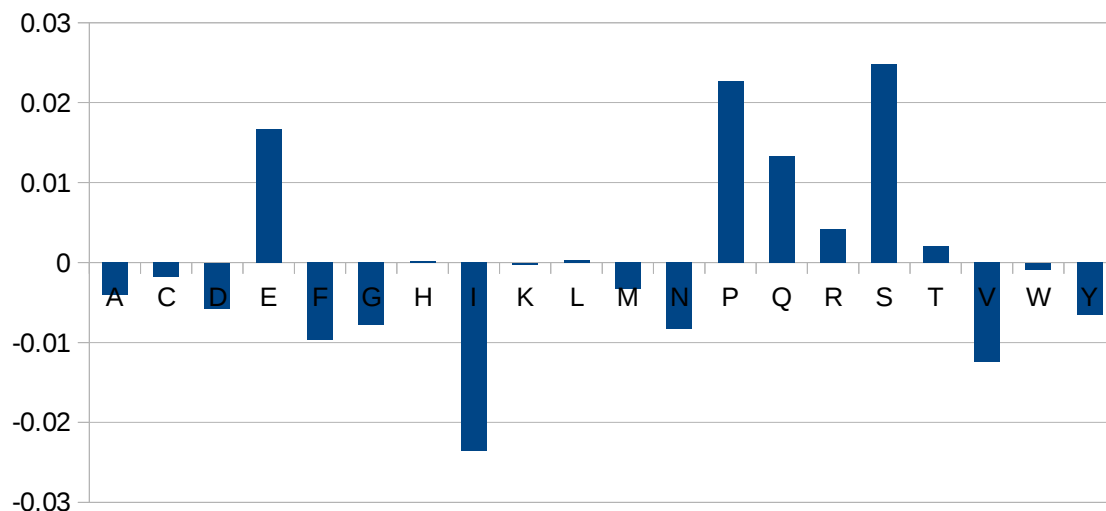
First graph shows both, HPRD and BLOSUM62 derived distributions. L (Leucine) is the most frequent amino acid in both distributions with the frequency of 0.1 and W (Tryptophan) is the least frequent amino acid with a frequency of about 0.01.

HPRD & BLOSUM62 Distributions



The following bar graph shows deltas between the HPRD and BLOSUM62 distributions with positive value representing higher frequencies in HPRD and negative values representing higher frequencies in the BLOSUM62 background distributions.

BLOSUM62 & HPRD Background Distribution Deltas



Code

```
'''
Created on 05/08/2014

@author: jacekrad
'''
from sequence import *
from prob import *
from symbol import *
from webservice import *
from sys import stderr

blosum62_background = readDistrib("blosum62.distrib")

def get_distrib_from_fasta(fasta_filename):
    '''
    This function creates a distribution from a set sequences
    read from a FASTA file. All sequences are read and every
    residue is used to construct the distribution. This
    function assumes that the FASTA file contains protein alphabet
    sequence. The function returns a Distrib object containing the
    generated distribution.
    '''
    protein_counts = {}
    # initilise the dictionary with zeros
    for residue in Protein_Alphabet.symbols:
        protein_counts[residue] = 0

    sequences = readFastaFile(fasta_filename)
    for sequence in sequences:
        for letter in sequence:
            protein_counts[letter] += 1

    return Distrib(Protein_Alphabet, protein_counts)

hprd_background = get_distrib_from_fasta("HPRD.fa")
hprd_background.writeDistrib("HPRD.distrib")

print hprd_background
print blosum62_background

# compare the two distributions by calculating deltas for each amino acid
for amino_acid in hprd_background.alpha:
    delta = hprd_background[amino_acid] - blosum62_background[amino_acid]
    sys.stderr.write(amino_acid + "," + str(delta) + "\n")
```

Raw Results

AA	HPRD	BLOSUM62	DELTA
A	0.0698457839	0.0738522954	-0.0040065115
C	0.0231226168	0.0249500998	-0.001827483
D	0.0481476988	0.0538922156	-0.0057445168
E	0.070644439	0.0538922156	0.0167522234
F	0.0372439945	0.0469061876	-0.0096621931
G	0.0660838698	0.0738522954	-0.0077684256
H	0.0261162961	0.0259481038	0.0001681923
I	0.044277412	0.0678642715	-0.0235868595
K	0.0576285349	0.0578842315	-0.0002556966
L	0.0991363806	0.0988023952	0.0003339854
M	0.0216587524	0.0249500998	-0.0032913474
N	0.0366184744	0.0449101796	-0.0082917052
P	0.0616506862	0.0389221557	0.0227285305
Q	0.0471915942	0.0339321357	0.0132594584
R	0.0560535647	0.0518962076	0.0041573571
S	0.0817464702	0.0568862275	0.0248602426
T	0.0529277466	0.0508982036	0.002029543
V	0.0604048745	0.0728542914	-0.0124494169
W	0.0120893881	0.0129740519	-0.0008846638
Y	0.0274114222	0.0339321357	-0.0065207135

Execution Output

```
Terminal
File Edit View Search Terminal Help
jacekrad@z400 ~/var/github-sem2/biol3014/prac02 $ python exerciselb.py 2> ex1b-d
eltas.csv
< A=0.07 C=0.02 D=0.05 E=0.07 F=0.04 G=0.07 H=0.03 I=0.04 K=0.06 L=0.10 M=0.02 N
=0.04 P=0.06 Q=0.05 R=0.06 S=0.08 T=0.05 V=0.06 W=0.01 Y=0.03 >
< A=0.07 C=0.02 D=0.05 E=0.05 F=0.05 G=0.07 H=0.03 I=0.07 K=0.06 L=0.10 M=0.02 N
=0.04 P=0.04 Q=0.03 R=0.05 S=0.06 T=0.05 V=0.07 W=0.01 Y=0.03 >
jacekrad@z400 ~/var/github-sem2/biol3014/prac02 $
```

Exercise 1C

HTH protein chosen was P56179 (<http://www.uniprot.org/uniprot/P56179>) whose sequence is:

```
MSHSQHSPYLQSYHNSSAAAQTRGDDTDQQKTTVIENGEIRFNGKGKKIRKPRTIYSSLQ
LQALNHRFQQTQYLALPERAELAASLGLTQTQVKIWFQNKRSKFKLLKQGSNPHESDPL
QGSAALSPRSPALPPVWDVSASAKGVSMPPNSYMPGYSHWYSSPHQDTMQRPQMM
```

Homeobox protein DLX-6 is located between positions 1 and 175 and the DNA binding Homeobox is between positions 49 and 108.

The homeobox is highlighted in the jpred output below with alpha helix predictions shown as well.

```
---51-----61-----71-----81-----91-----101-----
KIRKPRTIYSSLQALNHRFQQTQYLALPERAELAASLGLTQTQVKIWFQNKRSKFKLLKQ
-----EEE-----HHHHHHHHHHHH-----HHHHHHHHHHHH-----EEEE-----HHHHHHHH--
-----EEEE-----HHHHHHHHHHHH-----HHHHHHHHHHHH-----EEEEEEE-----HHHHHHHH--
-----E-----HHHHHHHHHHHH-----HHHHHHHHHH-----HHH-----HHHHHH--
```

Exercise 1D

Document code is shown below.

```
'''
Created on 06/08/2014
@author: jacekrad
'''
from gibbs import *
from sequence import *

seqs = readFastaFile("hth_40.fa", Protein_Alphabet)

W = 10 # the width of the motif sought

# create a GibbsMotif object from a list of sequences
# and of length W
g = GibbsMotif(seqs, W)

# execute the core Gibbs Sampling algorithm to discover
# the motif
q = g.discover()

# get the probability distribution for the background used
# in the discovery calculated above
p = g.getBackground()

# getAlignments is called and alignment for sequences seq
# is calculated from the foreground q and background p
# the resulting alignment is assigned to a
a = getAlignment(seqs, q, p)

k = 0
for seq in seqs:
    print "%s |t%s" % (seq.name, seq[a[k]:a[k]+W])
    k += 1
```

Exercise 1E

Code

Small change to gibbs.py

```
#print "LL @ %5d=\t%5.2f" % (round, LL)

if LL > self.maxLL:
    self.maxLL = LL
```

exercise1f.py

```
'''
Created on 07/08/2014

@author: jacekrad
'''
from gibbs import *
from sequence import *
import sys

seqs = readFastaFile("hth_40.fa", Protein_Alphabet)
width_values = [10, 24, 30]

# list of the files where we dump the results
# these will go to stderr for logo post processing
alignment_filenames = []

# maximum values for saving
maxLL = 0.0
max_p = None
max_q = None
p_filename = None
q_filename = None

for W in width_values:
    for i in range(1,4): # create 3 sets of results
        g = GibbsMotif(seqs, W)
        q = g.discover()
        p = g.getBackground()
        a = getAlignment(seqs, q, p)
        k = 0
        results_filename = "ex1e-W" + str(W) + "-iteration" + str(i) +
".aln"
        if g.maxLL > maxLL:
            maxLL = g.maxLL
            max_p = p
            max_q = q
            p_filename = "ex1e-W" + str(W) + "-iteration" + str(i) + "-p-
max.distrib"
            q_filename = "ex1e-W" + str(W) + "-iteration" + str(i) + "-q-
max.distrib"
            print "New maxLL distribution is ", q_filename
            sys.stderr.write(results_filename + "\n")
            results_file = open(results_filename, 'w')
```

```

    for seq in seqs:
        results_file.write("%s |t%s\n" % (seq.name, seq[a[k]:a[k]+W]))
        k += 1
    results_file.close()

# save distributions with highest log odds
print "Writing best distributions to ", p_filename, " and ", q_filename
max_p.writeDistrib(p_filename)
writeDistrib(max_q, q_filename)

```

BASH

```

#!/bin/bash

python exercisele.py 2>alignment_filenames.txt

for alignment_filename in `cat alignment_filenames.txt`; do
    export logo_filename=`echo ${alignment_filename} | cut -f 1 -d "."`.svg
    echo "generating ${logo_filename}"
    weblogo --format=svg < ${alignment_filename} > ${logo_filename}
done

```

Execution

```

Terminal
File Edit View Search Terminal Help
jacekrad@z400 ~/var/github-sem2/biol3014/prac02 $ time ./exle-create-logos.sh
New maxLL distribution is exle-W10-iteration1-q-max.distrib
New maxLL distribution is exle-W10-iteration2-q-max.distrib
New maxLL distribution is exle-W24-iteration1-q-max.distrib
New maxLL distribution is exle-W30-iteration1-q-max.distrib
New maxLL distribution is exle-W30-iteration2-q-max.distrib
Writing best distributions to exle-W30-iteration2-p-max.distrib and exle-W30-
iteration2-q-max.distrib
generating exle-W10-iteration1.svg
generating exle-W10-iteration2.svg
generating exle-W10-iteration3.svg
generating exle-W24-iteration1.svg
generating exle-W24-iteration2.svg
generating exle-W24-iteration3.svg
generating exle-W30-iteration1.svg
generating exle-W30-iteration2.svg
generating exle-W30-iteration3.svg

real    9m40.248s
user    9m38.267s
sys     0m1.474s
jacekrad@z400 ~/var/github-sem2/biol3014/prac02 $

```

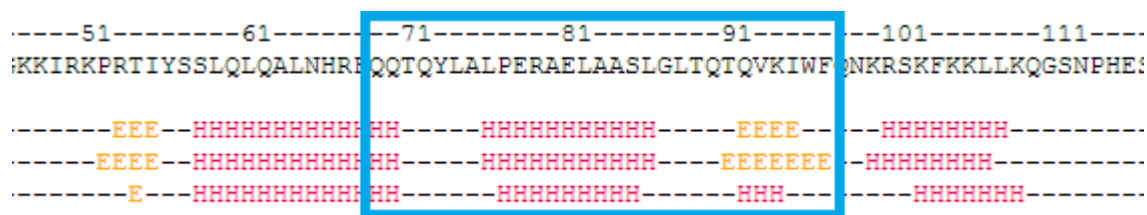

Logos

Inspecting motifs of different widths we can see a pattern of highly conserved region WFQNRR (and slightly less conserved surrounding residues) appearing in most logos. The exceptions are two of the W=10 and one of the W=30 logos. Inspecting the original amino acid sequence we can find this region starting at position 96 which is between the second and third alpha helices.

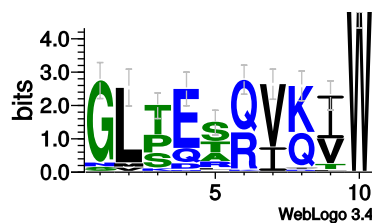
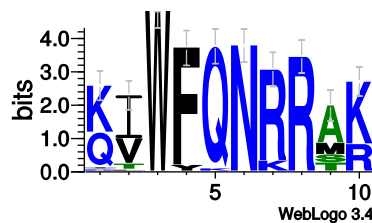
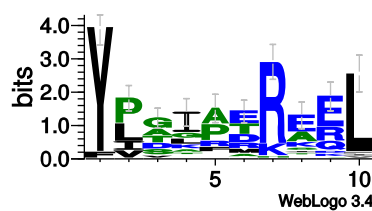
Furthermore, even for the logos of the same width motif is shifted, that starts and ends in different positions.

For the short width of W=10 two of the three motifs do not show the highly conserved region WFQNRR. The first of the logos does not seem to overlap either of the other two and there is an overlap of three positions between logo 2 and logo 3.

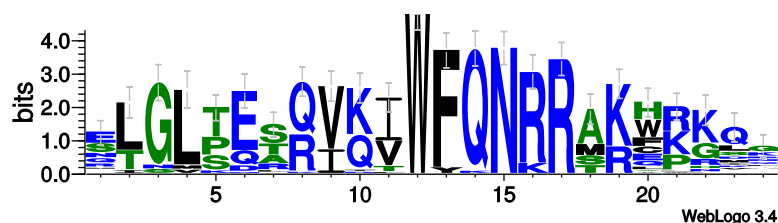
When W=30, two of the three logos provide a significant overlap of 28 positions. The overlap is from position 69 to 97 of the original sequence and covers 2 helices as highlighted in a blue box below.



W=10



W=24



Exercise 1f

To construct the two PWMs I have used the foreground saved in previous questions. For the backgrounds I've used the HPRD background from question 1B and background saved in last (1e).

I have had some problems with this questions as both of my PWMs matched hit every single one of the 14989 sequences searched. I then modified the threshold of the search but would have the value too high and no sequences were returned, or the value would be too low and all of the sequences would return hits. For pwm1 I found a threshold value of **4.59231187104470925** which returned most but not all sequences. Because of the time taken to experiment with this I didn't spend as much time on working out the best threshold for pwm2. My final run has abandoned this approach all together and printed

There are two possibilities here:

1. There is an error in either my approach or the code or both.
2. This motif is present in all proteins.

Because of the number of proteins found trying to get the report (getGOReport) would run for hours and not complete. Finally I left it running overnight producing a long list of results. Note, that the run was generated from one PWM only (pwm1) in order to save time.

I chose Q99440 as one of the proteins and checked in in uniprot (<http://www.uniprot.org/uniprot/Q99440>). It is unlikely to a HTH motif as there seems to be a problem with the number of results my code has returned.

Code

```
'''
Created on 06/08/2014

@author: s4361277
'''
from sequence import *
from reportlab.lib.set_ops import intersect

foreground = readDistrib("ex1e-W30-iteration2-p-max.distrib")
q1e_background = readDistrib("ex1e-W30-iteration2-q-max.distrib")
hprd_background = readDistrib("HPRD.distrib")

print type(foreground), type(q1e_background), type(hprd_background)

# create two Position Wighted Matrices. First used the background
# saved in question 1e and the second PWM is created using the
# background from question 1b, ie from the HPRD sequence data
pwm1 = PWM(foreground, q1e_background[0])
pwm2 = PWM(foreground, hprd_background[0])

print pwm1, pwm2
ids1 = []
ids2 = []
hprd_sequences = readFastaFile('HPRD.fa', Protein_Alphabet)
```

```

hth_sequences = readFastaFile('hth_40.fa', Protein_Alphabet)
hth_ids = [seq.name for seq in hth_sequences]

# these are the sequences we are going to search. These are the
# HPRD sequences that do not have an entry in our hth_40.fa FASTA file
search_sequences = [seq for seq in hprd_sequences if not(seq.name in
hth_ids)]

print "will search", len(search_sequences), "sequences out of a total
of", \
    len(hprd_sequences), "entries found."

# because each sequence is a match we'll count the total number of hits
# for the two different sequences

pwm1_hit_count = 0
pwm2_hit_count = 0
pwm1_theshhold = 4.5
count = 0
for sequence in search_sequences:
    hits1 = pwm1.search(sequence) # search using first PWM
    hits2 = pwm2.search(sequence) # search using second PWM
    pwm1_hit_count += len(hits1)
    pwm2_hit_count += len(hits2)
    if len(hits1) > 0:
        #print "%s \t%d \t%s \t%5.3f" % (sequence.name, hits1[0][0],
hits1[0][1], hits1[0][2])
        ids1.append(sequence.name)
    #if len(hits2) > 0:
    #    ids2.append(sequence.name)

#print "number of sequences matched by pwm1 and pwm2", len(ids1),
len(ids2), len(intersect(ids1, ids2))
#print "total hits by pwm1 and pwm2", pwm1_hit_count, pwm2_hit_count
print ids1
print "getting report"
report = getG0Report(ids1)
print "report rows"
for row in report:
    print "%s \t%d \t%s" % row

```

Output

PWMs

```

A    +4.59231187104470972571
C    -0.75522523905631300245
D    +3.17498245182345906201
E    -0.26582861907593180462
F    +0.02798567463261713434
G    +4.30332968772469914853
H    +0.02798567463261713434
I    -1.19336262521392066915
K    -1.92746413313828157676
L    +4.20981381202821491883
M    +2.44227746773204046349

```

```

N +2.70248809456029182030
P +4.56519783042241389381
Q -0.80902707783850980050
R -1.30051692762927095792
S +4.36641541115966269615
T +3.53386173184732665931
V +3.24396640703866045996
W +2.36507151000548576647
Y -1.70774517158982774845

```

```

A +0.56916260386476069666
C -0.62838704319051064129
D -0.47615359737981943766
E -0.18946438342253510423
F -0.32183919435603314252
G +0.33554657897056489047
H +0.03310351034586316021
I -1.04711236206315128072
K -0.36018379353077178973
L -0.16353528145197879229
M -0.41000005340910816720
N -0.67490827691591093185
P +0.66685193165766087908
Q +0.17501260361618561912
R +0.29447381337806322055
S +0.18594208355721397741
T -0.21192721623968954758
V -0.63396192461865674694
W +0.09591911309984096912
Y -0.40109685828777197347

```

GO report

I have deliberately included all of the 14285 terms returned by the report to illustrate the problems I've been having with this question. Because of the number of results it was impossible to predict the function.

```

GO:0016020 6197 membrane
GO:0005515 5534 protein binding
GO:0005634 5019 nucleus
GO:0005737 4988 cytoplasm
GO:0016021 4000 integral component of membrane
GO:0005886 3579 plasma membrane
GO:0046872 2975 metal ion binding
GO:0005829 2387 cytosol
GO:0070062 2346 extracellular vesicular exosome
GO:0006355 2020 regulation of transcription, DNA-templated
GO:0006351 1923 transcription, DNA-templated
GO:0007165 1848 signal transduction
GO:0003677 1842 DNA binding
GO:0000166 1707 nucleotide binding
GO:0005576 1641 extracellular region
GO:0005730 1538 nucleolus
GO:0006810 1537 transport
GO:0016787 1322 hydrolase activity
GO:0044281 1309 small molecule metabolic process
GO:0016740 1272 transferase activity

```

G0:0005739	1264	<u>mitochondrion</u>
G0:0005524	1262	ATP binding
G0:0005654	1057	<u>nucleoplasm</u>
G0:0005615	1047	<u>extracellular</u> space
G0:0008270	1044	zinc ion binding
G0:0003676	1023	<u>nucleic</u> acid binding
G0:0005887	1010	integral component of plasma membrane
G0:0005783	1001	<u>endoplasmic reticulum</u>
G0:0044822	971	<u>poly(A)</u> RNA binding
G0:0004871	947	signal <u>transducer</u> activity
G0:0005622	945	<u>intracellular</u>
G0:0005794	920	<u>Golgi</u> apparatus
G0:0005856	916	<u>cytoskeleton</u>
G0:0007275	893	multicellular <u>organismal</u> development
G0:0007186	865	G-protein coupled receptor signaling pathway
G0:0003700	835	sequence-specific DNA binding transcription factor activity
G0:0008152	781	<u>metabolic</u> process
G0:0045944	743	positive regulation of transcription from RNA <u>polymerase</u> II promoter
G0:0004930	741	G-protein coupled receptor activity
G0:0006915	672	<u>apoptotic</u> process
G0:0005789	657	<u>endoplasmic reticulum</u> membrane
G0:0003723	642	RNA binding
G0:0010467	642	gene expression
G0:0030154	599	cell differentiation
G0:0045087	597	innate immune response
G0:0016310	591	<u>phosphorylation</u>
G0:0016301	590	<u>kinase</u> activity
G0:0055085	585	<u>transmembrane</u> transport
G0:0005509	585	calcium ion binding
G0:0042803	580	protein <u>homodimerization</u> activity
G0:0003824	578	<u>catalytic</u> activity
G0:0055114	574	oxidation-reduction process
G0:0006468	571	protein <u>phosphorylation</u>
G0:0007155	565	cell adhesion
G0:0030054	561	cell junction
G0:0006811	544	ion transport
G0:0016032	539	viral process
G0:0015031	536	protein transport
G0:0007049	533	cell cycle
G0:0003674	528	molecular <u>function</u>
G0:0000122	521	negative regulation of transcription from RNA <u>polymerase</u> II promoter
G0:0045893	520	positive regulation of transcription, DNA- <u>templated</u>
G0:0006508	515	<u>proteolysis</u>
G0:0050896	500	response to stimulus
G0:0016772	496	<u>transferase</u> activity, transferring <u>phosphorus</u> -containing groups
G0:0004672	482	protein <u>kinase</u> activity
G0:0044267	481	cellular protein <u>metabolic</u> process
G0:0016491	473	<u>oxidoreductase</u> activity
G0:0042802	471	identical protein binding
G0:0043565	469	sequence-specific DNA binding
G0:0048471	469	<u>perinuclear</u> region of <u>cytoplasm</u>
G0:0042995	468	cell projection
G0:0008150	466	biological <u>process</u>
G0:0043066	459	negative regulation of <u>apoptotic</u> process
G0:0043231	451	<u>intracellular</u> membrane-bounded <u>organelle</u>
G0:0007596	449	blood coagulation
G0:0045892	443	negative regulation of transcription, DNA- <u>templated</u>
G0:0009986	435	cell surface
G0:0031410	435	<u>cytoplasmic vesicle</u>
G0:0000139	435	<u>Golgi</u> membrane
G0:0005768	430	<u>endosome</u>
G0:0008233	428	<u>peptidase</u> activity
G0:0007399	427	nervous system development
G0:0008284	416	positive regulation of cell proliferation
G0:0006366	410	transcription from RNA <u>polymerase</u> II promoter
G0:0006629	401	<u>lipid metabolic</u> process
G0:0016567	385	protein <u>ubiquitination</u>
G0:0007268	384	<u>synaptic</u> transmission
G0:0004674	376	protein <u>serine/threonine kinase</u> activity
G0:0008285	376	negative regulation of cell proliferation
G0:0007608	367	sensory perception of smell
G0:0000278	366	<u>mitotic</u> cell cycle
G0:0035556	360	<u>intracellular</u> signal <u>transduction</u>
G0:0043234	358	protein complex
G0:0045202	357	synapse

G0:0005975	356	carbohydrate <u>metabolic</u> process
G0:0005575	354	cellular <u>component</u>
G0:0046982	353	protein <u>heterodimerization</u> activity
G0:0005925	349	focal adhesion
G0:0006974	347	cellular response to DNA damage stimulus
G0:0006357	347	regulation of transcription from RNA <u>polymerase</u> II promoter
G0:0016874	342	<u>ligase</u> activity
G0:0004984	342	<u>olfactory</u> receptor activity
G0:0050911	342	detection of chemical stimulus involved in sensory perception of smell
G0:0008283	339	cell proliferation
G0:0006955	339	immune response
G0:0005102	336	receptor binding
G0:0002376	332	immune system process
G0:0007411	329	axon guidance
G0:0051301	316	cell division
G0:0030529	311	<u>ribonucleoprotein</u> complex
G0:0005525	307	GTP binding
G0:0042493	307	response to drug
G0:0005743	307	<u>mitochondrial</u> inner membrane
G0:0003682	305	<u>chromatin</u> binding
G0:0006281	304	DNA repair
G0:0019901	304	protein <u>kinase</u> binding
G0:0006954	300	<u>inflammatory</u> response
G0:0006412	299	translation
G0:0007283	297	<u>spermatogenesis</u>
G0:0003779	296	<u>actin</u> binding
G0:0006200	291	ATP <u>catabolic</u> process
G0:0030198	288	<u>extracellular</u> matrix organization
G0:0019899	286	<u>enzyme</u> binding
G0:0043065	286	positive regulation of <u>apoptotic</u> process
G0:0005813	281	<u>centrosome</u>
G0:0006397	281	mRNA processing
G0:0007264	280	small GTPase mediated signal <u>transduction</u>
G0:0005694	279	<u>chromosome</u>
G0:0005578	273	<u>proteinaceous</u> <u>extracellular</u> matrix
G0:0008380	268	RNA splicing
G0:0005764	262	<u>lysosome</u>
G0:0048011	260	<u>neurotrophin</u> TRK receptor signaling pathway
G0:0005815	254	<u>microtubule</u> organizing center
G0:0004842	253	<u>ubiquitin</u> -protein <u>transferase</u> activity
G0:0004872	249	receptor activity
G0:0016568	249	<u>chromatin</u> modification
G0:0043025	248	<u>neuronal</u> cell body
G0:0005874	247	<u>microtubule</u>
G0:0008134	246	transcription factor binding
G0:0030425	246	<u>dendrite</u>
G0:0043547	240	positive regulation of GTPase activity
G0:0007267	239	cell-cell signaling
G0:0008289	239	<u>lipid</u> binding
G0:0007067	237	<u>mitotic</u> nuclear division
G0:0019221	236	<u>cytokine</u> -mediated signaling pathway
G0:0016070	234	RNA <u>metabolic</u> process
G0:0007166	233	cell surface receptor signaling pathway
G0:0008219	230	cell death
G0:0001701	225	in utero embryonic development
G0:0005759	224	mitochondrial matrix
G0:0031012	220	extracellular matrix
G0:0005215	219	transporter activity
G0:0043005	218	neuron projection
G0:0001525	216	angiogenesis
G0:0003713	216	transcription coactivator activity
G0:0016192	211	vesicle-mediated transport
G0:0016071	209	mRNA metabolic process
G0:0005765	208	lysosomal membrane
G0:0006184	203	GTP catabolic process
G0:0005125	202	cytokine activity
G0:0030168	200	platelet activation
G0:0016324	200	apical plasma membrane
G0:0006886	194	intracellular protein transport
G0:0007420	192	brain development
G0:0034220	191	ion transmembrane transport
G0:0003924	190	GTPase activity
G0:0016757	189	transferase activity, transferring glycosyl groups
G0:0007173	187	epidermal growth factor receptor signaling pathway
G0:0032403	186	protein complex binding

G0:0007507	185	heart development
G0:0015629	184	actin cytoskeleton
G0:0005198	183	structural molecule activity
G0:0042981	183	regulation of apoptotic process
G0:0030424	183	axon
G0:0007601	182	visual perception
G0:0045211	181	postsynaptic membrane
G0:0019904	179	protein domain specific binding
G0:0034641	179	cellular nitrogen compound metabolic process
G0:0010628	178	positive regulation of gene expression
G0:0009897	176	external side of plasma membrane
G0:0006367	175	transcription initiation from RNA polymerase II promoter
G0:0005840	174	ribosome
G0:0005667	174	transcription factor complex
G0:0044212	174	transcription regulatory region DNA binding
G0:0016055	170	Wnt signaling pathway
G0:0005216	167	ion channel activity
G0:0043687	167	post-translational protein modification
G0:0016887	167	ATPase activity
G0:0005096	164	GTPase activator activity
G0:0004888	162	transmembrane signaling receptor activity
G0:0006457	161	protein folding
G0:0038095	160	Fc-epsilon receptor signaling pathway
G0:0046983	160	protein dimerization activity
G0:0010008	160	endosome membrane
G0:0045121	160	membrane raft
G0:0003714	160	transcription corepressor activity
G0:0000287	159	magnesium ion binding
G0:0031625	159	ubiquitin protein ligase binding
G0:0000398	159	mRNA splicing, via spliceosome
G0:0005516	159	calmodulin binding
G0:0005929	157	cilium
G0:0001666	157	response to hypoxia
G0:0008543	156	fibroblast growth factor receptor signaling pathway
G0:0016311	156	dephosphorylation
G0:0005788	155	endoplasmic reticulum lumen
G0:0008083	155	growth factor activity
G0:0046777	154	protein autophosphorylation
G0:0031965	154	nuclear membrane
G0:0016607	154	nuclear speck
G0:0006511	151	ubiquitin-dependent protein catabolic process
G0:0008022	151	protein C-terminus binding
G0:0051260	150	protein homooligomerization
G0:0008237	148	metallopeptidase activity
G0:0005769	147	early endosome
G0:0042127	147	regulation of cell proliferation
G0:0006897	146	endocytosis
G0:0032259	146	methylation
G0:0006935	145	chemotaxis
G0:0000082	145	G1/S transition of mitotic cell cycle
G0:0003735	144	structural constituent of ribosome
G0:0034765	143	regulation of ion transmembrane transport
G0:0006260	142	DNA replication
G0:0043123	142	positive regulation of I-kappaB kinase/NF-kappaB signaling
G0:0044255	141	cellular lipid metabolic process
G0:0032496	141	response to lipopolysaccharide
G0:0016477	140	cell migration
G0:0005244	139	voltage-gated ion channel activity
G0:0016746	139	transferase activity, transferring acyl groups
G0:0006805	137	xenobiotic metabolic process
G0:0016023	137	cytoplasmic membrane-bounded vesicle
G0:0008017	136	microtubule binding
G0:0001501	136	skeletal system development
G0:0005819	136	spindle
G0:0008286	136	insulin receptor signaling pathway
G0:0051607	136	defense response to virus
G0:0030246	135	carbohydrate binding
G0:0005882	134	intermediate filament
G0:0006486	134	protein glycosylation
G0:0061024	134	membrane organization
G0:0006644	132	phospholipid metabolic process
G0:0005506	132	iron ion binding
G0:0016323	132	basolateral plasma membrane
G0:0008168	132	methyltransferase activity
G0:0006816	132	calcium ion transport

G0:0006413	130	translational initiation
G0:0008201	130	heparin binding
G0:0018108	129	peptidyl-tyrosine phosphorylation
G0:0007156	129	homophilic cell adhesion
G0:0044237	129	cellular metabolic process
G0:0051056	127	regulation of small GTPase mediated signal transduction
G0:0030335	127	positive regulation of cell migration
G0:0031982	127	vesicle
G0:0005681	127	spliceosomal complex
G0:0009615	127	response to virus
G0:0000086	127	G2/M transition of mitotic cell cycle
G0:0051726	126	regulation of cell cycle
G0:0010468	126	regulation of gene expression
G0:0008236	125	serine-type peptidase activity
G0:0006813	125	potassium ion transport
G0:0030659	124	cytoplasmic vesicle membrane
G0:0006470	124	protein dephosphorylation
G0:0030036	124	actin cytoskeleton organization
G0:0010951	123	negative regulation of endopeptidase activity
G0:0051092	122	positive regulation of NF-kappaB transcription factor activity
G0:0005938	122	cell cortex
G0:0031225	122	anchored component of membrane
G0:0004252	121	serine-type endopeptidase activity
G0:0007568	121	aging
G0:0004386	121	helicase activity
G0:0000790	120	nuclear chromatin
G0:0005085	119	guanyl-nucleotide exchange factor activity
G0:0014070	119	response to organic cyclic compound
G0:0008234	118	cysteine-type peptidase activity
G0:0016829	118	lyase activity
G0:0007050	118	cell cycle arrest
G0:0007179	117	transforming growth factor beta receptor signaling pathway
G0:0009887	117	organ morphogenesis
G0:0043524	117	negative regulation of neuron apoptotic process
G0:0004721	117	phosphoprotein phosphatase activity
G0:0006631	117	fatty acid metabolic process
G0:0004713	117	protein tyrosine kinase activity
G0:0007417	116	central nervous system development
G0:0006461	115	protein complex assembly
G0:0006950	115	response to stress
G0:0000209	114	protein polyubiquitination
G0:0007219	114	Notch signaling pathway
G0:0000978	114	RNA polymerase II core promoter proximal region sequence-specific DNA binding
G0:0050900	114	leukocyte migration
G0:0007605	114	sensory perception of sound
G0:0048015	114	phosphatidylinositol-mediated signaling
G0:0001077	113	RNA polymerase II core promoter proximal region sequence-specific DNA binding
G0:0008202	113	steroid metabolic process
G0:0030027	113	lamellipodium
G0:0007204	112	positive regulation of cytosolic calcium ion concentration
G0:0005635	112	nuclear envelope
G0:0020037	112	heme binding
G0:0005911	112	cell-cell junction
G0:0006006	112	glucose metabolic process
G0:0030182	111	neuron differentiation
G0:0000775	111	chromosome, centromeric region
G0:0001934	111	positive regulation of protein phosphorylation
G0:0030308	110	negative regulation of cell growth
G0:0071805	110	potassium ion transmembrane transport
G0:0006979	109	response to oxidative stress
G0:0000184	109	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
G0:0072562	109	blood microparticle
G0:0019058	109	viral life cycle
G0:0022617	109	extracellular matrix disassembly
G0:0042742	109	defense response to bacterium
G0:0070588	108	calcium ion transmembrane transport
G0:0014069	108	postsynaptic density
G0:0005741	108	mitochondrial outer membrane
G0:0043235	108	receptor complex
G0:0030203	107	glycosaminoglycan metabolic process
G0:0097190	107	apoptotic signaling pathway
G0:0007218	106	neuropeptide signaling pathway
G0:0006614	106	SRP-dependent cotranslational protein targeting to membrane

G0:0006417	105	regulation of translation
G0:0006464	105	cellular protein modification process
G0:0006952	105	defense response
G0:0017124	105	SH3 domain binding
G0:0070374	105	positive regulation of ERK1 and ERK2 cascade
G0:0006812	104	cation transport
G0:0005802	103	trans-Golgi network
G0:0030496	103	midbody
G0:0002224	103	toll-like receptor signaling pathway
G0:0016853	102	isomerase activity
G0:0010466	102	negative regulation of peptidase activity
G0:0030414	101	peptidase inhibitor activity
G0:0006325	100	chromatin organization
G0:0016791	100	phosphatase activity
G0:0006364	99	rRNA processing
G0:0016337	98	single organismal cell-cell adhesion
G0:0006112	98	energy reserve metabolic process
G0:0031966	98	mitochondrial membrane
G0:0015630	98	microtubule cytoskeleton
G0:0030030	98	cell projection organization
G0:0005777	97	peroxisome
G0:0007409	97	axonogenesis
G0:0030324	97	lung development
G0:0009952	97	anterior/posterior pattern specification
G0:0008544	96	epidermis development
G0:0031175	96	neuron projection development
G0:0004222	96	metalloendopeptidase activity
G0:0001764	96	neuron migration
G0:0006928	96	cellular component movement
G0:0006814	96	sodium ion transport
G0:0000187	95	activation of MAPK activity
G0:0009653	95	anatomical structure morphogenesis
G0:0006414	95	translational elongation
G0:0005179	95	hormone activity
G0:0010629	95	negative regulation of gene expression
G0:0000776	94	kinetochore
G0:0007010	94	cytoskeleton organization
G0:0006936	94	muscle contraction
G0:0030426	94	growth cone
G0:0005923	93	tight junction
G0:0001649	93	osteoblast differentiation
G0:0051082	93	unfolded protein binding
G0:0008360	93	regulation of cell shape
G0:0001822	92	kidney development
G0:0045766	92	positive regulation of angiogenesis
G0:0006898	92	receptor-mediated endocytosis
G0:0042470	92	melanosome
G0:0051091	91	positive regulation of sequence-specific DNA binding transcription factor activity
G0:0005178	91	integrin binding
G0:0015293	91	symporter activity
G0:0004518	91	nuclease activity
G0:0045471	90	response to ethanol
G0:0022904	90	respiratory electron transport chain
G0:0002474	90	antigen processing and presentation of peptide antigen via MHC class I
G0:0006869	89	lipid transport
G0:0016605	88	PML body
G0:0034142	88	toll-like receptor 4 signaling pathway
G0:0047485	88	protein N-terminus binding
G0:0001503	88	ossification
G0:0005770	87	late endosome
G0:0007565	87	female pregnancy
G0:0010033	87	response to organic substance
G0:0005200	87	structural constituent of cytoskeleton
G0:0000981	87	sequence-specific DNA binding RNA polymerase II transcription factor activity
G0:0031090	86	organelle membrane
G0:0008584	86	male gonad development
G0:0007517	86	muscle organ development
G0:0008203	86	cholesterol metabolic process
G0:0009790	86	embryo development
G0:0004725	85	protein tyrosine phosphatase activity
G0:0012505	85	endomembrane system
G0:0035335	85	peptidyl-tyrosine dephosphorylation
G0:0030018	85	Z disc

G0:0006415	85	translational termination
G0:0016363	84	nuclear matrix
G0:0006914	84	autophagy
G0:0001726	84	ruffle
G0:0008021	84	synaptic vesicle
G0:0019886	84	antigen processing and presentation of exogenous peptide antigen via MHC class II
G0:0000785	84	chromatin
G0:0007160	84	cell-matrix adhesion
G0:0006874	84	cellular calcium ion homeostasis
G0:0000922	84	spindle pole
G0:0048511	83	rhythmic process
G0:0050852	83	T cell receptor signaling pathway
G0:0018279	83	protein N-linked glycosylation via asparagine
G0:0003690	83	double-stranded DNA binding
G0:0007603	83	phototransduction, visible light
G0:0071456	82	cellular response to hypoxia
G0:0050776	82	regulation of immune response
G0:0006396	82	RNA processing
G0:0007169	82	transmembrane receptor protein tyrosine kinase signaling pathway
G0:0090305	82	nucleic acid phosphodiester bond hydrolysis
G0:0030165	81	PDZ domain binding
G0:0006887	81	exocytosis
G0:0006766	81	vitamin metabolic process
G0:0019083	81	viral transcription
G0:0043086	81	negative regulation of catalytic activity
G0:0000165	81	MAPK cascade
G0:0002576	80	platelet degranulation
G0:0001889	80	liver development
G0:0050821	80	protein stabilization
G0:0004867	80	serine-type endopeptidase inhibitor activity
G0:0016042	80	lipid catabolic process
G0:0042060	80	wound healing
G0:0051028	80	mRNA transport
G0:0007626	79	locomotory behavior
G0:0090090	79	negative regulation of canonical Wnt signaling pathway
G0:0007584	79	response to nutrient
G0:0030336	79	negative regulation of cell migration
G0:0006919	78	activation of cysteine-type endopeptidase activity involved in apoptotic process
G0:0002755	78	MyD88-dependent toll-like receptor signaling pathway
G0:0050796	78	regulation of insulin secretion
G0:0031902	78	late endosome membrane
G0:0045177	77	apical part of cell
G0:0051384	77	response to glucocorticoid
G0:0051015	77	actin filament binding
G0:0031901	77	early endosome membrane
G0:0031145	77	anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process
G0:0006665	76	sphingolipid metabolic process
G0:0030968	76	endoplasmic reticulum unfolded protein response
G0:0006310	76	DNA recombination
G0:0055086	76	nucleobase-containing small molecule metabolic process
G0:0043197	75	dendritic spine
G0:0042590	75	antigen processing and presentation of exogenous peptide antigen via MHC class I
G0:0032355	75	response to estradiol
G0:0060070	75	canonical Wnt signaling pathway
G0:0009791	75	post-embryonic development
G0:0007229	74	integrin-mediated signaling pathway
G0:0034138	74	toll-like receptor 3 signaling pathway
G0:0071222	74	cellular response to lipopolysaccharide
G0:0071013	74	catalytic step 2 spliceosome
G0:0042593	74	glucose homeostasis
G0:0005262	74	calcium channel activity
G0:0005604	74	basement membrane
G0:0005796	74	Golgi lumen
G0:0050790	73	regulation of catalytic activity
G0:0044325	73	ion channel binding
G0:0006767	73	water-soluble vitamin metabolic process
G0:0043161	73	proteasome-mediated ubiquitin-dependent protein catabolic process
G0:0009636	73	response to toxic substance
G0:0050731	73	positive regulation of peptidyl-tyrosine phosphorylation
G0:0030900	73	forebrain development
G0:0042383	73	sarcolemma

G0:0046474	73	glycerophospholipid biosynthetic process
G0:0002756	73	MyD88-independent toll-like receptor signaling pathway
G0:0030097	73	hemopoiesis
G0:0005267	73	potassium channel activity
G0:0009055	72	electron carrier activity
G0:0042391	72	regulation of membrane potential
G0:0000777	72	condensed chromosome kinetochore
G0:0032321	72	positive regulation of Rho GTPase activity
G0:0030141	72	secretory granule
G0:0051439	72	regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle
G0:0004497	72	monooxygenase activity
G0:0035666	72	TRIF-dependent toll-like receptor signaling pathway
G0:0005581	72	collagen trimer
G0:0051216	71	cartilage development
G0:0042826	71	histone deacetylase binding
G0:0006821	71	chloride transport
G0:0002479	71	antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent
G0:0043410	70	positive regulation of MAPK cascade
G0:0043202	70	lysosomal lumen
G0:0030574	70	collagen catabolic process
G0:0038096	70	Fc-gamma receptor signaling pathway involved in phagocytosis
G0:0034329	70	cell junction assembly
G0:0016798	70	hydrolase activity, acting on glycosyl bonds
G0:0005543	70	phospholipid binding
G0:0035725	70	sodium ion transmembrane transport
G0:0007265	69	Ras protein signal transduction
G0:0030307	69	positive regulation of cell growth
G0:0030855	68	epithelial cell differentiation
G0:0034134	68	toll-like receptor 2 signaling pathway
G0:0051437	68	positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle
G0:0045095	68	keratin filament
G0:0051213	68	dioxygenase activity
G0:0016779	68	nucleotidyltransferase activity
G0:0038123	68	toll-like receptor TLR1:TLR2 signaling pathway
G0:0038124	68	toll-like receptor TLR6:TLR2 signaling pathway
G0:0007059	68	chromosome segregation
G0:0051897	67	positive regulation of protein kinase B signaling
G0:0045666	67	positive regulation of neuron differentiation
G0:0034162	67	toll-like receptor 9 signaling pathway
G0:0042384	67	cilium assembly
G0:0006338	67	chromatin remodeling
G0:0006289	67	nucleotide-excision repair
G0:0032587	66	ruffle membrane
G0:1902476	66	chloride transmembrane transport
G0:0006469	66	negative regulation of protein kinase activity
G0:0055037	66	recycling endosome
G0:0002020	66	protease binding
G0:0042393	65	histone binding
G0:0071260	65	cellular response to mechanical stimulus
G0:0060337	65	type I interferon signaling pathway
G0:0001558	65	regulation of cell growth
G0:0016705	64	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen
G0:0008076	64	voltage-gated potassium channel complex
G0:0060021	64	palate development
G0:0031295	64	T cell costimulation
G0:0045165	64	cell fate commitment
G0:0008144	64	drug binding
G0:0003774	64	motor activity
G0:0043627	64	response to estrogen
G0:0008104	64	protein localization
G0:0006977	63	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest
G0:0018105	63	peptidyl-serine phosphorylation
G0:0006368	63	transcription elongation from RNA polymerase II promoter
G0:0051436	63	negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle
G0:0001843	63	neural tube closure
G0:0003729	63	mRNA binding
G0:0009749	63	response to glucose
G0:0004843	63	ubiquitin-specific protease activity
G0:0060333	63	interferon-gamma-mediated signaling pathway

G0:0003697	63	single-stranded DNA binding
G0:0043085	63	positive regulation of catalytic activity
G0:0004175	63	endopeptidase activity
G0:0008033	63	tRNA processing
G0:0032869	62	cellular response to insulin stimulus
G0:0006302	62	double-strand break repair
G0:0030183	62	B cell differentiation
G0:0034097	62	response to cytokine
G0:0034166	62	toll-like receptor 10 signaling pathway
G0:0042254	62	ribosome biogenesis
G0:0019903	62	protein phosphatase binding
G0:0005814	62	centriole
G0:0034146	62	toll-like receptor 5 signaling pathway
G0:0043434	61	response to peptide hormone
G0:0005518	61	collagen binding
G0:0050679	61	positive regulation of epithelial cell proliferation
G0:0006334	61	nucleosome assembly
G0:0042472	61	inner ear morphogenesis
G0:0050728	61	negative regulation of inflammatory response
G0:0035091	60	phosphatidylinositol binding
G0:0005901	60	caveola
G0:0003705	60	RNA polymerase II distal enhancer sequence-specific DNA binding
transcription factor activity		
G0:0006987	60	activation of signaling protein activity involved in unfolded protein response
G0:0001938	60	positive regulation of endothelial cell proliferation
G0:0007126	60	meiotic nuclear division
G0:0030509	60	BMP signaling pathway
G0:0043154	59	negative regulation of cysteine-type endopeptidase activity involved in apoptotic process
G0:0008217	59	regulation of blood pressure
G0:0030512	59	negative regulation of transforming growth factor beta receptor signaling pathway
G0:0000502	59	proteasome complex
G0:0005905	59	coated pit
G0:0001570	59	vasculogenesis
G0:0019882	59	antigen processing and presentation
G0:0005643	59	nuclear pore
G0:0032481	59	positive regulation of type I interferon production
G0:0009725	59	response to hormone
G0:0005249	59	voltage-gated potassium channel activity
G0:0001669	59	acrosomal vesicle
G0:0040008	59	regulation of growth
G0:0004519	59	endonuclease activity
G0:0006139	59	nucleobase-containing compound metabolic process
G0:0009611	59	response to wounding
G0:0009612	59	response to mechanical stimulus
G0:0007202	58	activation of phospholipase C activity
G0:0035264	58	multicellular organism growth
G0:0051291	58	protein heterooligomerization
G0:0006968	58	cellular defense response
G0:0097193	58	intrinsic apoptotic signaling pathway
G0:0042475	58	odontogenesis of dentin-containing tooth
G0:0006406	58	mRNA export from nucleus
G0:0003777	58	microtubule motor activity
G0:0045216	58	cell-cell junction organization
G0:0050660	57	flavin adenine dinucleotide binding
G0:0032088	57	negative regulation of NF-kappaB transcription factor activity
G0:0015758	57	glucose transport
G0:0017137	57	Rab GTPase binding
G0:0015992	57	proton transport
G0:0000151	57	ubiquitin ligase complex
G0:0030176	57	integral component of endoplasmic reticulum membrane
G0:0030334	57	regulation of cell migration
G0:0006879	57	cellular iron ion homeostasis
G0:0043433	56	negative regulation of sequence-specific DNA binding transcription factor activity
G0:0008092	56	cytoskeletal protein binding
G0:0032580	56	Golgi cisterna membrane
G0:0030326	56	embryonic limb morphogenesis
G0:0009967	56	positive regulation of signal transduction
G0:0045669	56	positive regulation of osteoblast differentiation
G0:0008026	56	ATP-dependent helicase activity
G0:0043401	56	steroid hormone mediated signaling pathway
G0:0030216	56	keratinocyte differentiation

G0:0005758	56	mitochondrial intermembrane space
G0:0000226	55	microtubule cytoskeleton organization
G0:0051087	55	chaperone binding
G0:0007018	55	microtubule-based movement
G0:0000723	55	telomere maintenance
G0:0006959	55	humoral immune response
G0:0008013	55	beta-catenin binding
G0:0046330	55	positive regulation of JNK cascade
G0:0007623	54	circadian rhythm
G0:0045444	54	fat cell differentiation
G0:0071356	54	cellular response to tumor necrosis factor
G0:0008565	54	protein transporter activity
G0:0042734	54	presynaptic membrane
G0:0060041	54	retina development in camera-type eye
G0:0000977	54	RNA polymerase II regulatory region sequence-specific DNA binding
G0:0010976	54	positive regulation of neuron projection development
G0:0071300	54	cellular response to retinoic acid
G0:0006986	54	response to unfolded protein
G0:0071363	54	cellular response to growth factor stimulus
G0:0000902	54	cell morphogenesis
G0:0016525	54	negative regulation of angiogenesis
G0:0001568	54	blood vessel development
G0:0003684	54	damaged DNA binding
G0:0007599	54	hemostasis
G0:0030674	53	protein binding, bridging
G0:0042632	53	cholesterol homeostasis
G0:0000079	53	regulation of cyclin-dependent protein serine/threonine kinase activity
G0:0000910	53	cytokinesis
G0:0006694	53	steroid biosynthetic process
G0:0043204	53	perikaryon
G0:0000186	52	activation of MAPKK activity
G0:0022625	52	cytosolic large ribosomal subunit
G0:0070469	52	respiratory chain
G0:0051403	52	stress-activated MAPK cascade
G0:0044297	52	cell body
G0:0000786	52	nucleosome
G0:0004714	52	transmembrane receptor protein tyrosine kinase activity
G0:0007613	52	memory
G0:0008630	52	intrinsic apoptotic signaling pathway in response to DNA damage
G0:0048839	52	inner ear development
G0:0048704	52	embryonic skeletal system morphogenesis
G0:0050727	52	regulation of inflammatory response
G0:0005793	52	endoplasmic reticulum-Golgi intermediate compartment
G0:0042102	52	positive regulation of T cell proliferation
G0:0001523	52	retinoid metabolic process
G0:0051592	52	response to calcium ion
G0:0004197	51	cysteine-type endopeptidase activity
G0:00060326	51	cell chemotaxis
G0:0045860	51	positive regulation of protein kinase activity
G0:0003707	51	steroid hormone receptor activity
G0:0051536	51	iron-sulfur cluster binding
G0:0090263	51	positive regulation of canonical Wnt signaling pathway
G0:0007389	51	pattern specification process
G0:0035023	51	regulation of Rho protein signal transduction
G0:0030670	50	phagocytic vesicle membrane
G0:0005089	50	Rho guanyl-nucleotide exchange factor activity
G0:0032868	50	response to insulin
G0:0050680	50	negative regulation of epithelial cell proliferation
G0:0000932	50	cytoplasmic mRNA processing body
G0:0007586	50	digestion
G0:0006091	50	generation of precursor metabolites and energy
G0:0030175	50	filopodium
G0:0006521	50	regulation of cellular amino acid metabolic process
G0:0032851	50	positive regulation of Rab GTPase activity
G0:0007254	50	JNK cascade
G0:0019233	50	sensory perception of pain
G0:0031100	49	organ regeneration
G0:0016197	49	endosomal transport
G0:0016049	49	cell growth
G0:0006661	49	phosphatidylinositol biosynthetic process
G0:0005254	49	chloride channel activity
G0:1902600	49	hydrogen ion transmembrane transport
G0:0030666	49	endocytic vesicle membrane
G0:0048306	49	calcium-dependent protein binding
G0:0007269	49	neurotransmitter secretion

G0:0007286	49	spermatid development
G0:0002039	49	p53 binding
G0:0048666	49	neuron development
G0:0032526	49	response to retinoic acid
G0:0019827	49	stem cell maintenance
G0:0045454	49	cell redox homeostasis
G0:0030133	49	transport vesicle
G0:0042787	49	protein ubiquitination involved in ubiquitin-dependent protein catabolic process
G0:0019900	49	kinase binding
G0:0050729	49	positive regulation of inflammatory response
G0:0050830	48	defense response to Gram-positive bacterium
G0:0036459	48	ubiquitinyl hydrolase activity
G0:0001948	48	glycoprotein binding
G0:0003725	48	double-stranded RNA binding
G0:0043010	48	camera-type eye development
G0:0031093	48	platelet alpha granule lumen
G0:0003712	48	transcription cofactor activity
G0:0019369	48	arachidonic acid metabolic process
G0:0043406	48	positive regulation of MAP kinase activity
G0:0005201	48	extracellular matrix structural constituent
G0:0045732	48	positive regulation of protein catabolic process
G0:0005070	48	SH3/SH2 adaptor activity
G0:0007612	48	learning
G0:0005778	48	peroxisomal membrane
G0:0051259	48	protein oligomerization
G0:0051781	47	positive regulation of cell division
G0:0000288	47	nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay
G0:0006921	47	cellular component disassembly involved in execution phase of apoptosis
G0:0014068	47	positive regulation of phosphatidylinositol 3-kinase signaling
G0:0042110	47	T cell activation
G0:0042733	47	embryonic digit morphogenesis
G0:0034976	47	response to endoplasmic reticulum stress
G0:0033138	47	positive regulation of peptidyl-serine phosphorylation
G0:0071407	47	cellular response to organic cyclic compound
G0:0051289	47	protein homotetramerization
G0:0005811	47	lipid particle
G0:0034613	47	cellular protein localization
G0:0007519	47	skeletal muscle tissue development
G0:0045111	47	intermediate filament cytoskeleton
G0:0051591	47	response to cAMP
G0:0050839	46	cell adhesion molecule binding
G0:0008344	46	adult locomotory behavior
G0:0017053	46	transcriptional repressor complex
G0:0007015	46	actin filament organization
G0:0045596	46	negative regulation of cell differentiation
G0:0005507	46	copper ion binding
G0:0045665	46	negative regulation of neuron differentiation
G0:0007338	46	single fertilization
G0:0030136	46	clathrin-coated vesicle
G0:0019003	46	GDP binding
G0:0008009	46	chemokine activity
G0:0006283	46	transcription-coupled nucleotide-excision repair
G0:0006369	45	termination of RNA polymerase II transcription
G0:0007224	45	smoothened signaling pathway
G0:0001947	45	heart looping
G0:0007266	45	Rho protein signal transduction
G0:0031594	45	neuromuscular junction
G0:0016529	45	sarcoplasmic reticulum
G0:0021987	45	cerebral cortex development
G0:0001078	45	RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity involved in negative regulation of transcription
G0:0001657	45	ureteric bud development
G0:0003007	45	heart morphogenesis
G0:0000724	45	double-strand break repair via homologous recombination
G0:0006633	45	fatty acid biosynthetic process
G0:0035690	45	cellular response to drug
G0:0005912	45	adherens junction
G0:0006626	44	protein targeting to mitochondrion
G0:0032922	44	circadian regulation of gene expression
G0:0001756	44	somitogenesis
G0:0043588	44	skin development
G0:0007154	44	cell communication
G0:0016459	44	myosin complex
G0:0050434	44	positive regulation of viral transcription

G0:0050885	44	neuromuscular process controlling balance
G0:0001725	44	stress fiber
G0:0030170	44	pyridoxal phosphate binding
G0:0030178	44	negative regulation of Wnt signaling pathway
G0:0019722	44	calcium-mediated signaling
G0:0017148	44	negative regulation of translation
G0:0035064	44	methylated histone binding
G0:0030672	43	synaptic vesicle membrane
G0:0003743	43	translation initiation factor activity
G0:0006892	43	post-Golgi vesicle-mediated transport
G0:0016579	43	protein deubiquitination
G0:0001047	43	core promoter binding
G0:0048661	43	positive regulation of smooth muscle cell proliferation
G0:0009968	43	negative regulation of signal transduction
G0:0009411	43	response to UV
G0:0045786	43	negative regulation of cell cycle
G0:0048146	43	positive regulation of fibroblast proliferation
G0:0000781	43	chromosome, telomeric region
G0:0016881	43	acid-amino acid ligase activity
G0:0030017	43	sarcomere
G0:0010212	43	response to ionizing radiation
G0:0005871	43	kinesin complex
G0:0007416	43	synapse assembly
G0:0042542	42	response to hydrogen peroxide
G0:0007193	42	adenylate cyclase-inhibiting G-protein coupled receptor signaling pathway
G0:0005080	42	protein kinase C binding
G0:0034707	42	chloride channel complex
G0:0004715	42	non-membrane spanning protein tyrosine kinase activity
G0:0006888	42	ER to Golgi vesicle-mediated transport
G0:0005881	42	cytoplasmic microtubule
G0:0045727	42	positive regulation of translation
G0:0043525	42	positive regulation of neuron apoptotic process
G0:0006094	42	gluconeogenesis
G0:0007611	42	learning or memory
G0:0008277	42	regulation of G-protein coupled receptor protein signaling pathway
G0:0001933	42	negative regulation of protein phosphorylation
G0:0030139	42	endocytic vesicle
G0:0008047	42	enzyme activator activity
G0:0030155	42	regulation of cell adhesion
G0:0030521	42	androgen receptor signaling pathway
G0:0006520	42	cellular amino acid metabolic process
G0:0021766	42	hippocampus development
G0:0043130	42	ubiquitin binding
G0:0007368	41	determination of left/right symmetry
G0:0004857	41	enzyme inhibitor activity
G0:0007200	41	phospholipase C-activating G-protein coupled receptor signaling pathway
G0:0007189	41	adenylate cyclase-activating G-protein coupled receptor signaling pathway
G0:0005230	41	extracellular ligand-gated ion channel activity
G0:0001658	41	branching involved in ureteric bud morphogenesis
G0:0007588	41	excretion
G0:0030204	41	chondroitin sulfate metabolic process
G0:0007188	41	adenylate cyclase-modulating G-protein coupled receptor signaling pathway
G0:0031398	41	positive regulation of protein ubiquitination
G0:0005747	41	mitochondrial respiratory chain complex I
G0:0031047	41	gene silencing by RNA
G0:0006418	41	tRNA aminoacylation for protein translation
G0:0031424	41	keratinization
G0:0007595	41	lactation
G0:0021762	41	substantia nigra development
G0:0031124	41	mRNA 3'-end processing
G0:0004879	40	ligand-activated sequence-specific DNA binding RNA polymerase II transcription factor activity
G0:0048538	40	thymus development
G0:0004402	40	histone acetyltransferase activity
G0:0043966	40	histone H3 acetylation
G0:0019898	40	extrinsic component of membrane
G0:0001942	40	hair follicle development
G0:0048812	40	neuron projection morphogenesis
G0:0005902	40	microvillus
G0:0005044	40	scavenger receptor activity
G0:0006096	40	glycolytic process
G0:0042552	40	myelination
G0:0007187	40	G-protein coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger
G0:0031532	40	actin cytoskeleton reorganization

G0:0071320	40	cellular response to cAMP
G0:0008542	40	visual learning
G0:0016328	40	lateral plasma membrane
G0:0008654	40	phospholipid biosynthetic process
G0:0000980	40	RNA polymerase II distal enhancer sequence-specific DNA binding
G0:0035872	40	nucleotide-binding domain, leucine rich repeat containing receptor
signaling pathway		
G0:0009898	40	cytoplasmic side of plasma membrane
G0:0030145	40	manganese ion binding
G0:0008146	40	sulfotransferase activity
G0:0001541	40	ovarian follicle development
G0:0030218	40	erythrocyte differentiation
G0:0009953	40	dorsal/ventral pattern formation
G0:0031526	39	brush border membrane
G0:0006120	39	mitochondrial electron transport, NADH to ubiquinone
G0:0001750	39	photoreceptor outer segment
G0:0030819	39	positive regulation of cAMP biosynthetic process
G0:0032880	39	regulation of protein localization
G0:0006687	39	glycosphingolipid metabolic process
G0:0010595	39	positive regulation of endothelial cell migration
G0:0003151	39	outflow tract morphogenesis
G0:0008015	39	blood circulation
G0:0042157	39	lipoprotein metabolic process
G0:0060048	39	cardiac muscle contraction
G0:0007030	39	Golgi organization
G0:0045597	39	positive regulation of cell differentiation
G0:0070936	39	protein K48-linked ubiquitination
G0:0051865	39	protein autoubiquitination
G0:0060271	39	cilium morphogenesis
G0:0035914	39	skeletal muscle cell differentiation
G0:0008081	39	phosphoric diester hydrolase activity
G0:0009058	39	biosynthetic process
G0:0030199	39	collagen fibril organization
G0:0040007	39	growth
G0:0005057	39	receptor signaling protein activity
G0:0006836	39	neurotransmitter transport
G0:0043280	39	positive regulation of cysteine-type endopeptidase activity involved in
apoptotic process		
G0:0072659	38	protein localization to plasma membrane
G0:0010923	38	negative regulation of phosphatase activity
G0:0007205	38	protein kinase C-activating G-protein coupled receptor signaling pathway
G0:0038032	38	termination of G-protein coupled receptor signaling pathway
G0:0006635	38	fatty acid beta-oxidation
G0:0070301	38	cellular response to hydrogen peroxide
G0:0030049	38	muscle filament sliding
G0:0031667	38	response to nutrient levels
G0:0032755	38	positive regulation of interleukin-6 production
G0:0045740	38	positive regulation of DNA replication
G0:0050909	38	sensory perception of taste
G0:0008137	38	NADH dehydrogenase (ubiquinone) activity
G0:0022857	38	transmembrane transporter activity
G0:0055038	38	recycling endosome membrane
G0:0035176	38	social behavior
G0:0006284	38	base-excision repair
G0:0015030	38	Cajal body
G0:0006833	38	water transport
G0:0071230	38	cellular response to amino acid stimulus
G0:0032729	38	positive regulation of interferon-gamma production
G0:0048706	38	embryonic skeletal system development
G0:0006605	38	protein targeting
G0:0060548	38	negative regulation of cell death
G0:0046332	38	SMAD binding
G0:0008307	38	structural constituent of muscle
G0:0007628	37	adult walking behavior
G0:0031490	37	chromatin DNA binding
G0:0019838	37	growth factor binding
G0:0008645	37	hexose transport
G0:0050681	37	androgen receptor binding
G0:0004722	37	protein serine/threonine phosphatase activity
G0:0001656	37	metanephros development
G0:0048469	37	cell maturation
G0:0045785	37	positive regulation of cell adhesion
G0:0032508	37	DNA duplex unwinding
G0:0030593	37	neutrophil chemotaxis
G0:0071944	37	cell periphery

G0:0048705	37	skeletal system morphogenesis
G0:0030016	37	myofibril
G0:0030173	37	integral component of Golgi membrane
G0:0042645	37	mitochondrial nucleoid
G0:0051084	37	'de novo' posttranslational protein folding
G0:0007005	37	mitochondrion organization
G0:0009408	37	response to heat
G0:0030374	37	ligand-dependent nuclear receptor transcription coactivator activity
G0:0000737	37	DNA catabolic process, endonucleolytic
G0:0005109	36	frizzled binding
G0:0032436	36	positive regulation of proteasomal ubiquitin-dependent protein catabolic process
G0:0071377	36	cellular response to glucagon stimulus
G0:0008094	36	DNA-dependent ATPase activity
G0:0032154	36	cleavage furrow
G0:0022627	36	cytosolic small ribosomal subunit
G0:0051117	36	ATPase binding
G0:0097191	36	extrinsic apoptotic signaling pathway
G0:0035019	36	somatic stem cell maintenance
G0:0004527	36	exonuclease activity
G0:0031018	36	endocrine pancreas development
G0:0006259	36	DNA metabolic process
G0:0031514	36	motile cilium
G0:0008138	36	protein tyrosine/serine/threonine phosphatase activity
G0:0007631	36	feeding behavior
G0:0003899	36	DNA-directed RNA polymerase activity
G0:0007585	36	respiratory gaseous exchange
G0:0043407	36	negative regulation of MAP kinase activity
G0:2001235	36	positive regulation of apoptotic signaling pathway
G0:0019902	36	phosphatase binding
G0:0042277	36	peptide binding
G0:0043647	36	inositol phosphate metabolic process
G0:0030522	36	intracellular receptor signaling pathway
G0:0002062	36	chondrocyte differentiation
G0:0004553	36	hydrolase activity, hydrolyzing O-glycosyl compounds
G0:0048167	36	regulation of synaptic plasticity
G0:0004812	36	aminoacyl-tRNA ligase activity
G0:0006024	36	glycosaminoglycan biosynthetic process
G0:0070830	36	tight junction assembly
G0:0004896	36	cytokine receptor activity
G0:0006383	36	transcription from RNA polymerase III promoter
G0:0070527	36	platelet aggregation
G0:0018107	35	peptidyl-threonine phosphorylation
G0:0014704	35	intercalated disc
G0:0043195	35	terminal bouton
G0:0045668	35	negative regulation of osteoblast differentiation
G0:0030162	35	regulation of proteolysis
G0:0006144	35	purine nucleobase metabolic process
G0:0030315	35	T-tubule
G0:0032588	35	trans-Golgi network membrane
G0:0001890	35	placenta development
G0:0031252	35	cell leading edge
G0:0051219	35	phosphoprotein binding
G0:0019829	35	cation-transporting ATPase activity
G0:0023014	35	signal transduction by phosphorylation
G0:0048545	35	response to steroid hormone
G0:0001102	35	RNA polymerase II activating transcription factor binding
G0:0006909	35	phagocytosis
G0:0008206	35	bile acid metabolic process
G0:0051287	35	NAD binding
G0:0008625	35	extrinsic apoptotic signaling pathway via death domain receptors
G0:0001664	35	G-protein coupled receptor binding
G0:0043473	35	pigmentation
G0:0090382	35	phagosome maturation
G0:0006606	35	protein import into nucleus
G0:0090502	35	RNA phosphodiester bond hydrolysis, endonucleolytic
G0:0005245	35	voltage-gated calcium channel activity
G0:0051603	35	proteolysis involved in cellular protein catabolic process
G0:0002250	35	adaptive immune response
G0:0071333	34	cellular response to glucose stimulus
G0:0006641	34	triglyceride metabolic process
G0:0050661	34	NADP binding
G0:0016604	34	nuclear body
G0:0016266	34	O-glycan processing
G0:0060348	34	bone development

G0:0097192	34	extrinsic apoptotic signaling pathway in absence of ligand
G0:0002053	34	positive regulation of mesenchymal cell proliferation
G0:0032760	34	positive regulation of tumor necrosis factor production
G0:0006749	34	glutathione metabolic process
G0:0016758	34	transferase activity, transferring hexosyl groups
G0:0019432	34	triglyceride biosynthetic process
G0:0016773	34	phosphotransferase activity, alcohol group as acceptor
G0:0005782	34	peroxisomal matrix
G0:0006446	34	regulation of translational initiation
G0:0045599	34	negative regulation of fat cell differentiation
G0:0005884	34	actin filament
G0:0022008	34	neurogenesis
G0:0007077	34	mitotic nuclear envelope disassembly
G0:0005546	34	phosphatidylinositol-4,5-bisphosphate binding
G0:0004866	34	endopeptidase inhibitor activity
G0:0016616	34	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor
G0:0004221	34	ubiquitin thiolesterase activity
G0:0001837	34	epithelial to mesenchymal transition
G0:2001237	34	negative regulation of extrinsic apoptotic signaling pathway
G0:0007162	34	negative regulation of cell adhesion
G0:0042692	34	muscle cell differentiation
G0:0071560	34	cellular response to transforming growth factor beta stimulus
G0:0012507	34	ER to Golgi transport vesicle membrane
G0:0005834	34	heterotrimeric G-protein complex
G0:0043621	34	protein self-association
G0:0001580	34	detection of chemical stimulus involved in sensory perception of bitter taste
G0:0033077	34	T cell differentiation in thymus
G0:0006953	34	acute-phase response
G0:0005791	34	rough endoplasmic reticulum
G0:0021915	34	neural tube development
G0:0030658	33	transport vesicle membrane
G0:0043198	33	dendritic shaft
G0:0016485	33	protein processing
G0:0030838	33	positive regulation of actin filament polymerization
G0:0030163	33	protein catabolic process
G0:0035249	33	synaptic transmission, glutamatergic
G0:0007281	33	germ cell development
G0:0043679	33	axon terminus
G0:0042059	33	negative regulation of epidermal growth factor receptor signaling pathway
G0:0070098	33	chemokine-mediated signaling pathway
G0:0005251	33	delayed rectifier potassium channel activity
G0:0042113	33	B cell activation
G0:0030217	33	T cell differentiation
G0:0030901	33	midbrain development
G0:0045595	33	regulation of cell differentiation
G0:0048754	33	branching morphogenesis of an epithelial tube
G0:0001974	33	blood vessel remodeling
G0:0000413	33	protein peptidyl-prolyl isomerization
G0:0005097	33	Rab GTPase activator activity
G0:0032870	33	cellular response to hormone stimulus
G0:0006695	33	cholesterol biosynthetic process
G0:0051402	33	neuron apoptotic process
G0:0003755	33	peptidyl-prolyl cis-trans isomerase activity
G0:0032092	33	positive regulation of protein binding
G0:0034332	33	adherens junction organization
G0:0005930	33	axoneme
G0:0007498	33	mesoderm development
G0:0097110	33	scaffold protein binding
G0:0051539	33	4 iron, 4 sulfur cluster binding
G0:0005876	33	spindle microtubule
G0:0005913	33	cell-cell adherens junction
G0:0001569	33	patterning of blood vessels
G0:0005795	33	Golgi stack
G0:0001895	33	retina homeostasis
G0:0050890	33	cognition
G0:0032024	33	positive regulation of insulin secretion
G0:0030890	33	positive regulation of B cell proliferation
G0:0019905	33	syntaxin binding
G0:0030879	32	mammary gland development
G0:0001944	32	vasculature development
G0:0060325	32	face morphogenesis
G0:0007249	32	I-kappaB kinase/NF-kappaB signaling
G0:2001244	32	positive regulation of intrinsic apoptotic signaling pathway

G0:0016056	32	rhodopsin mediated signaling pathway
G0:0071310	32	cellular response to organic substance
G0:0055072	32	iron ion homeostasis
G0:0040018	32	positive regulation of multicellular organism growth
G0:0042752	32	regulation of circadian rhythm
G0:0007339	32	binding of sperm to zona pellucida
G0:0008016	32	regulation of heart contraction
G0:0030433	32	ER-associated ubiquitin-dependent protein catabolic process
G0:0006958	32	complement activation, classical pathway
G0:0042626	32	ATPase activity, coupled to transmembrane movement of substances
G0:0007257	32	activation of JUN kinase activity
G0:0060170	32	ciliary membrane
G0:0015297	32	antiporter activity
G0:0042476	32	odontogenesis
G0:0070555	32	response to interleukin-1
G0:0006261	32	DNA-dependent DNA replication
G0:0071277	32	cellular response to calcium ion
G0:0032956	32	regulation of actin cytoskeleton organization
G0:0036064	32	ciliary basal body
G0:0008652	32	cellular amino acid biosynthetic process
G0:0021549	32	cerebellum development
G0:0051496	32	positive regulation of stress fiber assembly
G0:0008180	32	COP9 signalosome
G0:0007040	32	lysosome organization
G0:0005875	32	microtubule associated complex
G0:0034446	32	substrate adhesion-dependent cell spreading
G0:0045171	32	intercellular bridge
G0:0015485	32	cholesterol binding
G0:0045429	32	positive regulation of nitric oxide biosynthetic process
G0:0070888	31	E-box binding
G0:0046677	31	response to antibiotic
G0:0045071	31	negative regulation of viral genome replication
G0:2001240	31	negative regulation of extrinsic apoptotic signaling pathway in absence of ligand
G0:0015459	31	potassium channel regulator activity
G0:0030514	31	negative regulation of BMP signaling pathway
G0:0007017	31	microtubule-based process
G0:0007157	31	heterophilic cell-cell adhesion
G0:0031072	31	heat shock protein binding
G0:0043330	31	response to exogenous dsRNA
G0:0015914	31	phospholipid transport
G0:0048589	31	developmental growth
G0:0010977	31	negative regulation of neuron projection development
G0:0016358	31	dendrite development
G0:0042594	31	response to starvation
G0:0007259	31	JAK-STAT cascade
G0:0032855	31	positive regulation of Rac GTPase activity
G0:0001085	31	RNA polymerase II transcription factor binding
G0:0031201	31	SNARE complex
G0:0045335	31	phagocytic vesicle
G0:0050918	31	positive chemotaxis
G0:0048013	31	ephrin receptor signaling pathway
G0:0042339	31	keratan sulfate metabolic process
G0:0030148	31	sphingolipid biosynthetic process
G0:0032570	31	response to progesterone
G0:0033209	31	tumor necrosis factor-mediated signaling pathway
G0:0006360	30	transcription from RNA polymerase I promoter
G0:0048536	30	spleen development
G0:0050853	30	B cell receptor signaling pathway
G0:0051701	30	interaction with host
G0:0018024	30	histone-lysine N-methyltransferase activity
G0:0021983	30	pituitary gland development
G0:0007094	30	mitotic spindle assembly checkpoint
G0:0007566	30	embryo implantation
G0:0048813	30	dendrite morphogenesis
G0:0031623	30	receptor internalization
G0:0016573	30	histone acetylation
G0:0005272	30	sodium channel activity
G0:0000979	30	RNA polymerase II core promoter sequence-specific DNA binding
G0:0043507	30	positive regulation of JUN kinase activity
G0:0034599	30	cellular response to oxidative stress
G0:0006865	30	amino acid transport
G0:0006271	30	DNA strand elongation involved in DNA replication
G0:0019825	30	oxygen binding
G0:0035116	30	embryonic hindlimb morphogenesis

G0:0001932	30	regulation of protein phosphorylation
G0:0006370	30	7-methylguanosine mRNA capping
G0:0071347	30	cellular response to interleukin-1
G0:2001238	30	positive regulation of extrinsic apoptotic signaling pathway
G0:0004693	30	cyclin-dependent protein serine/threonine kinase activity
G0:0032313	30	regulation of Rab GTPase activity
G0:0030501	30	positive regulation of bone mineralization
G0:0030282	30	bone mineralization
G0:0042147	30	retrograde transport, endosome to Golgi
G0:0009409	30	response to cold
G0:0030971	30	receptor tyrosine kinase binding
G0:0005164	30	tumor necrosis factor receptor binding
G0:0043491	30	protein kinase B signaling
G0:0048701	29	embryonic cranial skeleton morphogenesis
G0:0007190	29	activation of adenylate cyclase activity
G0:0006913	29	nucleocytoplasmic transport
G0:0048286	29	lung alveolus development
G0:0000794	29	condensed nuclear chromosome
G0:0010243	29	response to organonitrogen compound
G0:0070373	29	negative regulation of ERK1 and ERK2 cascade
G0:0004177	29	aminopeptidase activity
G0:0042220	29	response to cocaine
G0:0048487	29	beta-tubulin binding
G0:0061077	29	chaperone-mediated protein folding
G0:0007528	29	neuromuscular junction development
G0:0000976	29	transcription regulatory region sequence-specific DNA binding
G0:0005801	29	cis-Golgi network
G0:0032091	29	negative regulation of protein binding
G0:0001707	29	mesoderm formation
G0:0009117	29	nucleotide metabolic process
G0:0017046	29	peptide hormone binding
G0:0010494	29	cytoplasmic stress granule
G0:0032467	29	positive regulation of cytokinesis
G0:0004180	29	carboxypeptidase activity
G0:0004712	29	protein serine/threonine/tyrosine kinase activity
G0:0030317	29	sperm motility
G0:0005977	29	glycogen metabolic process
G0:0001228	29	RNA polymerase II transcription regulatory region sequence-specific DNA binding
G0:0022400	29	transcription factor activity involved in positive regulation of transcription
G0:0032720	29	regulation of rhodopsin mediated signaling pathway
G0:0035115	29	negative regulation of tumor necrosis factor production
G0:0035115	29	embryonic forelimb morphogenesis
G0:0090501	29	RNA phosphodiester bond hydrolysis
G0:0004864	29	protein phosphatase inhibitor activity
G0:0014823	29	response to activity
G0:0006956	29	complement activation
G0:0003887	28	DNA-directed DNA polymerase activity
G0:0001755	28	neural crest cell migration
G0:0007492	28	endoderm development
G0:0030669	28	clathrin-coated endocytic vesicle membrane
G0:0003727	28	single-stranded RNA binding
G0:0010827	28	regulation of glucose transport
G0:0008333	28	endosome to lysosome transport
G0:0031647	28	regulation of protein stability
G0:0007569	28	cell aging
G0:0010811	28	positive regulation of cell-substrate adhesion
G0:0005903	28	brush border
G0:0032320	28	positive regulation of Ras GTPase activity
G0:0019843	28	rRNA binding
G0:0016592	28	mediator complex
G0:0050770	28	regulation of axonogenesis
G0:0001975	28	response to amphetamine
G0:0005544	28	calcium-dependent phospholipid binding
G0:0005547	28	phosphatidylinositol-3,4,5-trisphosphate binding
G0:0070534	28	protein K63-linked ubiquitination
G0:0030073	28	insulin secretion
G0:0046875	28	ephrin receptor binding
G0:0006488	28	dolichol-linked oligosaccharide biosynthetic process
G0:0000049	28	tRNA binding
G0:0016788	28	hydrolase activity, acting on ester bonds
G0:0009566	28	fertilization
G0:0042169	28	SH2 domain binding
G0:0048662	28	negative regulation of smooth muscle cell proliferation
G0:0042100	28	B cell proliferation
G0:0045776	28	negative regulation of blood pressure

G0:0070491	28	repressing transcription factor binding
G0:0004869	28	cysteine-type endopeptidase inhibitor activity
G0:0043531	28	ADP binding
G0:0032947	28	protein complex scaffold
G0:0010942	28	positive regulation of cell death
G0:0005776	28	autophagic vacuole
G0:0007602	28	phototransduction
G0:0007369	27	gastrulation
G0:0086010	27	membrane depolarization during action potential
G0:0000188	27	inactivation of MAPK activity
G0:0030331	27	estrogen receptor binding
G0:0043928	27	exonucleolytic nuclear-transcribed mRNA catabolic process involved in deadenylation-dependent decay
G0:0050873	27	brown fat cell differentiation
G0:0000793	27	condensed chromosome
G0:0000228	27	nuclear chromosome
G0:0043200	27	response to amino acid
G0:0051149	27	positive regulation of muscle cell differentiation
G0:0005637	27	nuclear inner membrane
G0:0000077	27	DNA damage checkpoint
G0:0001618	27	virus receptor activity
G0:0008643	27	carbohydrate transport
G0:0031663	27	lipopolysaccharide-mediated signaling pathway
G0:0034612	27	response to tumor necrosis factor
G0:0000387	27	spliceosomal snRNP assembly
G0:0040014	27	regulation of multicellular organism growth
G0:0019228	27	neuronal action potential
G0:1900740	27	positive regulation of protein insertion into mitochondrial membrane
		involved in apoptotic signaling pathway
G0:0031016	27	pancreas development
G0:0048663	27	neuron fate commitment
G0:0043392	27	negative regulation of DNA binding
G0:0042177	27	negative regulation of protein catabolic process
G0:0042130	27	negative regulation of T cell proliferation
G0:0009966	27	regulation of signal transduction
G0:0043523	27	regulation of neuron apoptotic process
G0:0045765	27	regulation of angiogenesis
G0:0050714	27	positive regulation of protein secretion
G0:0046966	27	thyroid hormone receptor binding
G0:0016706	27	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors
G0:0033572	27	transferrin transport
G0:0007616	27	long-term memory
G0:0043124	27	negative regulation of I-kappaB kinase/NF-kappaB signaling
G0:0007422	27	peripheral nervous system development
G0:0009617	27	response to bacterium
G0:0030863	27	cortical cytoskeleton
G0:0050808	27	synapse organization
G0:0033116	27	endoplasmic reticulum-Golgi intermediate compartment membrane
G0:0001104	27	RNA polymerase II transcription cofactor activity
G0:0017048	27	Rho GTPase binding
G0:0060338	27	regulation of type I interferon-mediated signaling pathway
G0:0072593	27	reactive oxygen species metabolic process
G0:0045909	27	positive regulation of vasodilation
G0:0050690	27	regulation of defense response to virus by virus
G0:0009314	27	response to radiation
G0:0006730	27	one-carbon metabolic process
G0:0008060	27	ARF GTPase activator activity
G0:0032312	27	regulation of ARF GTPase activity
G0:0002088	27	lens development in camera-type eye
G0:0016925	27	protein sumoylation
G0:0035094	27	response to nicotine
G0:0008406	27	gonad development
G0:0002027	27	regulation of heart rate
G0:0048863	27	stem cell differentiation
G0:0008305	27	integrin complex
G0:0005891	27	voltage-gated calcium channel complex
G0:0015631	27	tubulin binding
G0:0004601	27	peroxidase activity
G0:0006361	26	transcription initiation from RNA polymerase I promoter
G0:0046676	26	negative regulation of insulin secretion
G0:0000792	26	heterochromatin
G0:0034644	26	cellular response to UV
G0:0019894	26	kinesin binding

G0:0045931	26	positive regulation of mitotic cell cycle
G0:0048514	26	blood vessel morphogenesis
G0:0008306	26	associative learning
G0:0003950	26	NAD+ ADP-ribosyltransferase activity
G0:0010862	26	positive regulation of pathway-restricted SMAD protein phosphorylation
G0:0004003	26	ATP-dependent DNA helicase activity
G0:0051209	26	release of sequestered calcium ion into cytosol
G0:0030534	26	adult behavior
G0:0001654	26	eye development
G0:0045494	26	photoreceptor cell maintenance
G0:0042771	26	intrinsic apoptotic signaling pathway in response to DNA damage by p53
class mediator		
G0:0016126	26	sterol biosynthetic process
G0:0001103	26	RNA polymerase II repressing transcription factor binding
G0:0004129	26	cytochrome-c oxidase activity
G0:0006654	26	phosphatidic acid biosynthetic process
G0:0070979	26	protein K11-linked ubiquitination
G0:0071556	26	integral component of lumenal side of endoplasmic reticulum membrane
G0:0042327	26	positive regulation of phosphorylation
G0:0001819	26	positive regulation of cytokine production
G0:0046326	26	positive regulation of glucose import
G0:0000118	26	histone deacetylase complex
G0:0048365	26	Rac GTPase binding
G0:0032480	26	negative regulation of type I interferon production
G0:0006099	26	tricarboxylic acid cycle
G0:0006090	26	pyruvate metabolic process
G0:0048008	26	platelet-derived growth factor receptor signaling pathway
G0:0051928	26	positive regulation of calcium ion transport
G0:0005158	26	insulin receptor binding
G0:0072686	26	mitotic spindle
G0:0045600	26	positive regulation of fat cell differentiation
G0:0045787	26	positive regulation of cell cycle
G0:0000722	26	telomere maintenance via recombination
G0:0051262	26	protein tetramerization
G0:0001937	26	negative regulation of endothelial cell proliferation
G0:0031492	26	nucleosomal DNA binding
G0:0015701	26	bicarbonate transport
G0:0035987	26	endodermal cell differentiation
G0:0030117	26	membrane coat
G0:0005921	26	gap junction
G0:0030177	26	positive regulation of Wnt signaling pathway
G0:0005261	26	cation channel activity
G0:0006501	26	C-terminal protein lipidation
G0:0010332	26	response to gamma radiation
G0:0045296	26	cadherin binding
G0:0016747	26	transferase activity, transferring acyl groups other than amino-acyl groups
G0:0017144	26	drug metabolic process
G0:0017147	26	Wnt-protein binding
G0:0003823	26	antigen binding
G0:0050766	26	positive regulation of phagocytosis
G0:0004860	26	protein kinase inhibitor activity
G0:0033017	26	sarcoplasmic reticulum membrane
G0:0018146	26	keratan sulfate biosynthetic process
G0:0051276	25	chromosome organization
G0:0071339	25	MLL1 complex
G0:0001772	25	immunological synapse
G0:0045664	25	regulation of neuron differentiation
G0:0050829	25	defense response to Gram-negative bacterium
G0:0031397	25	negative regulation of protein ubiquitination
G0:0031214	25	biomineral tissue development
G0:0004950	25	chemokine receptor activity
G0:0001892	25	embryonic placenta development
G0:0007093	25	mitotic cell cycle checkpoint
G0:0007159	25	leukocyte cell-cell adhesion
G0:0015991	25	ATP hydrolysis coupled proton transport
G0:0009267	25	cellular response to starvation
G0:0009925	25	basal plasma membrane
G0:0032735	25	positive regulation of interleukin-12 production
G0:0000096	25	sulfur amino acid metabolic process
G0:0042517	25	positive regulation of tyrosine phosphorylation of Stat3 protein
G0:1901687	25	glutathione derivative biosynthetic process
G0:0048565	25	digestive tract development
G0:0055010	25	ventricular cardiac muscle tissue morphogenesis
G0:0001917	25	photoreceptor inner segment

G0:0031519	25	PcG protein complex
G0:0046627	25	negative regulation of insulin receptor signaling pathway
G0:0043022	25	ribosome binding
G0:0006506	25	GPI anchor biosynthetic process
G0:0003730	25	mRNA 3'-UTR binding
G0:0006890	25	retrograde vesicle-mediated transport, Golgi to ER
G0:0034605	25	cellular response to heat
G0:0006754	25	ATP biosynthetic process
G0:0006027	25	glycosaminoglycan catabolic process
G0:0043552	25	positive regulation of phosphatidylinositol 3-kinase activity
G0:0061025	25	membrane fusion
G0:0001540	25	beta-amyloid binding
G0:0006206	25	pyrimidine nucleobase metabolic process
G0:0019005	25	SCF ubiquitin ligase complex
G0:0035329	25	hippo signaling
G0:2000379	25	positive regulation of reactive oxygen species metabolic process
G0:0051258	25	protein polymerization
G0:0060079	24	regulation of excitatory postsynaptic membrane potential
G0:0006363	24	termination of RNA polymerase I transcription
G0:0007194	24	negative regulation of adenylate cyclase activity
G0:0045861	24	negative regulation of proteolysis
G0:0015026	24	coreceptor activity
G0:0051899	24	membrane depolarization
G0:0051898	24	negative regulation of protein kinase B signaling
G0:0005083	24	small GTPase regulator activity
G0:1902042	24	negative regulation of extrinsic apoptotic signaling pathway via death domain receptors
G0:0015078	24	hydrogen ion transmembrane transporter activity
G0:0060349	24	bone morphogenesis
G0:0007131	24	reciprocal meiotic recombination
G0:0030041	24	actin filament polymerization
G0:0044070	24	regulation of anion transport
G0:0045859	24	regulation of protein kinase activity
G0:0019229	24	regulation of vasoconstriction
G0:0016575	24	histone deacetylation
G0:0050715	24	positive regulation of cytokine secretion
G0:0008135	24	translation factor activity, nucleic acid binding
G0:0005496	24	steroid binding
G0:0055074	24	calcium ion homeostasis
G0:0015935	24	small ribosomal subunit
G0:0033574	24	response to testosterone
G0:0005761	24	mitochondrial ribosome
G0:0048147	24	negative regulation of fibroblast proliferation
G0:0016339	24	calcium-dependent cell-cell adhesion
G0:0005978	24	glycogen biosynthetic process
G0:0001105	24	RNA polymerase II transcription coactivator activity
G0:0046854	24	phosphatidylinositol phosphorylation
G0:0007163	24	establishment or maintenance of cell polarity
G0:0045907	24	positive regulation of vasoconstriction
G0:0060173	24	limb development
G0:0043029	24	T cell homeostasis
G0:0030316	24	osteoclast differentiation
G0:0001816	24	cytokine production
G0:0045862	24	positive regulation of proteolysis
G0:0031069	24	hair follicle morphogenesis
G0:0001662	24	behavioral fear response
G0:0019216	24	regulation of lipid metabolic process
G0:0045840	24	positive regulation of mitosis
G0:0048678	24	response to axon injury
G0:0019706	24	protein-cysteine S-palmitoyltransferase activity
G0:0004114	24	3',5'-cyclic-nucleotide phosphodiesterase activity
G0:0006611	24	protein export from nucleus
G0:0034968	24	histone lysine methylation
G0:0035108	24	limb morphogenesis
G0:0030449	23	regulation of complement activation
G0:0061418	23	regulation of transcription from RNA polymerase II promoter in response to hypoxia
G0:0003678	23	DNA helicase activity
G0:0001968	23	fibronectin binding
G0:0016831	23	carboxy-lyase activity
G0:0005104	23	fibroblast growth factor receptor binding
G0:0090200	23	positive regulation of release of cytochrome c from mitochondria
G0:0071479	23	cellular response to ionizing radiation
G0:0030325	23	adrenal gland development
G0:0030513	23	positive regulation of BMP signaling pathway

G0:0042104	23	positive regulation of activated T cell proliferation
G0:0033344	23	cholesterol efflux
G0:0032281	23	alpha-amino-3-hydroxy-5-methyl-4-isoxazolepropionic acid selective glutamate receptor complex
G0:0060291	23	long-term synaptic potentiation
G0:0070423	23	nucleotide-binding oligomerization domain containing signaling pathway
G0:0071902	23	positive regulation of protein serine/threonine kinase activity
G0:0007032	23	endosome organization
G0:0042755	23	eating behavior
G0:0016597	23	amino acid binding
G0:0043484	23	regulation of RNA splicing
G0:0005154	23	epidermal growth factor receptor binding
G0:0045184	23	establishment of protein localization
G0:0060397	23	JAK-STAT cascade involved in growth hormone signaling pathway
G0:0008536	23	Ran GTPase binding
G0:0043967	23	histone H4 acetylation
G0:0051059	23	NF-kappaB binding
G0:0051491	23	positive regulation of filopodium assembly
G0:0051017	23	actin filament bundle assembly
G0:0042605	23	peptide antigen binding
G0:0071346	23	cellular response to interferon-gamma
G0:0008089	23	anterograde axon cargo transport
G0:0043425	23	bHLH transcription factor binding
G0:0004364	23	glutathione transferase activity
G0:2001141	23	regulation of RNA biosynthetic process
G0:0000045	23	autophagic vacuole assembly
G0:0030286	23	dynein complex
G0:0032147	23	activation of protein kinase activity
G0:0051965	23	positive regulation of synapse assembly
G0:0000060	23	protein import into nucleus, translocation
G0:0035235	23	ionotropic glutamate receptor signaling pathway
G0:0046686	23	response to cadmium ion
G0:0043278	23	response to morphine
G0:0051924	23	regulation of calcium ion transport
G0:0005484	23	SNAP receptor activity
G0:0001836	23	release of cytochrome c from mitochondria
G0:0045739	23	positive regulation of DNA repair
G0:0030032	23	lamellipodium assembly
G0:0000375	23	RNA splicing, via transesterification reactions
G0:0000149	23	SNARE binding
G0:0001972	23	retinoic acid binding
G0:0016209	23	antioxidant activity
G0:0043044	23	ATP-dependent chromatin remodeling
G0:0051281	23	positive regulation of release of sequestered calcium ion into cytosol
G0:0030212	23	hyaluronan metabolic process
G0:0009954	23	proximal/distal pattern formation
G0:0018149	23	peptide cross-linking
G0:0031463	23	Cul3-RING ubiquitin ligase complex
G0:0034504	23	protein localization to nucleus
G0:0005126	23	cytokine receptor binding
G0:0046658	22	anchored component of plasma membrane
G0:0036151	22	phosphatidylcholine acyl-chain remodeling
G0:0016620	22	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor
G0:0070509	22	calcium ion import
G0:0050870	22	positive regulation of T cell activation
G0:0005520	22	insulin-like growth factor binding
G0:0061098	22	positive regulation of protein tyrosine kinase activity
G0:0006513	22	protein monoubiquitination
G0:0031234	22	extrinsic component of cytoplasmic side of plasma membrane
G0:0019933	22	cAMP-mediated signaling
G0:0051930	22	regulation of sensory perception of pain
G0:0006479	22	protein methylation
G0:0043388	22	positive regulation of DNA binding
G0:0010575	22	positive regulation vascular endothelial growth factor production
G0:0042056	22	chemoattractant activity
G0:0006352	22	DNA-templated transcription, initiation
G0:0060412	22	ventricular septum morphogenesis
G0:0000381	22	regulation of alternative mRNA splicing, via spliceosome
G0:0014003	22	oligodendrocyte development
G0:0006298	22	mismatch repair
G0:0048468	22	cell development
G0:0006270	22	DNA replication initiation
G0:0032201	22	telomere maintenance via semi-conservative replication
G0:0090103	22	cochlea morphogenesis

G0:0036464	22	cytoplasmic ribonucleoprotein granule
G0:0010718	22	positive regulation of epithelial to mesenchymal transition
G0:0006493	22	protein O-linked glycosylation
G0:0006656	22	phosphatidylcholine biosynthetic process
G0:0006487	22	protein N-linked glycosylation
G0:0005689	22	U12-type spliceosomal complex
G0:0042474	22	middle ear morphogenesis
G0:0043021	22	ribonucleoprotein complex binding
G0:0043236	22	laminin binding
G0:0034660	22	ncRNA metabolic process
G0:0030057	22	desmosome
G0:0048169	22	regulation of long-term neuronal synaptic plasticity
G0:0004435	22	phosphatidylinositol phospholipase C activity
G0:0045214	22	sarcomere organization
G0:0033038	22	bitter taste receptor activity
G0:0086091	22	regulation of heart rate by cardiac conduction
G0:0030099	22	myeloid cell differentiation
G0:0006362	21	transcription elongation from RNA polymerase I promoter
G0:0005100	21	Rho GTPase activator activity
G0:0032438	21	melanosome organization
G0:0046847	21	filopodium assembly
G0:0007346	21	regulation of mitotic cell cycle
G0:0006939	21	smooth muscle contraction
G0:0046580	21	negative regulation of Ras protein signal transduction
G0:2001243	21	negative regulation of intrinsic apoptotic signaling pathway
G0:0006699	21	bile acid biosynthetic process
G0:0005184	21	neuropeptide hormone activity
G0:0017134	21	fibroblast growth factor binding
G0:0072372	21	primary cilium
G0:0010043	21	response to zinc ion
G0:0005242	21	inward rectifier potassium channel activity
G0:0034341	21	response to interferon-gamma
G0:0051480	21	cytosolic calcium ion homeostasis
G0:0006297	21	nucleotide-excision repair, DNA gap filling
G0:0043542	21	endothelial cell migration
G0:0016571	21	histone methylation
G0:0032689	21	negative regulation of interferon-gamma production
G0:0010634	21	positive regulation of epithelial cell migration
G0:0043393	21	regulation of protein binding
G0:0050905	21	neuromuscular process
G0:0001786	21	phosphatidylserine binding
G0:0031674	21	I band
G0:0034080	21	centromere-specific nucleosome assembly
G0:0070932	21	histone H3 deacetylation
G0:0031683	21	G-protein beta/gamma-subunit complex binding
G0:0070059	21	intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress
G0:0016338	21	calcium-independent cell-cell adhesion
G0:0001702	21	gastrulation with mouth forming second
G0:0006378	21	mRNA polyadenylation
G0:0060135	21	maternal process involved in female pregnancy
G0:0018345	21	protein palmitoylation
G0:0032420	21	stereocilium
G0:0030864	21	cortical actin cytoskeleton
G0:0030131	21	clathrin adaptor complex
G0:0051225	21	spindle assembly
G0:0005680	21	anaphase-promoting complex
G0:0031572	21	G2 DNA damage checkpoint
G0:0046835	21	carbohydrate phosphorylation
G0:0071364	21	cellular response to epidermal growth factor stimulus
G0:0042813	21	Wnt-activated receptor activity
G0:0001958	21	endochondral ossification
G0:0008045	21	motor neuron axon guidance
G0:0043001	21	Golgi to plasma membrane protein transport
G0:0003756	21	protein disulfide isomerase activity
G0:0032781	21	positive regulation of ATPase activity
G0:0042974	21	retinoic acid receptor binding
G0:0001046	21	core promoter sequence-specific DNA binding
G0:0002040	21	sprouting angiogenesis
G0:0008637	21	apoptotic mitochondrial changes
G0:0048646	21	anatomical structure formation involved in morphogenesis
G0:0070330	21	aromatase activity
G0:0032728	21	positive regulation of interferon-beta production
G0:0030318	21	melanocyte differentiation
G0:0048844	21	artery morphogenesis

G0:0090503	21	RNA phosphodiester bond hydrolysis, exonucleolytic
G0:0048265	21	response to pain
G0:0045747	21	positive regulation of Notch signaling pathway
G0:0000718	21	nucleotide-excision repair, DNA damage removal
G0:0048010	21	vascular endothelial growth factor receptor signaling pathway
G0:0005719	20	nuclear euchromatin
G0:0000289	20	nuclear-transcribed mRNA poly(A) tail shortening
G0:0035162	20	embryonic hemopoiesis
G0:0036152	20	phosphatidylethanolamine acyl-chain remodeling
G0:0016627	20	oxidoreductase activity, acting on the CH-CH group of donors
G0:0050662	20	coenzyme binding
G0:0006783	20	heme biosynthetic process
G0:0030100	20	regulation of endocytosis
G0:0000795	20	synaptonemal complex
G0:0007220	20	Notch receptor processing
G0:0015020	20	glucuronosyltransferase activity
G0:0050850	20	positive regulation of calcium-mediated signaling
G0:0006309	20	apoptotic DNA fragmentation
G0:0043014	20	alpha-tubulin binding
G0:0004623	20	phospholipase A2 activity
G0:0030301	20	cholesterol transport
G0:0051297	20	centrosome organization
G0:0007548	20	sex differentiation
G0:0000245	20	spliceosomal complex assembly
G0:0031648	20	protein destabilization
G0:0072332	20	intrinsic apoptotic signaling pathway by p53 class mediator
G0:0005212	20	structural constituent of eye lens
G0:0014065	20	phosphatidylinositol 3-kinase signaling
G0:0004298	20	threonine-type endopeptidase activity
G0:0019731	20	antibacterial humoral response
G0:0007178	20	transmembrane receptor protein serine/threonine kinase signaling pathway
G0:0050832	20	defense response to fungus
G0:0005844	20	polysome
G0:0071773	20	cellular response to BMP stimulus
G0:0045746	20	negative regulation of Notch signaling pathway
G0:0009060	20	aerobic respiration
G0:0001106	20	RNA polymerase II transcription corepressor activity
G0:0030902	20	hindbrain development
G0:0051090	20	regulation of sequence-specific DNA binding transcription factor activity
G0:0046329	20	negative regulation of JNK cascade
G0:0021537	20	telencephalon development
G0:0031435	20	mitogen-activated protein kinase kinase kinase binding
G0:0035924	20	cellular response to vascular endothelial growth factor stimulus
G0:0050771	20	negative regulation of axonogenesis
G0:0023019	20	signal transduction involved in regulation of gene expression
G0:0001502	20	cartilage condensation
G0:0048568	20	embryonic organ development
G0:0048041	20	focal adhesion assembly
G0:0021510	20	spinal cord development
G0:0042572	20	retinol metabolic process
G0:0045648	20	positive regulation of erythrocyte differentiation
G0:0006306	20	DNA methylation
G0:0032967	20	positive regulation of collagen biosynthetic process
G0:0001954	20	positive regulation of cell-matrix adhesion
G0:0002026	20	regulation of the force of heart contraction
G0:0006509	20	membrane protein ectodomain proteolysis
G0:0031593	20	polyubiquitin binding
G0:1901215	20	negative regulation of neuron death
G0:0050699	20	WW domain binding
G0:0030507	20	spectrin binding
G0:0005540	20	hyaluronic acid binding
G0:0030193	20	regulation of blood coagulation
G0:0070412	20	R-SMAD binding
G0:0007214	20	gamma-aminobutyric acid signaling pathway
G0:0032391	20	photoreceptor connecting cilium
G0:0071392	20	cellular response to estradiol stimulus
G0:0006471	20	protein ADP-ribosylation
G0:0000083	20	regulation of transcription involved in G1/S transition of mitotic cell cycle
G0:0005539	20	glycosaminoglycan binding
G0:0005248	20	voltage-gated sodium channel activity
G0:0055088	20	lipid homeostasis
G0:0045777	20	positive regulation of blood pressure
G0:0051412	20	response to corticosterone
G0:0050769	20	positive regulation of neurogenesis

G0:0005771	20	multivesicular body
G0:0055007	19	cardiac muscle cell differentiation
G0:0004190	19	aspartic-type endopeptidase activity
G0:0030878	19	thyroid gland development
G0:0042346	19	positive regulation of NF-kappaB import into nucleus
G0:0035145	19	exon-exon junction complex
G0:0006937	19	regulation of muscle contraction
G0:0044344	19	cellular response to fibroblast growth factor stimulus
G0:0010719	19	negative regulation of epithelial to mesenchymal transition
G0:0045930	19	negative regulation of mitotic cell cycle
G0:0010508	19	positive regulation of autophagy
G0:0043034	19	costamere
G0:0090190	19	positive regulation of branching involved in ureteric bud morphogenesis
G0:0004004	19	ATP-dependent RNA helicase activity
G0:0030552	19	cAMP binding
G0:0008156	19	negative regulation of DNA replication
G0:0046209	19	nitric oxide metabolic process
G0:0030539	19	male genitalia development
G0:0019955	19	cytokine binding
G0:0002076	19	osteoblast development
G0:0030511	19	positive regulation of transforming growth factor beta receptor signaling pathway
G0:0010001	19	glial cell differentiation
G0:0032757	19	positive regulation of interleukin-8 production
G0:0034361	19	very-low-density lipoprotein particle
G0:0045879	19	negative regulation of smoothened signaling pathway
G0:0012506	19	vesicle membrane
G0:0060045	19	positive regulation of cardiac muscle cell proliferation
G0:0051693	19	actin filament capping
G0:0021522	19	spinal cord motor neuron differentiation
G0:0017157	19	regulation of exocytosis
G0:0006807	19	nitrogen compound metabolic process
G0:0032715	19	negative regulation of interleukin-6 production
G0:0001578	19	microtubule bundle formation
G0:0048873	19	homeostasis of number of cells within a tissue
G0:0009880	19	embryonic pattern specification
G0:0030206	19	chondroitin sulfate biosynthetic process
G0:0050880	19	regulation of blood vessel size
G0:0001533	19	cornified envelope
G0:0007052	19	mitotic spindle organization
G0:0005720	19	nuclear heterochromatin
G0:0002092	19	positive regulation of receptor internalization
G0:0002286	19	T cell activation involved in immune response
G0:0090398	19	cellular senescence
G0:0004181	19	metallocarboxypeptidase activity
G0:0017022	19	myosin binding
G0:0071345	19	cellular response to cytokine stimulus
G0:0060716	19	labyrinthine layer blood vessel development
G0:0008601	19	protein phosphatase type 2A regulator activity
G0:0007250	19	activation of NF-kappaB-inducing kinase activity
G0:0050840	19	extracellular matrix binding
G0:0031941	19	filamentous actin
G0:0005640	19	nuclear outer membrane
G0:0017080	19	sodium channel regulator activity
G0:0050999	19	regulation of nitric-oxide synthase activity
G0:0005328	19	neurotransmitter:sodium symporter activity
G0:0006778	19	porphyrin-containing compound metabolic process
G0:0030010	19	establishment of cell polarity
G0:0005839	19	proteasome core complex
G0:0007088	19	regulation of mitosis
G0:0043027	19	cysteine-type endopeptidase inhibitor activity involved in apoptotic process
G0:0009755	19	hormone-mediated signaling pathway
G0:0030276	19	clathrin binding
G0:0007194	19	execution phase of apoptosis
G0:0000146	19	microfilament motor activity
G0:0009235	19	cobalamin metabolic process
G0:0048477	19	oogenesis
G0:0042311	19	vasodilation
G0:0005753	19	mitochondrial proton-transporting ATP synthase complex
G0:0019897	19	extrinsic component of plasma membrane
G0:0048387	18	negative regulation of retinoic acid receptor signaling pathway
G0:0000281	18	mitotic cytokinesis
G0:0004198	18	calcium-dependent cysteine-type endopeptidase activity
G0:0070064	18	proline-rich region binding

G0:0042098	18	T cell proliferation
G0:0048557	18	embryonic digestive tract morphogenesis
G0:0048738	18	cardiac muscle tissue development
G0:0048709	18	oligodendrocyte differentiation
G0:0071353	18	cellular response to interleukin-4
G0:0097503	18	sialylation
G0:0016818	18	hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides
G0:0016486	18	peptide hormone processing
G0:0034704	18	calcium channel complex
G0:0005657	18	replication fork
G0:0035097	18	histone methyltransferase complex
G0:0009190	18	cyclic nucleotide biosynthetic process
G0:0019915	18	lipid storage
G0:0046034	18	ATP metabolic process
G0:0051145	18	smooth muscle cell differentiation
G0:0005980	18	glycogen catabolic process
G0:0008585	18	female gonad development
G0:0004709	18	MAP kinase kinase kinase activity
G0:0005763	18	mitochondrial small ribosomal subunit
G0:0001673	18	male germ cell nucleus
G0:0042730	18	fibrinolysis
G0:0070328	18	triglyceride homeostasis
G0:0005234	18	extracellular-glutamate-gated ion channel activity
G0:0008656	18	cysteine-type endopeptidase activator activity involved in apoptotic process
G0:0034364	18	high-density lipoprotein particle
G0:0042326	18	negative regulation of phosphorylation
G0:0019226	18	transmission of nerve impulse
G0:0001824	18	blastocyst development
G0:0043548	18	phosphatidylinositol 3-kinase binding
G0:0016235	18	aggresome
G0:0008373	18	sialyltransferase activity
G0:0031290	18	retinal ganglion cell axon guidance
G0:0000159	18	protein phosphatase type 2A complex
G0:0007031	18	peroxisome organization
G0:0019370	18	leukotriene biosynthetic process
G0:0045921	18	positive regulation of exocytosis
G0:0005545	18	1-phosphatidylinositol binding
G0:0001708	18	cell fate specification
G0:0045453	18	bone resorption
G0:0015721	18	bile acid and bile salt transport
G0:0002931	18	response to ischemia
G0:0019433	18	triglyceride catabolic process
G0:0006904	18	vesicle docking involved in exocytosis
G0:0051881	18	regulation of mitochondrial membrane potential
G0:2001234	18	negative regulation of apoptotic signaling pathway
G0:0006541	18	glutamine metabolic process
G0:0000784	18	nuclear chromosome, telomeric region
G0:0015035	18	protein disulfide oxidoreductase activity
G0:0006693	18	prostaglandin metabolic process
G0:0030544	18	Hsp70 protein binding
G0:0035257	18	nuclear hormone receptor binding
G0:0005669	18	transcription factor TFIID complex
G0:0030520	18	intracellular estrogen receptor signaling pathway
G0:0045880	18	positive regulation of smoothened signaling pathway
G0:0043113	18	receptor clustering
G0:0045332	18	phospholipid translocation
G0:0006401	18	RNA catabolic process
G0:0030332	18	cyclin binding
G0:0046513	18	ceramide biosynthetic process
G0:0030506	18	ankyrin binding
G0:0008378	18	galactosyltransferase activity
G0:0009306	18	protein secretion
G0:0002009	18	morphogenesis of an epithelium
G0:0004890	18	GABA-A receptor activity
G0:0070371	18	ERK1 and ERK2 cascade
G0:0008301	18	DNA binding, bending
G0:0045773	18	positive regulation of axon extension
G0:0005246	18	calcium channel regulator activity
G0:0016581	18	NuRD complex
G0:0086005	18	ventricular cardiac muscle cell action potential
G0:0046488	18	phosphatidylinositol metabolic process
G0:0042310	18	vasoconstriction
G0:0016849	18	phosphorus-oxygen lyase activity

G0:0033613	18	activating transcription factor binding
G0:0071526	18	semaphorin-plexin signaling pathway
G0:0048699	18	generation of neurons
G0:0007597	18	blood coagulation, intrinsic pathway
G0:0032007	18	negative regulation of TOR signaling
G0:0048593	18	camera-type eye morphogenesis
G0:0016409	18	palmitoyltransferase activity
G0:2000352	18	negative regulation of endothelial cell apoptotic process
G0:0034199	17	activation of protein kinase A activity
G0:0045070	17	positive regulation of viral genome replication
G0:0015949	17	nucleobase-containing small molecule interconversion
G0:0042562	17	hormone binding
G0:0006970	17	response to osmotic stress
G0:0030101	17	natural killer cell activation
G0:0004407	17	histone deacetylase activity
G0:0016010	17	dystrophin-associated glycoprotein complex
G0:0051721	17	protein phosphatase 2A binding
G0:0004683	17	calmodulin-dependent protein kinase activity
G0:0006885	17	regulation of pH
G0:0000070	17	mitotic sister chromatid segregation
G0:0004970	17	ionotropic glutamate receptor activity
G0:0022624	17	proteasome accessory complex
G0:0008631	17	intrinsic apoptotic signaling pathway in response to oxidative stress
G0:1900026	17	positive regulation of substrate adhesion-dependent cell spreading
G0:0030532	17	small nuclear ribonucleoprotein complex
G0:0017112	17	Rab guanyl-nucleotide exchange factor activity
G0:0046697	17	decidualization
G0:0090002	17	establishment of protein localization to plasma membrane
G0:0034614	17	cellular response to reactive oxygen species
G0:0048485	17	sympathetic nervous system development
G0:0035035	17	histone acetyltransferase binding
G0:0002227	17	innate immune response in mucosa
G0:0001894	17	tissue homeostasis
G0:0016125	17	sterol metabolic process
G0:0035050	17	embryonic heart tube development
G0:0031418	17	L-ascorbic acid binding
G0:0032266	17	phosphatidylinositol-3-phosphate binding
G0:0050718	17	positive regulation of interleukin-1 beta secretion
G0:0009416	17	response to light stimulus
G0:0005504	17	fatty acid binding
G0:0009083	17	branched-chain amino acid catabolic process
G0:0050772	17	positive regulation of axonogenesis
G0:0005740	17	mitochondrial envelope
G0:0070933	17	histone H4 deacetylation
G0:0070207	17	protein homotrimerization
G0:0043536	17	positive regulation of blood vessel endothelial cell migration
G0:0019835	17	cytolysis
G0:0005319	17	lipid transporter activity
G0:0006612	17	protein targeting to membrane
G0:0006941	17	striated muscle contraction
G0:0043408	17	regulation of MAPK cascade
G0:0050427	17	3'-phosphoadenosine 5'-phosphosulfate metabolic process
G0:0004653	17	polypeptide N-acetylgalactosaminyltransferase activity
G0:0001916	17	positive regulation of T cell mediated cytotoxicity
G0:0017025	17	TBP-class protein binding
G0:0034394	17	protein localization to cell surface
G0:0072001	17	renal system development
G0:0005001	17	transmembrane receptor protein tyrosine phosphatase activity
G0:0006337	17	nucleosome disassembly
G0:0045926	17	negative regulation of growth
G0:0072661	17	protein targeting to plasma membrane
G0:0032402	17	melanosome transport
G0:0002548	17	monocyte chemotaxis
G0:0042744	17	hydrogen peroxide catabolic process
G0:0006691	17	leukotriene metabolic process
G0:0071837	17	HMG box domain binding
G0:0010506	17	regulation of autophagy
G0:0051966	17	regulation of synaptic transmission, glutamatergic
G0:0051968	17	positive regulation of synaptic transmission, glutamatergic
G0:0048786	17	presynaptic active zone
G0:0000062	17	fatty-acyl-CoA binding
G0:0090023	17	positive regulation of neutrophil chemotaxis
G0:0005605	17	basal lamina
G0:0008023	17	transcription elongation factor complex
G0:0032722	17	positive regulation of chemokine production

G0:0006796	17	phosphate-containing compound metabolic process
G0:0048675	17	axon extension
G0:0036342	17	post-anal tail morphogenesis
G0:0030234	17	enzyme regulator activity
G0:0000123	17	histone acetyltransferase complex
G0:0050767	17	regulation of neurogenesis
G0:0050768	17	negative regulation of neurogenesis
G0:0007405	17	neuroblast proliferation
G0:0006386	17	termination of RNA polymerase III transcription
G0:0031146	17	SCF-dependent proteasomal ubiquitin-dependent protein catabolic process
G0:0005922	17	connexon complex
G0:0008483	17	transaminase activity
G0:0032332	17	positive regulation of chondrocyte differentiation
G0:0048596	17	embryonic camera-type eye morphogenesis
G0:0033365	17	protein localization to organelle
G0:0006385	17	transcription elongation from RNA polymerase III promoter
G0:0010165	17	response to X-ray
G0:0045672	17	positive regulation of osteoclast differentiation
G0:0051879	16	Hsp90 protein binding
G0:0048384	16	retinoic acid receptor signaling pathway
G0:0048037	16	cofactor binding
G0:0045445	16	myoblast differentiation
G0:0071108	16	protein K48-linked deubiquitination
G0:2000811	16	negative regulation of anoikis
G0:0034719	16	SMN-Sm protein complex
G0:0002102	16	podosome
G0:0036150	16	phosphatidylserine acyl-chain remodeling
G0:0046849	16	bone remodeling
G0:0007026	16	negative regulation of microtubule depolymerization
G0:0033268	16	node of Ranvier
G0:0003951	16	NAD+ kinase activity
G0:0010507	16	negative regulation of autophagy
G0:0032504	16	multicellular organism reproduction
G0:0043209	16	myelin sheath
G0:0033141	16	positive regulation of peptidyl-serine phosphorylation of STAT protein
G0:0043015	16	gamma-tubulin binding
G0:0007263	16	nitric oxide mediated signal transduction
G0:0051482	16	positive regulation of cytosolic calcium ion concentration involved in phospholipase C-activating G-protein coupled signaling pathway
G0:0004540	16	ribonuclease activity
G0:0002052	16	positive regulation of neuroblast proliferation
G0:0019001	16	guanyl nucleotide binding
G0:0046716	16	muscle cell cellular homeostasis
G0:0001829	16	trophoblast cell differentiation
G0:0012501	16	programmed cell death
G0:0005024	16	transforming growth factor beta-activated receptor activity
G0:0004889	16	acetylcholine-activated cation-selective channel activity
G0:0006820	16	anion transport
G0:0030261	16	chromosome condensation
G0:0014047	16	glutamate secretion
G0:0071901	16	negative regulation of protein serine/threonine kinase activity
G0:0031032	16	actomyosin structure organization
G0:0030742	16	GTP-dependent protein binding
G0:0006801	16	superoxide metabolic process
G0:0016712	16	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced flavin or flavoprotein as one donor, and incorporation of one atom of oxygen
G0:0043691	16	reverse cholesterol transport
G0:0030224	16	monocyte differentiation
G0:0010881	16	regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion
G0:0010880	16	regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum
G0:0031430	16	M band
G0:0042307	16	positive regulation of protein import into nucleus
G0:0030949	16	positive regulation of vascular endothelial growth factor receptor signaling pathway
G0:0010765	16	positive regulation of sodium ion transport
G0:0021772	16	olfactory bulb development
G0:0060395	16	SMAD protein signal transduction
G0:0006940	16	regulation of smooth muscle contraction
G0:0048566	16	embryonic digestive tract development
G0:0036148	16	phosphatidylglycerol acyl-chain remodeling
G0:1902043	16	positive regulation of extrinsic apoptotic signaling pathway via death domain receptors

G0:0030665	16	clathrin-coated vesicle membrane
G0:0001530	16	lipopolysaccharide binding
G0:0048546	16	digestive tract morphogenesis
G0:2000134	16	negative regulation of G1/S transition of mitotic cell cycle
G0:0030866	16	cortical actin cytoskeleton organization
G0:0001659	16	temperature homeostasis
G0:0008353	16	RNA polymerase II carboxy-terminal domain kinase activity
G0:0060334	16	regulation of interferon-gamma-mediated signaling pathway
G0:0043409	16	negative regulation of MAPK cascade
G0:0006164	16	purine nucleotide biosynthetic process
G0:0016234	16	inclusion body
G0:0005099	16	Ras GTPase activator activity
G0:0006672	16	ceramide metabolic process
G0:0007271	16	synaptic transmission, cholinergic
G0:0007274	16	neuromuscular synaptic transmission
G0:0032148	16	activation of protein kinase B activity
G0:0060612	16	adipose tissue development
G0:0051894	16	positive regulation of focal adhesion assembly
G0:0030159	16	receptor signaling complex scaffold activity
G0:0007292	16	female gamete generation
G0:0030279	16	negative regulation of ossification
G0:0005666	16	DNA-directed RNA polymerase III complex
G0:0016254	16	preassembly of GPI anchor in ER membrane
G0:0090004	16	positive regulation of establishment of protein localization to plasma membrane
G0:0006891	16	intra-Golgi vesicle-mediated transport
G0:0042445	16	hormone metabolic process
G0:0030500	16	regulation of bone mineralization
G0:0016922	16	ligand-dependent nuclear receptor binding
G0:0004550	16	nucleoside diphosphate kinase activity
G0:0048168	16	regulation of neuronal synaptic plasticity
G0:0003333	16	amino acid transmembrane transport
G0:0030502	16	negative regulation of bone mineralization
G0:0050804	16	regulation of synaptic transmission
G0:0001508	16	action potential
G0:0042149	16	cellular response to glucose starvation
G0:0030295	16	protein kinase activator activity
G0:0043984	16	histone H4-K16 acetylation
G0:0033198	16	response to ATP
G0:0050919	16	negative chemotaxis
G0:0005892	16	acetylcholine-gated channel complex
G0:0032982	16	myosin filament
G0:0005247	16	voltage-gated chloride channel activity
G0:0007140	16	male meiosis
G0:0015171	16	amino acid transmembrane transporter activity
G0:0045638	16	negative regulation of myeloid cell differentiation
G0:0008484	16	sulfuric ester hydrolase activity
G0:0048598	16	embryonic morphogenesis
G0:0004602	16	glutathione peroxidase activity
G0:0046427	16	positive regulation of JAK-STAT cascade
G0:0043281	16	regulation of cysteine-type endopeptidase activity involved in apoptotic process
G0:0042523	16	positive regulation of tyrosine phosphorylation of Stat5 protein
G0:0006165	16	nucleoside diphosphate phosphorylation
G0:0045671	16	negative regulation of osteoclast differentiation
G0:0006595	15	polyamine metabolic process
G0:0017015	15	regulation of transforming growth factor beta receptor signaling pathway
G0:0015711	15	organic anion transport
G0:0005132	15	type I interferon receptor binding
G0:0009165	15	nucleotide biosynthetic process
G0:0009168	15	purine ribonucleoside monophosphate biosynthetic process
G0:0001759	15	organ induction
G0:0016810	15	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds
G0:0016817	15	hydrolase activity, acting on acid anhydrides
G0:0071371	15	cellular response to gonadotropin stimulus
G0:0045343	15	regulation of MHC class I biosynthetic process
G0:0035267	15	NuA4 histone acetyltransferase complex
G0:0042246	15	tissue regeneration
G0:0006303	15	double-strand break repair via nonhomologous end joining
G0:0031954	15	positive regulation of protein autophosphorylation
G0:0017075	15	syntaxin-1 binding
G0:0043153	15	entrainment of circadian clock by photoperiod
G0:0016820	15	hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances
G0:0001158	15	enhancer sequence-specific DNA binding

G0:0003746	15	translation elongation factor activity
G0:0043011	15	myeloid dendritic cell differentiation
G0:0051146	15	striated muscle cell differentiation
G0:0006182	15	cGMP biosynthetic process
G0:0090201	15	negative regulation of release of cytochrome c from mitochondria
G0:0030554	15	adenyl nucleotide binding
G0:0004012	15	phospholipid-translocating ATPase activity
G0:0016079	15	synaptic vesicle exocytosis
G0:0060347	15	heart trabecula formation
G0:0001056	15	RNA polymerase III activity
G0:0031668	15	cellular response to extracellular stimulus
G0:0004702	15	receptor signaling protein serine/threonine kinase activity
G0:0004708	15	MAP kinase kinase activity
G0:0031589	15	cell-substrate adhesion
G0:0001676	15	long-chain fatty acid metabolic process
G0:0010800	15	positive regulation of peptidyl-threonine phosphorylation
G0:0030048	15	actin filament-based movement
G0:0005671	15	Ada2/Gcn5/Ada3 transcription activator complex
G0:0000038	15	very long-chain fatty acid metabolic process
G0:0003281	15	ventricular septum development
G0:0007158	15	neuron cell-cell adhesion
G0:0016514	15	SWI/SNF complex
G0:0031258	15	lamellipodium membrane
G0:0001655	15	urogenital system development
G0:0002323	15	natural killer cell activation involved in immune response
G0:0043277	15	apoptotic cell clearance
G0:0023026	15	MHC class II protein complex binding
G0:0036092	15	phosphatidylinositol-3-phosphate biosynthetic process
G0:0006826	15	iron ion transport
G0:0032733	15	positive regulation of interleukin-10 production
G0:0001556	15	oocyte maturation
G0:2000311	15	regulation of alpha-amino-3-hydroxy-5-methyl-4-isoxazole propionate
selective glutamate		receptor activity
G0:0007520	15	myoblast fusion
G0:0035861	15	site of double-strand break
G0:0050901	15	leukocyte tethering or rolling
G0:0045104	15	intermediate filament cytoskeleton organization
G0:0001782	15	B cell homeostasis
G0:0006071	15	glycerol metabolic process
G0:0005528	15	FK506 binding
G0:0046907	15	intracellular transport
G0:0003785	15	actin monomer binding
G0:0048870	15	cell motility
G0:0021904	15	dorsal/ventral neural tube patterning
G0:0010460	15	positive regulation of heart rate
G0:0048066	15	developmental pigmentation
G0:0000302	15	response to reactive oxygen species
G0:0009948	15	anterior/posterior axis specification
G0:0050431	15	transforming growth factor beta binding
G0:0042136	15	neurotransmitter biosynthetic process
G0:0071285	15	cellular response to lithium ion
G0:0044130	15	negative regulation of growth of symbiont in host
G0:0001516	15	prostaglandin biosynthetic process
G0:0004143	15	diacylglycerol kinase activity
G0:0005159	15	insulin-like growth factor receptor binding
G0:0000102	15	cochlea development
G0:0001709	15	cell fate determination
G0:0010744	15	positive regulation of macrophage derived foam cell differentiation
G0:0051018	15	protein kinase A binding
G0:0097381	15	photoreceptor disc membrane
G0:0005112	15	Notch binding
G0:0008574	15	plus-end-directed microtubule motor activity
G0:0043395	15	heparan sulfate proteoglycan binding
G0:0050806	15	positive regulation of synaptic transmission
G0:0008080	15	N-acetyltransferase activity
G0:0042832	15	defense response to protozoan
G0:0071158	15	positive regulation of cell cycle arrest
G0:0071157	15	negative regulation of cell cycle arrest
G0:0030111	15	regulation of Wnt signaling pathway
G0:0032874	15	positive regulation of stress-activated MAPK cascade
G0:0005665	15	DNA-directed RNA polymerase II, core complex
G0:0042809	15	vitamin D receptor binding
G0:0060076	15	excitatory synapse
G0:0004697	15	protein kinase C activity
G0:0007276	15	gamete generation

G0:0006198	15	cAMP catabolic process
G0:0015012	15	heparan sulfate proteoglycan biosynthetic process
G0:0035255	15	ionotropic glutamate receptor binding
G0:0045089	15	positive regulation of innate immune response
G0:0010035	15	response to inorganic substance
G0:0008209	15	androgen metabolic process
G0:0070848	15	response to growth factor
G0:0002042	15	cell migration involved in sprouting angiogenesis
G0:0048490	15	anterograde synaptic vesicle transport
G0:0015986	15	ATP synthesis coupled proton transport
G0:0002028	15	regulation of sodium ion transport
G0:0060441	15	epithelial tube branching involved in lung morphogenesis
G0:0031226	15	intrinsic component of plasma membrane
G0:0033280	15	response to vitamin D
G0:0008188	15	neuropeptide receptor activity
G0:0048266	15	behavioral response to pain
G0:0045987	15	positive regulation of smooth muscle contraction
G0:0045736	15	negative regulation of cyclin-dependent protein serine/threonine kinase activity
G0:0032456	15	endocytic recycling
G0:0060037	15	pharyngeal system development
G0:0007029	15	endoplasmic reticulum organization
G0:0052695	15	cellular glucuronidation
G0:0043325	15	phosphatidylinositol-3,4-bisphosphate binding
G0:0005537	15	mannose binding
G0:0045778	15	positive regulation of ossification
G0:0050930	15	induction of positive chemotaxis
G0:0031307	15	integral component of mitochondrial outer membrane
G0:0006996	15	organelle organization
G0:0051602	15	response to electrical stimulus
G0:0035327	15	transcriptionally active chromatin
G0:0042462	15	eye photoreceptor cell development
G0:0031143	15	pseudopodium
G0:0032331	15	negative regulation of chondrocyte differentiation
G0:0055117	15	regulation of cardiac muscle contraction
G0:0048025	15	negative regulation of mRNA splicing, via spliceosome
G0:0031122	15	cytoplasmic microtubule organization
G0:0005773	15	vacuole
G0:0048018	15	receptor agonist activity
G0:0008527	15	taste receptor activity
G0:0010906	14	regulation of glucose metabolic process
G0:0007625	14	grooming behavior
G0:0006978	14	DNA damage response, signal transduction by p53 class mediator resulting in transcription of p21 class mediator
G0:0090280	14	positive regulation of calcium ion import
G0:0001731	14	formation of translation preinitiation complex
G0:0031672	14	A band
G0:0001965	14	G-protein alpha-subunit binding
G0:0030169	14	low-density lipoprotein particle binding
G0:0016811	14	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides
G0:0050877	14	neurological system process
G0:0042613	14	MHC class II protein complex
G0:0051233	14	spindle midzone
G0:0060425	14	lung morphogenesis
G0:0006536	14	glutamate metabolic process
G0:0008093	14	cytoskeletal adaptor activity
G0:0030833	14	regulation of actin filament polymerization
G0:0045190	14	isotype switching
G0:0042267	14	natural killer cell mediated cytotoxicity
G0:0031091	14	platelet alpha granule
G0:2001241	14	positive regulation of extrinsic apoptotic signaling pathway in absence of ligand
G0:0010842	14	retina layer formation
G0:0017091	14	AU-rich element binding
G0:0030553	14	cGMP binding
G0:0031369	14	translation initiation factor binding
G0:0031210	14	phosphatidylcholine binding
G0:0010596	14	negative regulation of endothelial cell migration
G0:0004707	14	MAP kinase activity
G0:0033189	14	response to vitamin A
G0:0030518	14	intracellular steroid hormone receptor signaling pathway
G0:0048488	14	synaptic vesicle endocytosis
G0:0030705	14	cytoskeleton-dependent intracellular transport
G0:0046718	14	viral entry into host cell

G0:0031528	14	microvillus membrane
G0:0008299	14	isoprenoid biosynthetic process
G0:0017156	14	calcium ion-dependent exocytosis
G0:0008198	14	ferrous iron binding
G0:0008375	14	acetylglucosaminyltransferase activity
G0:0004089	14	carbonate dehydratase activity
G0:0042776	14	mitochondrial ATP synthesis coupled proton transport
G0:0090316	14	positive regulation of intracellular protein transport
G0:0046928	14	regulation of neurotransmitter secretion
G0:0042176	14	regulation of protein catabolic process
G0:0031293	14	membrane protein intracellular domain proteolysis
G0:2000463	14	positive regulation of excitatory postsynaptic membrane potential
G0:0071385	14	cellular response to glucocorticoid stimulus
G0:0048535	14	lymph node development
G0:0032993	14	protein-DNA complex
G0:0042325	14	regulation of phosphorylation
G0:0051393	14	alpha-actinin binding
G0:0035815	14	positive regulation of renal sodium excretion
G0:0035338	14	long-chain fatty-acyl-CoA biosynthetic process
G0:0019371	14	cyclooxygenase pathway
G0:0060749	14	mammary gland alveolus development
G0:0002244	14	hematopoietic progenitor cell differentiation
G0:0002407	14	dendritic cell chemotaxis
G0:0005161	14	platelet-derived growth factor receptor binding
G0:0030889	14	negative regulation of B cell proliferation
G0:0046961	14	proton-transporting ATPase activity, rotational mechanism
G0:0001518	14	voltage-gated sodium channel complex
G0:0048009	14	insulin-like growth factor receptor signaling pathway
G0:0006171	14	cAMP biosynthetic process
G0:0001706	14	endoderm formation
G0:0034185	14	apolipoprotein binding
G0:0007398	14	ectoderm development
G0:0050775	14	positive regulation of dendrite morphogenesis
G0:0051019	14	mitogen-activated protein kinase binding
G0:0036149	14	phosphatidylinositol acyl-chain remodeling
G0:0070536	14	protein K63-linked deubiquitination
G0:0030667	14	secretory granule membrane
G0:0032924	14	activin receptor signaling pathway
G0:0042573	14	retinoic acid metabolic process
G0:0001101	14	response to acid
G0:0031513	14	nonmotile primary cilium
G0:0033276	14	transcription factor TFTC complex
G0:0070577	14	lysine-acetylated histone binding
G0:0042622	14	photoreceptor outer segment membrane
G0:0042629	14	mast cell granule
G0:0042026	14	protein refolding
G0:0048741	14	skeletal muscle fiber development
G0:0034451	14	centriolar satellite
G0:0048821	14	erythrocyte development
G0:0060314	14	regulation of ryanodine-sensitive calcium-release channel activity
G0:0071276	14	cellular response to cadmium ion
G0:0071889	14	14-3-3 protein binding
G0:0014032	14	neural crest cell development
G0:0007512	14	adult heart development
G0:0032314	14	regulation of Rac GTPase activity
G0:0002526	14	acute inflammatory response
G0:0046579	14	positive regulation of Ras protein signal transduction
G0:0046688	14	response to copper ion
G0:0045088	14	regulation of innate immune response
G0:0050995	14	negative regulation of lipid catabolic process
G0:0005762	14	mitochondrial large ribosomal subunit
G0:0045333	14	cellular respiration
G0:0046965	14	retinoid X receptor binding
G0:0051493	14	regulation of cytoskeleton organization
G0:0005487	14	nucleocytoplasmic transporter activity
G0:0071682	14	endocytic vesicle lumen
G0:0021954	14	central nervous system neuron development
G0:0034375	14	high-density lipoprotein particle remodeling
G0:0005852	14	eukaryotic translation initiation factor 3 complex
G0:0005859	14	muscle myosin complex
G0:0008408	14	3'-5' exonuclease activity
G0:0000987	14	core promoter proximal region sequence-specific DNA binding
G0:0006839	14	mitochondrial transport
G0:0051537	14	2 iron, 2 sulfur cluster binding
G0:0006607	14	NLS-bearing protein import into nucleus

G0:0043981	14	histone H4-K5 acetylation
G0:0070372	14	regulation of ERK1 and ERK2 cascade
G0:0045582	14	positive regulation of T cell differentiation
G0:0032270	14	positive regulation of cellular protein metabolic process
G0:0061028	14	establishment of endothelial barrier
G0:0007141	14	male meiosis I
G0:0002230	14	positive regulation of defense response to virus by host
G0:0015908	14	fatty acid transport
G0:0022011	14	myelination in peripheral nervous system
G0:0043982	14	histone H4-K8 acetylation
G0:0001190	14	RNA polymerase II transcription factor binding transcription factor
G0:2000377	14	activity involved in positive regulation of transcription
G0:0002089	14	regulation of reactive oxygen species metabolic process
G0:0005149	14	lens morphogenesis in camera-type eye
G0:0048854	14	interleukin-1 receptor binding
G0:0005779	14	brain morphogenesis
G0:0051000	14	integral component of peroxisomal membrane
G0:0007413	14	positive regulation of nitric-oxide synthase activity
G0:0030675	13	axonal fasciculation
G0:0030673	13	Rac GTPase activator activity
G0:0004993	13	axolemma
G0:0017017	13	serotonin receptor activity
G0:0017016	13	MAP kinase tyrosine/serine/threonine phosphatase activity
G0:0006103	13	Ras GTPase binding
G0:0060445	13	2-oxoglutarate metabolic process
G0:0042554	13	branching involved in salivary gland morphogenesis
G0:0006646	13	superoxide anion generation
G0:0030126	13	phosphatidylethanolamine biosynthetic process
G0:0021527	13	COPI vesicle coat
G0:0001967	13	spinal cord association neuron differentiation
G0:0001964	13	suckling behavior
G0:0001963	13	startle response
G0:0006349	13	synaptic transmission, dopaminergic
G0:0016601	13	regulation of gene expression by genetic imprinting
G0:0070742	13	Rac protein signal transduction
G0:0030818	13	C2H2 zinc finger domain binding
G0:0046827	13	negative regulation of cAMP biosynthetic process
G0:0001779	13	positive regulation of protein export from nucleus
G0:000421	13	natural killer cell differentiation
G0:0005086	13	autophagic vacuole membrane
G0:0022891	13	ARF guanyl-nucleotide exchange factor activity
G0:0008210	13	substrate-specific transmembrane transporter activity
G0:0006790	13	estrogen metabolic process
G0:0033327	13	sulfur compound metabolic process
G0:0010524	13	Leydig cell differentiation
G0:0030663	13	positive regulation of calcium ion transport into cytosol
G0:0031235	13	COPI-coated vesicle membrane
G0:0016050	13	intrinsic component of the cytoplasmic side of the plasma membrane
G0:0060038	13	vesicle organization
G0:0010038	13	cardiac muscle cell proliferation
G0:0031988	13	response to metal ion
G0:0071398	13	membrane-bounded vesicle
G0:0045954	13	cellular response to fatty acid
G0:0045086	13	positive regulation of natural killer cell mediated cytotoxicity
G0:0000242	13	positive regulation of interleukin-2 biosynthetic process
G0:0060216	13	pericentriolar material
G0:0005942	13	definitive hemopoiesis
G0:0014911	13	phosphatidylinositol 3-kinase complex
G0:0015269	13	positive regulation of smooth muscle cell migration
G0:0070403	13	calcium-activated potassium channel activity
G0:0034362	13	NAD+ binding
G0:0031529	13	low-density lipoprotein particle
G0:0060292	13	ruffle organization
G0:0001823	13	long term synaptic depression
G0:0016282	13	mesonephros development
G0:0045725	13	eukaryotic 43S preinitiation complex
G0:0031011	13	positive regulation of glycogen biosynthetic process
G0:0000178	13	Ino80 complex
G0:0000175	13	exosome (RNase complex)
G0:0006825	13	3'-5'-exoribonuclease activity
G0:0030001	13	copper ion transport
G0:0003995	13	metal ion transport
G0:0000975	13	acyl-CoA dehydrogenase activity
G0:0042288	13	regulatory region DNA binding
		MHC class I protein binding

G0:0035198	13	miRNA binding
G0:0006809	13	nitric oxide biosynthetic process
G0:0001784	13	phosphotyrosine binding
G0:0005868	13	cytoplasmic dynein complex
G0:0050730	13	regulation of peptidyl-tyrosine phosphorylation
G0:0019841	13	retinol binding
G0:0043616	13	keratinocyte proliferation
G0:0048255	13	mRNA stabilization
G0:0000132	13	establishment of mitotic spindle orientation
G0:0007016	13	cytoskeletal anchoring at plasma membrane
G0:0030225	13	macrophage differentiation
G0:0045780	13	positive regulation of bone resorption
G0:0031434	13	mitogen-activated protein kinase kinase binding
G0:0051568	13	histone H3-K4 methylation
G0:0030207	13	chondroitin sulfate catabolic process
G0:0005746	13	mitochondrial respiratory chain
G0:0032012	13	regulation of ARF protein signal transduction
G0:0043101	13	purine-containing compound salvage
G0:0004806	13	triglyceride lipase activity
G0:0035909	13	aorta morphogenesis
G0:0090314	13	positive regulation of protein targeting to membrane
G0:0043539	13	protein serine/threonine kinase activator activity
G0:0046969	13	NAD-dependent histone deacetylase activity (H3-K9 specific)
G0:0016331	13	morphogenesis of embryonic epithelium
G0:0035584	13	calcium-mediated signaling using intracellular calcium source
G0:0048205	13	COPI coating of Golgi vesicle
G0:0010971	13	positive regulation of G2/M transition of mitotic cell cycle
G0:0010745	13	negative regulation of macrophage derived foam cell differentiation
G0:0006376	13	mRNA splice site selection
G0:0009395	13	phospholipid catabolic process
G0:0005160	13	transforming growth factor beta receptor binding
G0:0044257	13	cellular protein catabolic process
G0:0007215	13	glutamate receptor signaling pathway
G0:0042417	13	dopamine metabolic process
G0:0060134	13	prepulse inhibition
G0:0009116	13	nucleoside metabolic process
G0:0010288	13	response to lead ion
G0:0006119	13	oxidative phosphorylation
G0:0032094	13	response to food
G0:0046856	13	phosphatidylinositol dephosphorylation
G0:0005685	13	U1 snRNP
G0:0021675	13	nerve development
G0:0050868	13	negative regulation of T cell activation
G0:0033137	13	negative regulation of peptidyl-serine phosphorylation
G0:0050860	13	negative regulation of T cell receptor signaling pathway
G0:0005095	13	GTPase inhibitor activity
G0:0045022	13	early endosome to late endosome transport
G0:0010875	13	positive regulation of cholesterol efflux
G0:0042789	13	mRNA transcription from RNA polymerase II promoter
G0:0002504	13	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II
G0:0035265	13	organ growth
G0:0042274	13	ribosomal small subunit biogenesis
G0:0032784	13	regulation of DNA-templated transcription, elongation
G0:0015464	13	acetylcholine receptor activity
G0:0006957	13	complement activation, alternative pathway
G0:0005003	13	ephrin receptor activity
G0:0002063	13	chondrocyte development
G0:0050750	13	low-density lipoprotein particle receptor binding
G0:0006779	13	porphyrin-containing compound biosynthetic process
G0:0015276	13	ligand-gated ion channel activity
G0:0006402	13	mRNA catabolic process
G0:0035810	13	positive regulation of urine volume
G0:0043046	13	DNA methylation involved in gamete generation
G0:0030195	13	negative regulation of blood coagulation
G0:0042953	13	lipoprotein transport
G0:0007080	13	mitotic metaphase plate congression
G0:0022409	13	positive regulation of cell-cell adhesion
G0:0008610	13	lipid biosynthetic process
G0:0060444	13	branching involved in mammary gland duct morphogenesis
G0:0050482	13	arachidonic acid secretion
G0:0048260	13	positive regulation of receptor-mediated endocytosis
G0:0007043	13	cell-cell junction assembly
G0:0019395	13	fatty acid oxidation
G0:0050910	13	detection of mechanical stimulus involved in sensory perception of sound

G0:0045807	13	positive regulation of endocytosis
G0:0034113	13	heterotypic cell-cell adhesion
G0:0032981	13	mitochondrial respiratory chain complex I assembly
G0:0031362	13	anchored component of external side of plasma membrane
G0:0046939	13	nucleotide phosphorylation
G0:0042101	13	T cell receptor complex
G0:0071044	13	histone mRNA catabolic process
G0:0048268	13	clathrin coat assembly
G0:0010181	13	FMN binding
G0:0071542	13	dopaminergic neuron differentiation
G0:0030214	13	hyaluronan catabolic process
G0:0042312	13	regulation of vasodilation
G0:0043537	13	negative regulation of blood vessel endothelial cell migration
G0:0003009	13	skeletal muscle contraction
G0:0035326	13	enhancer binding
G0:0048208	13	COPII vesicle coating
G0:0007062	13	sister chromatid cohesion
G0:0043560	13	insulin receptor substrate binding
G0:0021542	13	dentate gyrus development
G0:0002080	13	acrosomal membrane
G0:0031461	13	cullin-RING ubiquitin ligase complex
G0:0090179	13	planar cell polarity pathway involved in neural tube closure
G0:0051020	13	GTPase binding
G0:0032968	13	positive regulation of transcription elongation from RNA polymerase II promoter
G0:0060384	13	innervation
G0:0060389	13	pathway-restricted SMAD protein phosphorylation
G0:0009651	13	response to salt stress
G0:0034774	12	secretory granule lumen
G0:0006590	12	thyroid hormone generation
G0:0097502	12	mannosylation
G0:0071397	12	cellular response to cholesterol
G0:1902230	12	negative regulation of intrinsic apoptotic signaling pathway in response to DNA damage
G0:0097150	12	neuronal stem cell maintenance
G0:0034236	12	protein kinase A catalytic subunit binding
G0:0031527	12	filopodium membrane
G0:0007340	12	acrosome reaction
G0:2000310	12	regulation of N-methyl-D-aspartate selective glutamate receptor activity
G0:0051044	12	positive regulation of membrane protein ectodomain proteolysis
G0:0046135	12	pyrimidine nucleoside catabolic process
G0:0031267	12	small GTPase binding
G0:0007600	12	sensory perception
G0:0005736	12	DNA-directed RNA polymerase I complex
G0:0043968	12	histone H2A acetylation
G0:0071375	12	cellular response to peptide hormone stimulus
G0:1900087	12	positive regulation of G1/S transition of mitotic cell cycle
G0:0005523	12	tropomyosin binding
G0:0000422	12	mitochondrion degradation
G0:0043039	12	tRNA aminoacylation
G0:0019079	12	viral genome replication
G0:0008066	12	glutamate receptor activity
G0:0060307	12	regulation of ventricular cardiac muscle cell membrane repolarization
G0:0002687	12	positive regulation of leukocyte migration
G0:0035098	12	ESC/E(Z) complex
G0:0030140	12	trans-Golgi network transport vesicle
G0:0061178	12	regulation of insulin secretion involved in cellular response to glucose stimulus
G0:0035066	12	positive regulation of histone acetylation
G0:0043220	12	Schmidt-Lanterman incisure
G0:1902187	12	negative regulation of viral release from host cell
G0:0008589	12	regulation of smoothened signaling pathway
G0:0070584	12	mitochondrion morphogenesis
G0:0060644	12	mammary gland epithelial cell differentiation
G0:0051298	12	centrosome duplication
G0:0015813	12	L-glutamate transport
G0:1902176	12	negative regulation of oxidative stress-induced intrinsic apoptotic signaling pathway
G0:0015267	12	channel activity
G0:0050321	12	tau-protein kinase activity
G0:0030517	12	negative regulation of axon extension
G0:0043292	12	contractile fiber
G0:0043623	12	cellular protein complex assembly
G0:0030515	12	snoRNA binding
G0:0034399	12	nuclear periphery

G0:0031640	12	killing of cells of other organism
G0:0035774	12	positive regulation of insulin secretion involved in cellular response to glucose stimulus
G0:0050678	12	regulation of epithelial cell proliferation
G0:0048814	12	regulation of dendrite morphogenesis
G0:0040015	12	negative regulation of multicellular organism growth
G0:0042043	12	neurexin family protein binding
G0:0060042	12	retina morphogenesis in camera-type eye
G0:0050710	12	negative regulation of cytokine secretion
G0:0008191	12	metalloendopeptidase inhibitor activity
G0:0097372	12	NAD-dependent histone deacetylase activity (H3-K18 specific)
G0:0019430	12	removal of superoxide radicals
G0:0000346	12	transcription export complex
G0:0015671	12	oxygen transport
G0:0032041	12	NAD-dependent histone deacetylase activity (H3-K14 specific)
G0:0033290	12	eukaryotic 48S preinitiation complex
G0:0055093	12	response to hyperoxia
G0:0042641	12	actomyosin
G0:0030247	12	polysaccharide binding
G0:0042340	12	keratan sulfate catabolic process
G0:0031996	12	thioesterase binding
G0:0008154	12	actin polymerization or depolymerization
G0:0008334	12	histone mRNA metabolic process
G0:0030220	12	platelet formation
G0:0060766	12	negative regulation of androgen receptor signaling pathway
G0:0016594	12	glycine binding
G0:0009888	12	tissue development
G0:0042491	12	auditory receptor cell differentiation
G0:0031432	12	titin binding
G0:0007076	12	mitotic chromosome condensation
G0:0031333	12	negative regulation of protein complex assembly
G0:0033762	12	response to glucagon
G0:0021794	12	thalamus development
G0:0070935	12	3'-UTR-mediated mRNA stabilization
G0:0007051	12	spindle organization
G0:0043488	12	regulation of mRNA stability
G0:0031641	12	regulation of myelination
G0:0030208	12	dermatan sulfate biosynthetic process
G0:0051604	12	protein maturation
G0:0002003	12	angiotensin maturation
G0:0001935	12	endothelial cell proliferation
G0:0046887	12	positive regulation of hormone secretion
G0:0006379	12	mRNA cleavage
G0:0045667	12	regulation of osteoblast differentiation
G0:0045662	12	negative regulation of myoblast differentiation
G0:0033391	12	chromatoid body
G0:0006637	12	acyl-CoA metabolic process
G0:0004675	12	transmembrane receptor protein serine/threonine kinase activity
G0:0007210	12	serotonin receptor signaling pathway
G0:0050673	12	epithelial cell proliferation
G0:0071625	12	vocalization behavior
G0:0006906	12	vesicle fusion
G0:0016805	12	dipeptidase activity
G0:0007252	12	I-kappaB phosphorylation
G0:2000678	12	negative regulation of transcription regulatory region DNA binding
G0:0003954	12	NADH dehydrogenase activity
G0:0048745	12	smooth muscle tissue development
G0:0032465	12	regulation of cytokinesis
G0:0080111	12	DNA demethylation
G0:0019048	12	modulation by virus of host morphology or physiology
G0:0009311	12	oligosaccharide metabolic process
G0:0010259	12	multicellular organismal aging
G0:2000378	12	negative regulation of reactive oxygen species metabolic process
G0:0042273	12	ribosomal large subunit biogenesis
G0:0032008	12	positive regulation of TOR signaling
G0:0045948	12	positive regulation of translational initiation
G0:0005123	12	death receptor binding
G0:0009650	12	UV protection
G0:2000251	12	positive regulation of actin cytoskeleton reorganization
G0:0036065	12	fucosylation
G0:0045502	12	dynein binding
G0:0003148	12	outflow tract septum morphogenesis
G0:0051926	12	negative regulation of calcium ion transport
G0:1902166	12	negative regulation of intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator

G0:0043922	12	negative regulation by host of viral transcription
G0:0014902	12	myotube differentiation
G0:0030330	12	DNA damage response, signal transduction by p53 class mediator
G0:0042994	12	cytoplasmic sequestering of transcription factor
G0:0032743	12	positive regulation of interleukin-2 production
G0:0045295	12	gamma-catenin binding
G0:0070410	12	co-SMAD binding
G0:0040029	12	regulation of gene expression, epigenetic
G0:0010812	12	negative regulation of cell-substrate adhesion
G0:0006750	12	glutathione biosynthetic process
G0:0048148	12	behavioral response to cocaine
G0:0022408	12	negative regulation of cell-cell adhesion
G0:0018298	12	protein-chromophore linkage
G0:0060071	12	Wnt signaling pathway, planar cell polarity pathway
G0:0009303	12	rRNA transcription
G0:0071565	12	nBAF complex
G0:0000989	12	transcription factor binding transcription factor activity
G0:0043087	12	regulation of GTPase activity
G0:0005916	12	fascia adherens
G0:0048185	12	activin binding
G0:0042162	12	telomeric DNA binding
G0:0045055	12	regulated secretory pathway
G0:0048246	12	macrophage chemotaxis
G0:0000145	12	exocyst
G0:0007020	12	microtubule nucleation
G0:0005790	12	smooth endoplasmic reticulum
G0:0006044	12	N-acetylglucosamine metabolic process
G0:0016580	12	Sin3 complex
G0:0017187	12	peptidyl-glutamic acid carboxylation
G0:0035307	12	positive regulation of protein dephosphorylation
G0:0015693	12	magnesium ion transport
G0:0031305	12	integral component of mitochondrial inner membrane
G0:0005513	12	detection of calcium ion
G0:0050953	12	sensory perception of light stimulus
G0:0035102	12	PRC1 complex
G0:0006855	12	drug transmembrane transport
G0:0051593	12	response to folic acid
G0:0008324	12	cation transmembrane transporter activity
G0:0030897	12	HOPS complex
G0:0003906	12	DNA-(apurinic or apyrimidinic site) lyase activity
G0:0046970	12	NAD-dependent histone deacetylase activity (H4-K16 specific)
G0:0004620	12	phospholipase activity
G0:0021895	12	cerebral cortex neuron differentiation
G0:0002087	12	regulation of respiratory gaseous exchange by neurological system process
G0:2000145	12	regulation of cell motility
G0:0016407	12	acetyltransferase activity
G0:0061436	12	establishment of skin barrier
G0:0048712	12	negative regulation of astrocyte differentiation
G0:0070528	12	protein kinase C signaling
G0:0045670	12	regulation of osteoclast differentiation
G0:0050786	11	RAGE receptor binding
G0:0030676	11	Rac guanyl-nucleotide exchange factor activity
G0:0055008	11	cardiac muscle tissue morphogenesis
G0:0051272	11	positive regulation of cellular component movement
G0:0016702	11	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen
G0:0009100	11	glycoprotein metabolic process
G0:0045019	11	negative regulation of nitric oxide biosynthetic process
G0:0006911	11	phagocytosis, engulfment
G0:0035631	11	CD40 receptor complex
G0:0006342	11	chromatin silencing
G0:2000060	11	positive regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process
G0:0005031	11	tumor necrosis factor-activated receptor activity
G0:0043923	11	positive regulation by host of viral transcription
G0:0000407	11	pre-autophagosomal structure
G0:0032886	11	regulation of microtubule-based process
G0:0043194	11	axon initial segment
G0:0005675	11	holo TFIIH complex
G0:0001775	11	cell activation
G0:0008239	11	dipeptidyl-peptidase activity
G0:0042800	11	histone methyltransferase activity (H3-K4 specific)
G0:0070542	11	response to fatty acid
G0:0032695	11	negative regulation of interleukin-12 production
G0:0016226	11	iron-sulfur cluster assembly

G0:0051895	11	negative regulation of focal adhesion assembly
G0:0042633	11	hair cycle
G0:0008430	11	selenium binding
G0:0000050	11	urea cycle
G0:0044548	11	S100 protein binding
G0:0032797	11	SMN complex
G0:0005355	11	glucose transmembrane transporter activity
G0:0042446	11	hormone biosynthetic process
G0:0043950	11	positive regulation of cAMP-mediated signaling
G0:0021854	11	hypothalamus development
G0:0050921	11	positive regulation of chemotaxis
G0:0009987	11	cellular process
G0:0015075	11	ion transmembrane transporter activity
G0:0005798	11	Golgi-associated vesicle
G0:0001841	11	neural tube formation
G0:0047496	11	vesicle transport along microtubule
G0:0051290	11	protein heterotetramerization
G0:0032793	11	positive regulation of CREB transcription factor activity
G0:0006884	11	cell volume homeostasis
G0:0042073	11	intraciliary transport
G0:0005614	11	interstitial matrix
G0:0033993	11	response to lipid
G0:0006707	11	cholesterol catabolic process
G0:0060081	11	membrane hyperpolarization
G0:0001891	11	phagocytic cup
G0:0031581	11	hemidesmosome assembly
G0:0022604	11	regulation of cell morphogenesis
G0:0043267	11	negative regulation of potassium ion transport
G0:0060413	11	atrial septum morphogenesis
G0:0043518	11	negative regulation of DNA damage response, signal transduction by p53
class mediator		
G0:0031078	11	histone deacetylase activity (H3-K14 specific)
G0:0008354	11	germ cell migration
G0:0055089	11	fatty acid homeostasis
G0:0004065	11	arylsulfatase activity
G0:0032753	11	positive regulation of interleukin-4 production
G0:0071257	11	cellular response to electrical stimulus
G0:0010613	11	positive regulation of cardiac muscle hypertrophy
G0:0021680	11	cerebellar Purkinje cell layer development
G0:0008199	11	ferric iron binding
G0:0048407	11	platelet-derived growth factor binding
G0:0006829	11	zinc ion transport
G0:0051443	11	positive regulation of ubiquitin-protein transferase activity
G0:0048714	11	positive regulation of oligodendrocyte differentiation
G0:0045744	11	negative regulation of G-protein coupled receptor protein signaling
pathway		
G0:0002011	11	morphogenesis of an epithelial sheet
G0:0033628	11	regulation of cell adhesion mediated by integrin
G0:0046902	11	regulation of mitochondrial membrane permeability
G0:0043508	11	negative regulation of JUN kinase activity
G0:0060009	11	Sertoli cell development
G0:0097067	11	cellular response to thyroid hormone stimulus
G0:0048872	11	homeostasis of number of cells
G0:0034698	11	response to gonadotropin
G0:0009881	11	photoreceptor activity
G0:0006195	11	purine nucleotide catabolic process
G0:0002199	11	zona pellucida receptor complex
G0:0032039	11	integrator complex
G0:0008242	11	omega peptidase activity
G0:0046328	11	regulation of JNK cascade
G0:0060391	11	positive regulation of SMAD protein import into nucleus
G0:0001076	11	RNA polymerase II transcription factor binding transcription factor
activity		
G0:0042301	11	phosphate ion binding
G0:0032897	11	negative regulation of viral transcription
G0:0009435	11	NAD biosynthetic process
G0:0055078	11	sodium ion homeostasis
G0:0034260	11	negative regulation of GTPase activity
G0:0035136	11	forelimb morphogenesis
G0:0035137	11	hindlimb morphogenesis
G0:0034739	11	histone deacetylase activity (H4-K16 specific)
G0:0048747	11	muscle fiber development
G0:2000406	11	positive regulation of T cell migration
G0:0043122	11	regulation of I-kappaB kinase/NF-kappaB signaling
G0:0060394	11	negative regulation of pathway-restricted SMAD protein phosphorylation

G0:0035589	11	G-protein coupled purinergic nucleotide receptor signaling pathway
G0:0060707	11	trophoblast giant cell differentiation
G0:0010975	11	regulation of neuron projection development
G0:0021756	11	striatum development
G0:0042438	11	melanin biosynthetic process
G0:2000114	11	regulation of establishment of cell polarity
G0:0016180	11	snRNA processing
G0:0060272	11	embryonic skeletal joint morphogenesis
G0:0031396	11	regulation of protein ubiquitination
G0:0045060	11	negative thymic T cell selection
G0:0007212	11	dopamine receptor signaling pathway
G0:0007213	11	G-protein coupled acetylcholine receptor signaling pathway
G0:0033700	11	phospholipid efflux
G0:0086004	11	regulation of cardiac muscle cell contraction
G0:0043162	11	ubiquitin-dependent protein catabolic process via the multivesicular body sorting pathway
G0:0001741	11	XY body
G0:0046888	11	negative regulation of hormone secretion
G0:0015939	11	pantothenate metabolic process
G0:0042834	11	peptidoglycan binding
G0:0071480	11	cellular response to gamma radiation
G0:0016493	11	C-C chemokine receptor activity
G0:0045947	11	negative regulation of translational initiation
G0:0016239	11	positive regulation of macroautophagy
G0:0046597	11	negative regulation of viral entry into host cell
G0:0046621	11	negative regulation of organ growth
G0:0031571	11	mitotic G1 DNA damage checkpoint
G0:2001239	11	regulation of extrinsic apoptotic signaling pathway in absence of ligand
G0:0045028	11	G-protein coupled purinergic nucleotide receptor activity
G0:0042627	11	chylomicron
G0:0042623	11	ATPase activity, coupled
G0:0001953	11	negative regulation of cell-matrix adhesion
G0:0090303	11	positive regulation of wound healing
G0:0008235	11	metalloexopeptidase activity
G0:0017166	11	vinculin binding
G0:0010510	11	regulation of acetyl-CoA biosynthetic process from pyruvate
G0:0005344	11	oxygen transporter activity
G0:0009312	11	oligosaccharide biosynthetic process
G0:0006744	11	ubiquinone biosynthetic process
G0:0002690	11	positive regulation of leukocyte chemotaxis
G0:0042711	11	maternal behavior
G0:0051770	11	positive regulation of nitric-oxide synthase biosynthetic process
G0:0048333	11	mesodermal cell differentiation
G0:0071425	11	hematopoietic stem cell proliferation
G0:0032839	11	dendrite cytoplasm
G0:0032786	11	positive regulation of DNA-templated transcription, elongation
G0:0043252	11	sodium-independent organic anion transport
G0:0015250	11	water channel activity
G0:0033197	11	response to vitamin E
G0:0017127	11	cholesterol transporter activity
G0:0043069	11	negative regulation of programmed cell death
G0:0050998	11	nitric-oxide synthase binding
G0:0071564	11	npBAF complex
G0:0043274	11	phospholipase binding
G0:0007610	11	behavior
G0:0010039	11	response to iron ion
G0:0032590	11	dendrite membrane
G0:0060047	11	heart contraction
G0:0030194	11	positive regulation of blood coagulation
G0:0060674	11	placenta blood vessel development
G0:0051131	11	chaperone-mediated protein complex assembly
G0:0034453	11	microtubule anchoring
G0:0050927	11	positive regulation of positive chemotaxis
G0:0071236	11	cellular response to antibiotic
G0:0032129	11	histone deacetylase activity (H3-K9 specific)
G0:0043206	11	extracellular fibril organization
G0:0004532	11	exoribonuclease activity
G0:0075733	11	intracellular transport of virus
G0:0001833	11	inner cell mass cell proliferation
G0:0035413	11	positive regulation of catenin import into nucleus
G0:0034374	11	low-density lipoprotein particle remodeling
G0:0035025	11	positive regulation of Rho protein signal transduction
G0:0048617	11	embryonic foregut morphogenesis
G0:0015095	11	magnesium ion transmembrane transporter activity
G0:0042640	11	anagen

G0:0000160	11	phosphorelay signal transduction system
G0:0000982	11	RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity
G0:2000273	11	positive regulation of receptor activity
G0:0035518	11	histone H2A monoubiquitination
G0:0006241	11	CTP biosynthetic process
G0:0007168	11	receptor guanylyl cyclase signaling pathway
G0:0006069	11	ethanol oxidation
G0:0042166	11	acetylcholine binding
G0:0006476	11	protein deacetylation
G0:0010952	11	positive regulation of peptidase activity
G0:0030238	11	male sex determination
G0:0033630	11	positive regulation of cell adhesion mediated by integrin
G0:2000045	11	regulation of G1/S transition of mitotic cell cycle
G0:0043517	11	positive regulation of DNA damage response, signal transduction by p53 class mediator
G0:0045821	11	positive regulation of glycolytic process
G0:0070498	11	interleukin-1-mediated signaling pathway
G0:0007004	11	telomere maintenance via telomerase
G0:0097481	11	neuronal postsynaptic density
G0:0002237	11	response to molecule of bacterial origin
G0:0032026	11	response to magnesium ion
G0:0016303	11	1-phosphatidylinositol-3-kinase activity
G0:0071294	11	cellular response to zinc ion
G0:0033540	11	fatty acid beta-oxidation using acyl-CoA oxidase
G0:0030898	11	actin-dependent ATPase activity
G0:0035024	11	negative regulation of Rho protein signal transduction
G0:0048715	11	negative regulation of oligodendrocyte differentiation
G0:0006228	11	UTP biosynthetic process
G0:0006081	11	cellular aldehyde metabolic process
G0:0016327	11	apicolateral plasma membrane
G0:0048599	11	oocyte development
G0:0043116	11	negative regulation of vascular permeability
G0:0060402	11	calcium ion transport into cytosol
G0:0044262	11	cellular carbohydrate metabolic process
G0:0021952	11	central nervous system projection neuron axonogenesis
G0:0000738	11	DNA catabolic process, exonucleolytic
G0:0051642	11	centrosome localization
G0:0045995	11	regulation of embryonic development
G0:0008385	11	IkappaB kinase complex
G0:0014912	11	negative regulation of smooth muscle cell migration
G0:0019372	11	lipoxigenase pathway
G0:0019373	11	epoxygenase P450 pathway
G0:0006596	10	polyamine biosynthetic process
G0:0006622	10	protein targeting to lysosome
G0:0048038	10	quinone binding
G0:0034389	10	lipid particle organization
G0:0006107	10	oxaloacetate metabolic process
G0:0008361	10	regulation of cell size
G0:0032435	10	negative regulation of proteasomal ubiquitin-dependent protein catabolic process
G0:0019953	10	sexual reproduction
G0:0045651	10	positive regulation of macrophage differentiation
G0:0030877	10	beta-catenin destruction complex
G0:0007191	10	adenylate cyclase-activating dopamine receptor signaling pathway
G0:0008757	10	S-adenosylmethionine-dependent methyltransferase activity
G0:0008340	10	determination of adult lifespan
G0:0045078	10	positive regulation of interferon-gamma biosynthetic process
G0:0030215	10	semaphorin receptor binding
G0:0050872	10	white fat cell differentiation
G0:0042612	10	MHC class I protein complex
G0:0019674	10	NAD metabolic process
G0:0001945	10	lymph vessel development
G0:0001946	10	lymphangiogenesis
G0:0014701	10	junctional sarcoplasmic reticulum membrane
G0:0042581	10	specific granule
G0:0019363	10	pyridine nucleotide biosynthetic process
G0:0032479	10	regulation of type I interferon production
G0:0030837	10	negative regulation of actin filament polymerization
G0:0090307	10	spindle assembly involved in mitosis
G0:0045618	10	positive regulation of keratinocyte differentiation
G0:0032863	10	activation of Rac GTPase activity
G0:0021879	10	forebrain neuron differentiation
G0:0045579	10	positive regulation of B cell differentiation
G0:0048103	10	somatic stem cell division

G0:0060306	10	regulation of membrane repolarization
G0:0016208	10	AMP binding
G0:0016051	10	carbohydrate biosynthetic process
G0:0048730	10	epidermis morphogenesis
G0:0006183	10	GTP biosynthetic process
G0:0005639	10	integral component of nuclear inner membrane
G0:0051918	10	negative regulation of fibrinolysis
G0:0008276	10	protein methyltransferase activity
G0:0016918	10	retinal binding
G0:0015804	10	neutral amino acid transport
G0:0010544	10	negative regulation of platelet activation
G0:0033160	10	positive regulation of protein import into nucleus, translocation
G0:0003724	10	RNA helicase activity
G0:0050982	10	detection of mechanical stimulus
G0:0032434	10	regulation of proteasomal ubiquitin-dependent protein catabolic process
G0:0032794	10	GTPase activating protein binding
G0:0043249	10	erythrocyte maturation
G0:0045956	10	positive regulation of calcium ion-dependent exocytosis
G0:0005243	10	gap junction channel activity
G0:0070306	10	lens fiber cell differentiation
G0:0007130	10	synaptonemal complex assembly
G0:0030983	10	mismatched DNA binding
G0:0017119	10	Golgi transport complex
G0:0061136	10	regulation of proteasomal protein catabolic process
G0:0006000	10	fructose metabolic process
G0:0030277	10	maintenance of gastrointestinal epithelium
G0:0031274	10	positive regulation of pseudopodium assembly
G0:0010369	10	chromocenter
G0:0001678	10	cellular glucose homeostasis
G0:0042054	10	histone methyltransferase activity
G0:0043268	10	positive regulation of potassium ion transport
G0:0007099	10	centriole replication
G0:0007095	10	mitotic G2 DNA damage checkpoint
G0:0010801	10	negative regulation of peptidyl-threonine phosphorylation
G0:0006768	10	biotin metabolic process
G0:0000380	10	alternative mRNA splicing, via spliceosome
G0:0060065	10	uterus development
G0:0060068	10	vagina development
G0:0009268	10	response to pH
G0:0030296	10	protein tyrosine kinase activator activity
G0:0004526	10	ribonuclease P activity
G0:0004520	10	endodeoxyribonuclease activity
G0:0014067	10	negative regulation of phosphatidylinositol 3-kinase signaling
G0:0031624	10	ubiquitin conjugating enzyme binding
G0:0016574	10	histone ubiquitination
G0:0002031	10	G-protein coupled receptor internalization
G0:0045263	10	proton-transporting ATP synthase complex, coupling factor F(o)
G0:2000484	10	positive regulation of interleukin-8 secretion
G0:0040037	10	negative regulation of fibroblast growth factor receptor signaling pathway
G0:0005845	10	mRNA cap binding complex
G0:0042770	10	signal transduction in response to DNA damage
G0:0015672	10	monovalent inorganic cation transport
G0:0008417	10	fucosyltransferase activity
G0:0016558	10	protein import into peroxisome matrix
G0:0045745	10	positive regulation of G-protein coupled receptor protein signaling pathway
G0:0050908	10	detection of light stimulus involved in visual perception
G0:0005041	10	low-density lipoprotein receptor activity
G0:0031297	10	replication fork processing
G0:0033598	10	mammary gland epithelial cell proliferation
G0:0061036	10	positive regulation of cartilage development
G0:0050732	10	negative regulation of peptidyl-tyrosine phosphorylation
G0:0034045	10	pre-autophagosomal structure membrane
G0:0008331	10	high voltage-gated calcium channel activity
G0:0045598	10	regulation of fat cell differentiation
G0:0010469	10	regulation of receptor activity
G0:0030595	10	leukocyte chemotaxis
G0:0010944	10	negative regulation of transcription by competitive promoter binding
G0:0001817	10	regulation of cytokine production
G0:0050435	10	beta-amyloid metabolic process
G0:0009950	10	dorsal/ventral axis specification
G0:0055091	10	phospholipid homeostasis
G0:0016595	10	glutamate binding
G0:0060999	10	positive regulation of dendritic spine development
G0:0060993	10	kidney morphogenesis

G0:0050884	10	neuromuscular process controlling posture
G0:0031334	10	positive regulation of protein complex assembly
G0:0060218	10	hematopoietic stem cell differentiation
G0:0050777	10	negative regulation of immune response
G0:0050778	10	positive regulation of immune response
G0:0015934	10	large ribosomal subunit
G0:0006098	10	pentose-phosphate shunt
G0:0010226	10	response to lithium ion
G0:0008272	10	sulfate transport
G0:0043296	10	apical junction complex
G0:0043295	10	glutathione binding
G0:0042535	10	positive regulation of tumor necrosis factor biosynthetic process
G0:0043129	10	surfactant homeostasis
G0:0016651	10	oxidoreductase activity, acting on NAD(P)H
G0:0031115	10	negative regulation of microtubule polymerization
G0:0031116	10	positive regulation of microtubule polymerization
G0:0046641	10	positive regulation of alpha-beta T cell proliferation
G0:0060213	10	positive regulation of nuclear-transcribed mRNA poly(A) tail shortening
G0:0033235	10	positive regulation of protein sumoylation
G0:0048935	10	peripheral nervous system neuron development
G0:0090129	10	positive regulation of synapse maturation
G0:0005833	10	hemoglobin complex
G0:0045663	10	positive regulation of myoblast differentiation
G0:0034709	10	methylosome
G0:0071806	10	protein transmembrane transport
G0:0030660	10	Golgi-associated vesicle membrane
G0:0055015	10	ventricular cardiac muscle cell development
G0:0034122	10	negative regulation of toll-like receptor signaling pathway
G0:0042574	10	retinal metabolic process
G0:0086002	10	cardiac muscle cell action potential involved in contraction
G0:0042416	10	dopamine biosynthetic process
G0:0003215	10	cardiac right ventricle morphogenesis
G0:0043394	10	proteoglycan binding
G0:0030014	10	CCR4-NOT complex
G0:0035458	10	cellular response to interferon-beta
G0:0032495	10	response to muramyl dipeptide
G0:0002480	10	antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-independent
G0:0033270	10	paranode region of axon
G0:0006336	10	DNA replication-independent nucleosome assembly
G0:0060484	10	lung-associated mesenchyme development
G0:0014898	10	cardiac muscle hypertrophy in response to stress
G0:0043403	10	skeletal muscle tissue regeneration
G0:0002544	10	chronic inflammatory response
G0:0060315	10	negative regulation of ryanodine-sensitive calcium-release channel activity
G0:0060317	10	cardiac epithelial to mesenchymal transition
G0:0060174	10	limb bud formation
G0:0001054	10	RNA polymerase I activity
G0:0031083	10	BLOC-1 complex
G0:0051967	10	negative regulation of synaptic transmission, glutamatergic
G0:0050965	10	detection of temperature stimulus involved in sensory perception of pain
G0:0090026	10	positive regulation of monocyte chemotaxis
G0:0021846	10	cell proliferation in forebrain
G0:0032727	10	positive regulation of interferon-alpha production
G0:0046685	10	response to arsenic-containing substance
G0:0006600	10	creatine metabolic process
G0:0015279	10	store-operated calcium channel activity
G0:0030992	10	intraciliary transport particle B
G0:0032740	10	positive regulation of interleukin-17 production
G0:0070411	10	I-SMAD binding
G0:0007435	10	salivary gland morphogenesis
G0:0006029	10	proteoglycan metabolic process
G0:0006569	10	tryptophan catabolic process
G0:0031000	10	response to caffeine
G0:0017146	10	N-methyl-D-aspartate selective glutamate receptor complex
G0:0021953	10	central nervous system neuron differentiation
G0:0035418	10	protein localization to synapse
G0:0048856	10	anatomical structure development
G0:0014059	10	regulation of dopamine secretion
G0:0006895	10	Golgi to endosome transport
G0:0045737	10	positive regulation of cyclin-dependent protein serine/threonine kinase activity
G0:0030431	10	sleep
G0:0031284	10	positive regulation of guanylate cyclase activity

G0:0014075	10	response to amine
G0:0006835	10	dicarboxylic acid transport
G0:0016540	10	protein autoprocessing
G0:0042359	10	vitamin D metabolic process
G0:0071391	10	cellular response to estrogen stimulus
G0:0045806	10	negative regulation of endocytosis
G0:0010390	10	histone monoubiquitination
G0:0036126	10	sperm flagellum
G0:0051085	10	chaperone mediated protein folding requiring cofactor
G0:0005890	10	sodium:potassium-exchanging ATPase complex
G0:0048843	10	negative regulation of axon extension involved in axon guidance
G0:0006268	10	DNA unwinding involved in DNA replication
G0:0048665	10	neuron fate specification
G0:0050707	10	regulation of cytokine secretion
G0:0002218	10	activation of innate immune response
G0:0004115	10	3',5'-cyclic-AMP phosphodiesterase activity
G0:0019855	10	calcium channel inhibitor activity
G0:0030914	10	STAGA complex
G0:0008143	10	poly(A) binding
G0:0006878	10	cellular copper ion homeostasis
G0:0090009	10	primitive streak formation
G0:0071549	10	cellular response to dexamethasone stimulus
G0:0019538	10	protein metabolic process
G0:0016442	10	RISC complex
G0:0048193	10	Golgi vesicle transport
G0:0006998	10	nuclear envelope organization
G0:0045792	10	negative regulation of cell size
G0:0021702	10	cerebellar Purkinje cell differentiation
G0:0007129	10	synapsis
G0:0043568	10	positive regulation of insulin-like growth factor receptor signaling pathway
G0:0031325	10	positive regulation of cellular metabolic process
G0:0043229	10	intracellular organelle
G0:0048853	10	forebrain morphogenesis
G0:0051775	10	response to redox state
G0:0005774	10	vacuolar membrane
G0:0048016	10	inositol phosphate-mediated signaling
G0:0000731	10	DNA synthesis involved in DNA repair
G0:0008266	10	poly(U) RNA binding
G0:2000353	10	positive regulation of endothelial cell apoptotic process
G0:0001921	10	positive regulation of receptor recycling
G0:0045109	10	intermediate filament organization
G0:0048711	10	positive regulation of astrocyte differentiation
G0:0030850	9	prostate gland development
G0:0031105	9	septin complex
G0:0031103	9	axon regeneration
G0:0046655	9	folic acid metabolic process
G0:0006621	9	protein retention in ER lumen
G0:0097504	9	Gemini of coiled bodies
G0:0055003	9	cardiac myofibril assembly
G0:0006972	9	hyperosmotic response
G0:0045446	9	endothelial cell differentiation
G0:0080182	9	histone H3-K4 trimethylation
G0:0006105	9	succinate metabolic process
G0:0004859	9	phospholipase inhibitor activity
G0:0071577	9	zinc ion transmembrane transport
G0:0001736	9	establishment of planar polarity
G0:0006111	9	regulation of gluconeogenesis
G0:0048703	9	embryonic viscerocranium morphogenesis
G0:0035058	9	nonmotile primary cilium assembly
G0:0007342	9	fusion of sperm to egg plasma membrane
G0:0003197	9	endocardial cushion development
G0:0086014	9	atrial cardiac muscle cell action potential
G0:0000185	9	activation of MAPKKK activity
G0:0000400	9	four-way junction DNA binding
G0:0021819	9	layer formation in cerebral cortex
G0:0048245	9	eosinophil chemotaxis
G0:0017056	9	structural constituent of nuclear pore
G0:0008091	9	spectrin
G0:0043032	9	positive regulation of macrophage activation
G0:0004935	9	adrenergic receptor activity
G0:0061303	9	cornea development in camera-type eye
G0:0031953	9	negative regulation of protein autophosphorylation
G0:0050795	9	regulation of behavior
G0:0004029	9	aldehyde dehydrogenase (NAD) activity

G0:0035240	9	dopamine binding
G0:0042993	9	positive regulation of transcription factor import into nucleus
G0:0006516	9	glycoprotein catabolic process
G0:0044306	9	neuron projection terminus
G0:0055119	9	relaxation of cardiac muscle
G0:0004985	9	opioid receptor activity
G0:0043240	9	Fanconi anaemia nuclear complex
G0:0046549	9	retinal cone cell development
G0:0034464	9	BBSome
G0:0072358	9	cardiovascular system development
G0:0000266	9	mitochondrial fission
G0:0047555	9	3',5'-cyclic-GMP phosphodiesterase activity
G0:0042074	9	cell migration involved in gastrulation
G0:0010820	9	positive regulation of T cell chemotaxis
G0:0006702	9	androgen biosynthetic process
G0:0046933	9	proton-transporting ATP synthase activity, rotational mechanism
G0:0010569	9	regulation of double-strand break repair via homologous recombination
G0:0070307	9	lens fiber cell development
G0:0043583	9	ear development
G0:0043589	9	skin morphogenesis
G0:0006559	9	L-phenylalanine catabolic process
G0:0031588	9	AMP-activated protein kinase complex
G0:0001675	9	acrosome assembly
G0:0001671	9	ATPase activator activity
G0:0032040	9	small-subunit processome
G0:0034616	9	response to laminar fluid shear stress
G0:0048484	9	enteric nervous system development
G0:0046426	9	negative regulation of JAK-STAT cascade
G0:0048156	9	tau protein binding
G0:0014002	9	astrocyte development
G0:0008343	9	adult feeding behavior
G0:0003094	9	glomerular filtration
G0:0031076	9	embryonic camera-type eye development
G0:0060603	9	mammary gland duct morphogenesis
G0:0048541	9	Peyer's patch development
G0:0005005	9	transmembrane-ephrin receptor activity
G0:0008603	9	cAMP-dependent protein kinase regulator activity
G0:0070402	9	NADPH binding
G0:2000249	9	regulation of actin cytoskeleton reorganization
G0:0071203	9	WASH complex
G0:0006450	9	regulation of translational fidelity
G0:0004521	9	endoribonuclease activity
G0:0009743	9	response to carbohydrate
G0:0071435	9	potassium ion export
G0:2000036	9	regulation of stem cell maintenance
G0:0007171	9	activation of transmembrane receptor protein tyrosine kinase activity
G0:0016578	9	histone deubiquitination
G0:0043097	9	pyrimidine nucleoside salvage
G0:0031017	9	exocrine pancreas development
G0:0017154	9	semaphorin receptor activity
G0:0001227	9	RNA polymerase II transcription regulatory region sequence-specific DNA binding transcription factor activity involved in negative regulation of transcription
G0:0043586	9	tongue development
G0:0003214	9	cardiac left ventricle morphogenesis
G0:0045176	9	apical protein localization
G0:0005847	9	mRNA cleavage and polyadenylation specificity factor complex
G0:0061053	9	somite development
G0:0005501	9	retinoid binding
G0:1990090	9	cellular response to nerve growth factor stimulus
G0:0006012	9	galactose metabolic process
G0:0043422	9	protein kinase B binding
G0:0014044	9	Schwann cell development
G0:0090399	9	replicative senescence
G0:2000648	9	positive regulation of stem cell proliferation
G0:0002827	9	positive regulation of T-helper 1 type immune response
G0:2000649	9	regulation of sodium ion transmembrane transporter activity
G0:0010633	9	negative regulation of epithelial cell migration
G0:0045742	9	positive regulation of epidermal growth factor receptor signaling pathway
G0:0045741	9	positive regulation of epidermal growth factor-activated receptor activity
G0:0019864	9	IgG binding
G0:0010388	9	cullin deneddylation
G0:0010389	9	regulation of G2/M transition of mitotic cell cycle
G0:0044224	9	juxtaparanode region of axon
G0:0008179	9	adenylate cyclase binding
G0:0070628	9	proteasome binding

G0:0051428	9	peptide hormone receptor binding
G0:0042347	9	negative regulation of NF-kappaB import into nucleus
G0:0009451	9	RNA modification
G0:0000956	9	nuclear-transcribed mRNA catabolic process
G0:0042119	9	neutrophil activation
G0:0030903	9	notochord development
G0:0045839	9	negative regulation of mitosis
G0:0016538	9	cyclin-dependent protein serine/threonine kinase regulator activity
G0:0003810	9	protein-glutamine gamma-glutamyltransferase activity
G0:0031419	9	cobalamin binding
G0:0005883	9	neurofilament
G0:0043306	9	positive regulation of mast cell degranulation
G0:0006275	9	regulation of DNA replication
G0:0060765	9	regulation of androgen receptor signaling pathway
G0:0021984	9	adenohypophysis development
G0:0070016	9	armadillo repeat domain binding
G0:0003016	9	respiratory system process
G0:0016591	9	DNA-directed RNA polymerase II, holoenzyme
G0:0034067	9	protein localization to Golgi apparatus
G0:0046325	9	negative regulation of glucose import
G0:0034237	9	protein kinase A regulatory subunit binding
G0:0009086	9	methionine biosynthetic process
G0:0033558	9	protein deacetylase activity
G0:0046790	9	virion binding
G0:0060740	9	prostate gland epithelium morphogenesis
G0:0050773	9	regulation of dendrite development
G0:0001973	9	adenosine receptor signaling pathway
G0:0007589	9	body fluid secretion
G0:0001522	9	pseudouridine synthesis
G0:0070206	9	protein trimerization
G0:0070208	9	protein heterotrimerization
G0:0042738	9	exogenous drug catabolic process
G0:1900153	9	positive regulation of nuclear-transcribed mRNA catabolic process,
		deadenylation-dependent decay
G0:0010225	9	response to UV-C
G0:0033555	9	multicellular organismal response to stress
G0:0008494	9	translation activator activity
G0:0071897	9	DNA biosynthetic process
G0:0005687	9	U4 snRNP
G0:0035371	9	microtubule plus-end
G0:0048762	9	mesenchymal cell differentiation
G0:2000179	9	positive regulation of neural precursor cell proliferation
G0:0045603	9	positive regulation of endothelial cell differentiation
G0:0006613	9	cotranslational protein targeting to membrane
G0:0006942	9	regulation of striated muscle contraction
G0:0042088	9	T-helper 1 type immune response
G0:0042551	9	neuron maturation
G0:0043149	9	stress fiber assembly
G0:0051497	9	negative regulation of stress fiber assembly
G0:0060113	9	inner ear receptor cell differentiation
G0:0051010	9	microtubule plus-end binding
G0:0051016	9	barbed-end actin filament capping
G0:0030031	9	cell projection assembly
G0:0008514	9	organic anion transmembrane transporter activity
G0:0005952	9	cAMP-dependent protein kinase complex
G0:0019985	9	translesion synthesis
G0:0004983	9	neuropeptide Y receptor activity
G0:0032395	9	MHC class II receptor activity
G0:0030137	9	COPI-coated vesicle
G0:0021799	9	cerebral cortex radially oriented cell migration
G0:0021795	9	cerebral cortex cell migration
G0:0042592	9	homeostatic process
G0:0044295	9	axonal growth cone
G0:0008088	9	axon cargo transport
G0:0009404	9	toxin metabolic process
G0:0046628	9	positive regulation of insulin receptor signaling pathway
G0:0046620	9	regulation of organ growth
G0:0000783	9	nuclear telomere cap complex
G0:0016064	9	immunoglobulin mediated immune response
G0:0001952	9	regulation of cell-matrix adhesion
G0:0006782	9	protoporphyrinogen IX biosynthetic process
G0:0016973	9	poly(A)+ mRNA export from nucleus
G0:0005662	9	DNA replication factor A complex
G0:0000042	9	protein targeting to Golgi
G0:0015299	9	solute:proton antiporter activity

G0:0032461	9	positive regulation of protein oligomerization
G0:0030828	9	positive regulation of cGMP biosynthetic process
G0:0035278	9	negative regulation of translation involved in gene silencing by miRNA
G0:0031224	9	intrinsic component of membrane
G0:0016024	9	CDP-diacylglycerol biosynthetic process
G0:0035646	9	endosome to melanosome transport
G0:0061314	9	Notch signaling involved in heart development
G0:0008593	9	regulation of Notch signaling pathway
G0:0016272	9	prefoldin complex
G0:0016279	9	protein-lysine N-methyltransferase activity
G0:0033179	9	proton-transporting V-type ATPase, V0 domain
G0:0004016	9	adenylate cyclase activity
G0:0032836	9	glomerular basement membrane development
G0:0016045	9	detection of bacterium
G0:0060429	9	epithelium development
G0:0010832	9	negative regulation of myotube differentiation
G0:0004716	9	receptor signaling protein tyrosine kinase activity
G0:0032319	9	regulation of Rho GTPase activity
G0:0031045	9	dense core granule
G0:0004385	9	guanylate kinase activity
G0:0009072	9	aromatic amino acid family metabolic process
G0:0005388	9	calcium-transporting ATPase activity
G0:0004033	9	aldo-keto reductase (NADP) activity
G0:0043024	9	ribosomal small subunit binding
G0:0071872	9	cellular response to epinephrine stimulus
G0:0043666	9	regulation of phosphoprotein phosphatase activity
G0:0010224	9	response to UV-B
G0:0000800	9	lateral element
G0:0097202	9	activation of cysteine-type endopeptidase activity
G0:0043117	9	positive regulation of vascular permeability
G0:0016281	9	eukaryotic translation initiation factor 4F complex
G0:0016504	9	peptidase activator activity
G0:0033690	9	positive regulation of osteoblast proliferation
G0:0097028	9	dendritic cell differentiation
G0:0060840	9	artery development
G0:0033151	9	V(D)J recombination
G0:0005832	9	chaperonin-containing T-complex
G0:0002675	9	positive regulation of acute inflammatory response
G0:0035435	9	phosphate ion transmembrane transport
G0:0022407	9	regulation of cell-cell adhesion
G0:0002021	9	response to dietary excess
G0:0008347	9	glial cell migration
G0:0030278	9	regulation of ossification
G0:0031080	9	nuclear pore outer ring
G0:0045730	9	respiratory burst
G0:0043088	9	regulation of Cdc42 GTPase activity
G0:0097038	9	perinuclear endoplasmic reticulum
G0:0003323	9	type B pancreatic cell development
G0:0003841	9	1-acylglycerol-3-phosphate 0-acyltransferase activity
G0:0032330	9	regulation of chondrocyte differentiation
G0:0032703	9	negative regulation of interleukin-2 production
G0:0015175	9	neutral amino acid transmembrane transporter activity
G0:0007167	9	enzyme linked receptor protein signaling pathway
G0:0007530	9	sex determination
G0:0038003	9	opioid receptor signaling pathway
G0:0045580	9	regulation of T cell differentiation
G0:0015301	9	anion:anion antiporter activity
G0:1901653	9	cellular response to peptide
G0:0061029	9	eyelid development in camera-type eye
G0:0031985	9	Golgi cisterna
G0:0001893	9	maternal placenta development
G0:0032516	9	positive regulation of phosphoprotein phosphatase activity
G0:0070266	9	necroptotic process
G0:0000940	9	condensed chromosome outer kinetochore
G0:0045779	9	negative regulation of bone resorption
G0:0003796	9	lysozyme activity
G0:0019852	9	L-ascorbic acid metabolic process
G0:0051571	9	positive regulation of histone H3-K4 methylation
G0:0010459	9	negative regulation of heart rate
G0:0016446	9	somatic hypermutation of immunoglobulin genes
G0:0035455	9	response to interferon-alpha
G0:0061001	9	regulation of dendritic spine morphogenesis
G0:0002437	9	inflammatory response to antigenic stimulus
G0:0015909	9	long-chain fatty acid transport
G0:0006388	9	tRNA splicing, via endonucleolytic cleavage and ligation

G0:0006853	9	carnitine shuttle
G0:0003222	9	ventricular trabecula myocardium morphogenesis
G0:0008327	9	methyl-CpG binding
G0:0032230	9	positive regulation of synaptic transmission, GABAergic
G0:0051457	9	maintenance of protein location in nucleus
G0:0042698	9	ovulation cycle
G0:0004629	9	phospholipase C activity
G0:0004622	9	lysophospholipase activity
G0:2000147	9	positive regulation of cell motility
G0:0045059	9	positive thymic T cell selection
G0:0006264	9	mitochondrial DNA replication
G0:0019789	9	SUMO ligase activity
G0:0006265	9	DNA topological change
G0:0046622	8	positive regulation of organ growth
G0:0030856	8	regulation of epithelial cell differentiation
G0:0030857	8	negative regulation of epithelial cell differentiation
G0:0030858	8	positive regulation of epithelial cell differentiation
G0:0006625	8	protein targeting to peroxisome
G0:0006975	8	DNA damage induced protein phosphorylation
G0:0002456	8	T cell mediated immunity
G0:0034383	8	low-density lipoprotein particle clearance
G0:0042405	8	nuclear inclusion body
G0:0010107	8	potassium ion import
G0:0005869	8	dynactin complex
G0:0032926	8	negative regulation of activin receptor signaling pathway
G0:0016998	8	cell wall macromolecule catabolic process
G0:0045650	8	negative regulation of macrophage differentiation
G0:0045654	8	positive regulation of megakaryocyte differentiation
G0:0050810	8	regulation of steroid biosynthetic process
G0:0050811	8	GABA receptor binding
G0:0007199	8	G-protein coupled receptor signaling pathway coupled to cGMP nucleotide
second messenger		
G0:0034587	8	piRNA metabolic process
G0:0004467	8	long-chain fatty acid-CoA ligase activity
G0:0032835	8	glomerulus development
G0:0071354	8	cellular response to interleukin-6
G0:0003198	8	epithelial to mesenchymal transition involved in endocardial cushion
formation		
G0:0072075	8	metanephric mesenchyme development
G0:0016812	8	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in
cyclic amides		
G0:0016814	8	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in
cyclic amidines		
G0:0008595	8	anterior/posterior axis specification, embryo
G0:0005313	8	L-glutamate transmembrane transporter activity
G0:0071372	8	cellular response to follicle-stimulating hormone stimulus
G0:0045116	8	protein neddylation
G0:0006903	8	vesicle targeting
G0:0060322	8	head development
G0:0060324	8	face development
G0:0005521	8	lamin binding
G0:0015280	8	ligand-gated sodium channel activity
G0:0032693	8	negative regulation of interleukin-10 production
G0:0032691	8	negative regulation of interleukin-1 beta production
G0:0046638	8	positive regulation of alpha-beta T cell differentiation
G0:0051893	8	regulation of focal adhesion assembly
G0:0043995	8	histone acetyltransferase activity (H4-K5 specific)
G0:0032862	8	activation of Rho GTPase activity
G0:0006308	8	DNA catabolic process
G0:0051974	8	negative regulation of telomerase activity
G0:0009308	8	amine metabolic process
G0:0090197	8	positive regulation of chemokine secretion
G0:0035095	8	behavioral response to nicotine
G0:0007494	8	midgut development
G0:0004745	8	retinol dehydrogenase activity
G0:0051378	8	serotonin binding
G0:0051371	8	muscle alpha-actinin binding
G0:0033147	8	negative regulation of intracellular estrogen receptor signaling pathway
G0:0033148	8	positive regulation of intracellular estrogen receptor signaling pathway
G0:0031095	8	platelet dense tubular network membrane
G0:0031092	8	platelet alpha granule membrane
G0:0090037	8	positive regulation of protein kinase C signaling
G0:0043651	8	linoleic acid metabolic process
G0:0071360	8	cellular response to exogenous dsRNA
G0:0008053	8	mitochondrial fusion

G0:0016876	8	ligase activity, forming aminoacyl-tRNA and related compounds
G0:0000075	8	cell cycle checkpoint
G0:0070723	8	response to cholesterol
G0:0002674	8	negative regulation of acute inflammatory response
G0:0046548	8	retinal rod cell development
G0:0033169	8	histone H3-K9 demethylation
G0:0033162	8	melanosome membrane
G0:0004022	8	alcohol dehydrogenase (NAD) activity
G0:0051292	8	nuclear pore complex assembly
G0:0032825	8	positive regulation of natural killer cell differentiation
G0:0008157	8	protein phosphatase 1 binding
G0:0071243	8	cellular response to arsenic-containing substance
G0:0060346	8	bone trabecula formation
G0:0006703	8	estrogen biosynthetic process
G0:0006527	8	arginine catabolic process
G0:0008253	8	5'-nucleotidase activity
G0:0008250	8	oligosaccharyltransferase complex
G0:0060487	8	lung epithelial cell differentiation
G0:0006704	8	glucocorticoid biosynthetic process
G0:0032584	8	growth cone membrane
G0:2000810	8	regulation of tight junction assembly
G0:0017110	8	nucleoside-diphosphatase activity
G0:0009062	8	fatty acid catabolic process
G0:0005391	8	sodium:potassium-exchanging ATPase activity
G0:0000812	8	Swr1 complex
G0:0016868	8	intramolecular transferase activity, phosphotransferases
G0:1900006	8	positive regulation of dendrite development
G0:0051489	8	regulation of filopodium assembly
G0:0051481	8	negative regulation of cytosolic calcium ion concentration
G0:0007096	8	regulation of exit from mitosis
G0:0010804	8	negative regulation of tumor necrosis factor-mediated signaling pathway
G0:0031669	8	cellular response to nutrient levels
G0:0048489	8	synaptic vesicle transport
G0:0019206	8	nucleoside kinase activity
G0:0019205	8	nucleobase-containing compound kinase activity
G0:0019752	8	carboxylic acid metabolic process
G0:0004861	8	cyclin-dependent protein serine/threonine kinase inhibitor activity
G0:0009266	8	response to temperature stimulus
G0:0006893	8	Golgi to plasma membrane transport
G0:0046889	8	positive regulation of lipid biosynthetic process
G0:0019773	8	proteasome core complex, alpha-subunit complex
G0:0034366	8	spherical high-density lipoprotein particle
G0:0016799	8	hydrolase activity, hydrolyzing N-glycosyl compounds
G0:0035871	8	protein K11-linked deubiquitination
G0:0008037	8	cell recognition
G0:0008290	8	F-actin capping protein complex
G0:0019227	8	neuronal action potential propagation
G0:0001510	8	RNA methylation
G0:0007175	8	negative regulation of epidermal growth factor-activated receptor activity
G0:0007172	8	signal complex assembly
G0:0000993	8	RNA polymerase II core binding
G0:0016572	8	histone phosphorylation
G0:0045723	8	positive regulation of fatty acid biosynthetic process
G0:1900745	8	positive regulation of p38MAPK cascade
G0:0060044	8	negative regulation of cardiac muscle cell proliferation
G0:0017158	8	regulation of calcium ion-dependent exocytosis
G0:0017153	8	sodium:dicarboxylate symporter activity
G0:0030728	8	ovulation
G0:0045120	8	pronucleus
G0:0045124	8	regulation of bone resorption
G0:0019509	8	L-methionine biosynthetic process from methylthioadenosine
G0:0045178	8	basal part of cell
G0:0042487	8	regulation of odontogenesis of dentin-containing tooth
G0:0003680	8	AT DNA binding
G0:0060080	8	regulation of inhibitory postsynaptic membrane potential
G0:0016559	8	peroxisome fission
G0:0006465	8	signal peptide processing
G0:0000155	8	phosphorelay sensor kinase activity
G0:0015385	8	sodium:proton antiporter activity
G0:0019388	8	galactose catabolic process
G0:0005861	8	troponin complex
G0:0071711	8	basement membrane organization
G0:0061037	8	negative regulation of cartilage development
G0:0042135	8	neurotransmitter catabolic process
G0:0035970	8	peptidyl-threonine dephosphorylation

G0:0000098	8	sulfur amino acid catabolic process
G0:0042754	8	negative regulation of circadian rhythm
G0:0043522	8	leucine zipper domain binding
G0:0005522	8	profilin binding
G0:0043996	8	histone acetyltransferase activity (H4-K8 specific)
G0:0042116	8	macrophage activation
G0:0050663	8	cytokine secretion
G0:0030904	8	retromer complex
G0:0061202	8	clathrin-sculpted gamma-aminobutyric acid transport vesicle membrane
G0:0032801	8	receptor catabolic process
G0:0005068	8	transmembrane receptor protein tyrosine kinase adaptor activity
G0:0035313	8	wound healing, spreading of epidermal cells
G0:0007606	8	sensory perception of chemical stimulus
G0:0071316	8	cellular response to nicotine
G0:0010888	8	negative regulation of lipid storage
G0:0000307	8	cyclin-dependent protein kinase holoenzyme complex
G0:0042053	8	regulation of dopamine metabolic process
G0:0001886	8	endothelial cell morphogenesis
G0:0060997	8	dendritic spine morphogenesis
G0:0034063	8	stress granule assembly
G0:0046324	8	regulation of glucose import
G0:0008139	8	nuclear localization sequence binding
G0:0009629	8	response to gravity
G0:0003203	8	endocardial cushion morphogenesis
G0:0035567	8	non-canonical Wnt signaling pathway
G0:0051567	8	histone H3-K9 methylation
G0:0033559	8	unsaturated fatty acid metabolic process
G0:0016471	8	vacuolar proton-transporting V-type ATPase complex
G0:0006983	8	ER overload response
G0:0003351	8	epithelial cilium movement
G0:0045416	8	positive regulation of interleukin-8 biosynthetic process
G0:0042511	8	positive regulation of tyrosine phosphorylation of Stat1 protein
G0:0042473	8	outer ear morphogenesis
G0:0009607	8	response to biotic stimulus
G0:0032228	8	regulation of synaptic transmission, GABAergic
G0:0036109	8	alpha-linolenic acid metabolic process
G0:0032486	8	Rap protein signal transduction
G0:0086069	8	bundle of His cell to Purkinje myocyte communication
G0:0031681	8	G-protein beta-subunit binding
G0:0007617	8	mating behavior
G0:0051246	8	regulation of protein metabolic process
G0:0010763	8	positive regulation of fibroblast migration
G0:0034244	8	negative regulation of transcription elongation from RNA polymerase II promoter
G0:0002467	8	germinal center formation
G0:0006390	8	transcription from mitochondrial promoter
G0:0060396	8	growth hormone receptor signaling pathway
G0:0042987	8	amyloid precursor protein catabolic process
G0:0008535	8	respiratory chain complex IV assembly
G0:0016655	8	oxidoreductase activity, acting on NAD(P)H, quinone or similar compound as acceptor
G0:0032609	8	interferon-gamma production
G0:0031110	8	regulation of microtubule polymerization or depolymerization
G0:0097105	8	presynaptic membrane assembly
G0:0048029	8	monosaccharide binding
G0:0001931	8	uropod
G0:0072164	8	mesonephric tubule development
G0:0042555	8	MCM complex
G0:0005744	8	mitochondrial inner membrane presequence translocase complex
G0:0048708	8	astrocyte differentiation
G0:0030299	8	intestinal cholesterol absorption
G0:0016188	8	synaptic vesicle maturation
G0:0070530	8	K63-linked polyubiquitin binding
G0:0033962	8	cytoplasmic mRNA processing body assembly
G0:0006359	8	regulation of transcription from RNA polymerase III promoter
G0:0004535	8	poly(A)-specific ribonuclease activity
G0:0005113	8	patched binding
G0:0014824	8	artery smooth muscle contraction
G0:0045647	8	negative regulation of erythrocyte differentiation
G0:2001214	8	positive regulation of vasculogenesis
G0:0004659	8	prenyltransferase activity
G0:0033018	8	sarcoplasmic reticulum lumen
G0:0030118	8	clathrin coat
G0:0010700	8	negative regulation of norepinephrine secretion
G0:0046855	8	inositol phosphate dephosphorylation

G0:0006335	8	DNA replication-dependent nucleosome assembly
G0:0030119	8	AP-type membrane coat adaptor complex
G0:0017049	8	GTP-Rho binding
G0:0042596	8	fear response
G0:0043186	8	P granule
G0:0097284	8	hepatocyte apoptotic process
G0:0060155	8	platelet dense granule organization
G0:0060158	8	phospholipase C-activating dopamine receptor signaling pathway
G0:0001763	8	morphogenesis of a branching structure
G0:0016494	8	C-X-C chemokine receptor activity
G0:0021670	8	lateral ventricle development
G0:0075713	8	establishment of integrated proviral latency
G0:0005092	8	GDP-dissociation inhibitor activity
G0:0032872	8	regulation of stress-activated MAPK cascade
G0:0071361	8	cellular response to ethanol
G0:2000679	8	positive regulation of transcription regulatory region DNA binding
G0:0031748	8	D1 dopamine receptor binding
G0:0005664	8	nuclear origin of replication recognition complex
G0:0016290	8	palmitoyl-CoA hydrolase activity
G0:0032469	8	endoplasmic reticulum calcium ion homeostasis
G0:0032464	8	positive regulation of protein homooligomerization
G0:0034101	8	erythrocyte homeostasis
G0:0034450	8	ubiquitin-ubiquitin ligase activity
G0:0046972	8	histone acetyltransferase activity (H4-K16 specific)
G0:0001055	8	RNA polymerase II activity
G0:0035414	8	negative regulation of catenin import into nucleus
G0:0043020	8	NADPH oxidase complex
G0:0031227	8	intrinsic component of endoplasmic reticulum membrane
G0:0007270	8	neuron-neuron synaptic transmission
G0:0008469	8	histone-arginine N-methyltransferase activity
G0:0032854	8	positive regulation of Rap GTPase activity
G0:0005641	8	nuclear envelope lumen
G0:0008046	8	axon guidance receptor activity
G0:0005452	8	inorganic anion exchanger activity
G0:0035259	8	glucocorticoid receptor binding
G0:0035253	8	ciliary rootlet
G0:0030695	8	GTPase regulator activity
G0:0097267	8	omega-hydroxylase P450 pathway
G0:0048339	8	paraxial mesoderm development
G0:0070102	8	interleukin-6-mediated signaling pathway
G0:0033689	8	negative regulation of osteoblast proliferation
G0:0031929	8	TOR signaling
G0:0045945	8	positive regulation of transcription from RNA polymerase III promoter
G0:0016322	8	neuron remodeling
G0:0000002	8	mitochondrial genome maintenance
G0:0006688	8	glycosphingolipid biosynthetic process
G0:2000573	8	positive regulation of DNA biosynthetic process
G0:0000983	8	RNA polymerase II core promoter sequence-specific DNA binding
transcription factor activity		
G0:0035239	8	tube morphogenesis
G0:0061299	8	retina vasculature morphogenesis in camera-type eye
G0:0043068	8	positive regulation of programmed cell death
G0:0031702	8	type 1 angiotensin receptor binding
G0:0090005	8	negative regulation of establishment of protein localization to plasma
membrane		
G0:0004383	8	guanylate cyclase activity
G0:0005385	8	zinc ion transmembrane transporter activity
G0:0004032	8	alditol:NADP+ 1-oxidoreductase activity
G0:0070474	8	positive regulation of uterine smooth muscle contraction
G0:0030056	8	hemidesmosome
G0:0045721	8	negative regulation of gluconeogenesis
G0:0005542	8	folic acid binding
G0:0015278	8	calcium-release channel activity
G0:0060670	8	branching involved in labyrinthine layer morphogenesis
G0:0080025	8	phosphatidylinositol-3,5-bisphosphate binding
G0:0005838	8	proteasome regulatory particle
G0:0007084	8	mitotic nuclear envelope reassembly
G0:0006285	8	base-excision repair, AP site formation
G0:0048149	8	behavioral response to ethanol
G0:0005227	8	calcium activated cation channel activity
G0:0010592	8	positive regulation of lamellipodium assembly
G0:0003084	8	positive regulation of systemic arterial blood pressure
G0:0045719	8	negative regulation of glycogen biosynthetic process
G0:0045717	8	negative regulation of fatty acid biosynthetic process
G0:0042975	8	peroxisome proliferator activated receptor binding

G0:0034379	8	very-low-density lipoprotein particle assembly
G0:0008374	8	0-acyltransferase activity
G0:0003857	8	3-hydroxyacyl-CoA dehydrogenase activity
G0:0042379	8	chemokine receptor binding
G0:1902358	8	sulfate transmembrane transport
G0:0019725	8	cellular homeostasis
G0:0035855	8	megakaryocyte development
G0:0030432	8	peristalsis
G0:0061180	8	mammary gland epithelium development
G0:0048846	8	axon extension involved in axon guidance
G0:0008409	8	5'-3' exonuclease activity
G0:0070989	8	oxidative demethylation
G0:0070986	8	left/right axis specification
G0:0000578	8	embryonic axis specification
G0:0032700	8	negative regulation of interleukin-17 production
G0:0043551	8	regulation of phosphatidylinositol 3-kinase activity
G0:0061045	8	negative regulation of wound healing
G0:0042355	8	L-fucose catabolic process
G0:0042769	8	DNA damage response, detection of DNA damage
G0:0043983	8	histone H4-K12 acetylation
G0:0060059	8	embryonic retina morphogenesis in camera-type eye
G0:0090084	8	negative regulation of inclusion body assembly
G0:0006817	8	phosphate ion transport
G0:0031406	8	carboxylic acid binding
G0:0030235	8	nitric-oxide synthase regulator activity
G0:0006554	8	lysine catabolic process
G0:0035067	8	negative regulation of histone acetylation
G0:0071949	8	FAD binding
G0:0072321	8	chaperone-mediated protein transport
G0:0072546	8	ER membrane protein complex
G0:0050708	8	regulation of protein secretion
G0:0050709	8	negative regulation of protein secretion
G0:0005536	8	glucose binding
G0:0001542	8	ovulation from ovarian follicle
G0:0045822	8	negative regulation of heart contraction
G0:0070493	8	thrombin receptor signaling pathway
G0:0009635	8	response to herbicide
G0:0004862	8	cAMP-dependent protein kinase inhibitor activity
G0:0007009	8	plasma membrane organization
G0:0030219	8	megakaryocyte differentiation
G0:0035457	8	cellular response to interferon-alpha
G0:0000339	8	RNA cap binding
G0:0050892	8	intestinal absorption
G0:0001527	8	microfibril
G0:0043534	8	blood vessel endothelial cell migration
G0:0045793	8	positive regulation of cell size
G0:0021707	8	cerebellar granule cell differentiation
G0:0048752	8	semicircular canal morphogenesis
G0:0003337	8	mesenchymal to epithelial transition involved in metanephros morphogenesis
G0:0051597	8	response to methylmercury
G0:0032940	8	secretion by cell
G0:0032494	8	response to peptidoglycan
G0:0043495	8	protein anchor
G0:0001191	8	RNA polymerase II transcription factor binding transcription factor activity involved in negative regulation of transcription
G0:0005577	8	fibrinogen complex
G0:0051006	8	positive regulation of lipoprotein lipase activity
G0:0000904	8	cell morphogenesis involved in differentiation
G0:0032006	8	regulation of TOR signaling
G0:0032000	8	positive regulation of fatty acid beta-oxidation
G0:0030955	8	potassium ion binding
G0:0046930	8	pore complex
G0:0043114	8	regulation of vascular permeability
G0:0031464	8	Cul4A-RING E3 ubiquitin ligase complex
G0:0048513	8	organ development
G0:0001205	8	RNA polymerase II distal enhancer sequence-specific DNA binding transcription factor activity involved in positive regulation of transcription
G0:0033691	8	sialic acid binding
G0:0000733	8	DNA strand renaturation
G0:0071312	8	cellular response to alkaloid
G0:0045197	8	establishment or maintenance of epithelial cell apical/basal polarity
G0:0051001	8	negative regulation of nitric-oxide synthase activity
G0:0001939	8	female pronucleus
G0:0051787	7	misfolded protein binding
G0:0046653	7	tetrahydrofolate metabolic process

G0:0010759	7	positive regulation of macrophage chemotaxis
G0:0008429	7	phosphatidylethanolamine binding
G0:0090136	7	epithelial cell-cell adhesion
G0:0009101	7	glycoprotein biosynthetic process
G0:0032433	7	filopodium tip
G0:0006110	7	regulation of glycolytic process
G0:0007196	7	adenylate cyclase-inhibiting G-protein coupled glutamate receptor
signaling pathway		
G0:0005732	7	small nucleolar ribonucleoprotein complex
G0:0030122	7	AP-2 adaptor complex
G0:0030127	7	COPII vesicle coat
G0:0034235	7	GPI anchor binding
G0:0032816	7	positive regulation of natural killer cell activation
G0:0021520	7	spinal cord motor neuron cell fate specification
G0:0061099	7	negative regulation of protein tyrosine kinase activity
G0:0060907	7	positive regulation of macrophage cytokine production
G0:0001960	7	negative regulation of cytokine-mediated signaling pathway
G0:0086012	7	membrane depolarization during cardiac muscle cell action potential
G0:0000183	7	chromatin silencing at rDNA
G0:0050665	7	hydrogen peroxide biosynthetic process
G0:0060124	7	positive regulation of growth hormone secretion
G0:0032418	7	lysosome localization
G0:0015108	7	chloride transmembrane transporter activity
G0:0048070	7	regulation of developmental pigmentation
G0:0090073	7	positive regulation of protein homodimerization activity
G0:0046826	7	negative regulation of protein export from nucleus
G0:0046822	7	regulation of nucleocytoplasmic transport
G0:0016018	7	cyclosporin A binding
G0:0042589	7	zymogen granule membrane
G0:0035612	7	AP-2 adaptor complex binding
G0:0060323	7	head morphogenesis
G0:0009142	7	nucleoside triphosphate biosynthetic process
G0:0001778	7	plasma membrane repair
G0:0015288	7	porin activity
G0:0071499	7	cellular response to laminar fluid shear stress
G0:0070544	7	histone H3-K36 demethylation
G0:0032471	7	negative regulation of endoplasmic reticulum calcium ion concentration
G0:2000505	7	regulation of energy homeostasis
G0:0030836	7	positive regulation of actin filament depolymerization
G0:0046632	7	alpha-beta T cell differentiation
G0:0043030	7	regulation of macrophage activation
G0:0005088	7	Ras guanyl-nucleotide exchange factor activity
G0:0004931	7	extracellular ATP-gated cation channel activity
G0:0048096	7	chromatin-mediated maintenance of transcription
G0:0090050	7	positive regulation of cell migration involved in sprouting angiogenesis
G0:0015377	7	cation:chloride symporter activity
G0:0034706	7	sodium channel complex
G0:0032059	7	bleb
G0:0006307	7	DNA dealkylation involved in DNA repair
G0:0006301	7	postreplication repair
G0:0043208	7	glycosphingolipid binding
G0:0010863	7	positive regulation of phospholipase C activity
G0:0010867	7	positive regulation of triglyceride biosynthetic process
G0:0015116	7	sulfate transmembrane transporter activity
G0:0014037	7	Schwann cell differentiation
G0:0005721	7	centromeric heterochromatin
G0:0019441	7	tryptophan catabolic process to kynurenine
G0:0034115	7	negative regulation of heterotypic cell-cell adhesion
G0:0019919	7	peptidyl-arginine methylation, to asymmetrical-dimethyl arginine
G0:0002162	7	dystroglycan binding
G0:0030239	7	myofibril assembly
G0:0031232	7	extrinsic component of external side of plasma membrane
G0:0036010	7	protein localization to endosome
G0:0043653	7	mitochondrial fragmentation involved in apoptotic process
G0:0009982	7	pseudouridine synthase activity
G0:0031491	7	nucleosome binding
G0:0004767	7	sphingomyelin phosphodiesterase activity
G0:0008271	7	secondary active sulfate transmembrane transporter activity
G0:0051354	7	negative regulation of oxidoreductase activity
G0:0051353	7	positive regulation of oxidoreductase activity
G0:0010172	7	embryonic body morphogenesis
G0:2000543	7	positive regulation of gastrulation
G0:0019934	7	cGMP-mediated signaling
G0:0001849	7	complement component C1q binding
G0:0016265	7	death

G0:0016264	7	gap junction assembly
G0:0044597	7	daunorubicin metabolic process
G0:0071679	7	commissural neuron axon guidance
G0:0030306	7	ADP-ribosylation factor binding
G0:0047498	7	calcium-dependent phospholipase A2 activity
G0:0047497	7	mitochondrion transport along microtubule
G0:0004972	7	N-methyl-D-aspartate selective glutamate receptor activity
G0:0051168	7	nuclear export
G0:0008635	7	activation of cysteine-type endopeptidase activity involved in apoptotic process by cytochrome c
G0:0001614	7	purinergic nucleotide receptor activity
G0:0006882	7	cellular zinc ion homeostasis
G0:0008509	7	anion transmembrane transporter activity
G0:1900025	7	negative regulation of substrate adhesion-dependent cell spreading
G0:0050072	7	m7G(5')pppN diphosphatase activity
G0:0071318	7	cellular response to ATP
G0:0006700	7	C21-steroid hormone biosynthetic process
G0:0072657	7	protein localization to membrane
G0:0004568	7	chitinase activity
G0:0048172	7	regulation of short-term neuronal synaptic plasticity
G0:0048170	7	positive regulation of long-term neuronal synaptic plasticity
G0:0000012	7	single strand break repair
G0:0031666	7	positive regulation of lipopolysaccharide-mediated signaling pathway
G0:0031665	7	negative regulation of lipopolysaccharide-mediated signaling pathway
G0:0004703	7	G-protein coupled receptor kinase activity
G0:0006701	7	progesterone biosynthetic process
G0:0001867	7	complement activation, lectin pathway
G0:0032589	7	neuron projection membrane
G0:1901030	7	positive regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway
G0:0060316	7	positive regulation of ryanodine-sensitive calcium-release channel activity
G0:0060664	7	epithelial cell proliferation involved in salivary gland morphogenesis
G0:0033523	7	histone H2B ubiquitination
G0:0051099	7	positive regulation of binding
G0:0034983	7	peptidyl-lysine deacetylation
G0:0034713	7	type I transforming growth factor beta receptor binding
G0:0070688	7	MLL5-L complex
G0:0071223	7	cellular response to lipoteichoic acid
G0:0003360	7	brainstem development
G0:0007091	7	metaphase/anaphase transition of mitotic cell cycle
G0:0050688	7	regulation of defense response to virus
G0:0005114	7	type II transforming growth factor beta receptor binding
G0:0060411	7	cardiac septum morphogenesis
G0:0000030	7	mannosyltransferase activity
G0:0004726	7	non-membrane spanning protein tyrosine phosphatase activity
G0:0031642	7	negative regulation of myelination
G0:0007567	7	parturition
G0:1901016	7	regulation of potassium ion transmembrane transporter activity
G0:0004017	7	adenylate kinase activity
G0:0015884	7	folic acid transport
G0:0060017	7	parathyroid gland development
G0:0032288	7	myelin assembly
G0:0008608	7	attachment of spindle microtubules to kinetochore
G0:0040011	7	locomotion
G0:0040016	7	embryonic cleavage
G0:0040019	7	positive regulation of embryonic development
G0:0033089	7	positive regulation of T cell differentiation in thymus
G0:0002606	7	positive regulation of dendritic cell antigen processing and presentation
G0:0030285	7	integral component of synaptic vesicle membrane
G0:0006032	7	chitin catabolic process
G0:0008035	7	high-density lipoprotein particle binding
G0:0003073	7	regulation of systemic arterial blood pressure
G0:0045722	7	positive regulation of gluconeogenesis
G0:0032421	7	stereocilium bundle
G0:0008190	7	eukaryotic initiation factor 4E binding
G0:0008376	7	acetylgalactosaminyltransferase activity
G0:0040036	7	regulation of fibroblast growth factor receptor signaling pathway
G0:0032731	7	positive regulation of interleukin-1 beta production
G0:0071599	7	otic vesicle development
G0:0005606	7	laminin-1 complex
G0:0048667	7	cell morphogenesis involved in neuron differentiation
G0:0003993	7	acid phosphatase activity
G0:0031054	7	pre-miRNA processing
G0:0072357	7	PTW/PP1 phosphatase complex

G0:0060351	7	cartilage development involved in endochondral bone morphogenesis
G0:0042178	7	xenobiotic catabolic process
G0:0043566	7	structure-specific DNA binding
G0:0043569	7	negative regulation of insulin-like growth factor receptor signaling pathway
G0:0070365	7	hepatocyte differentiation
G0:0008366	7	axon ensheathment
G0:0008312	7	7S RNA binding
G0:0070997	7	neuron death
G0:0032717	7	negative regulation of interleukin-8 production
G0:0033627	7	cell adhesion mediated by integrin
G0:0042753	7	positive regulation of circadian rhythm
G0:0042756	7	drinking behavior
G0:0050733	7	RS domain binding
G0:0048644	7	muscle organ morphogenesis
G0:0036057	7	slit diaphragm
G0:0042117	7	monocyte activation
G0:0097060	7	synaptic membrane
G0:0045835	7	negative regulation of meiosis
G0:0042921	7	glucocorticoid receptor signaling pathway
G0:0005885	7	Arp2/3 protein complex
G0:0016458	7	gene silencing
G0:0061549	7	sympathetic ganglion development
G0:0010886	7	positive regulation of cholesterol storage
G0:1900116	7	extracellular negative regulation of signal transduction
G0:0002221	7	pattern recognition receptor signaling pathway
G0:0001553	7	luteinization
G0:0001881	7	receptor recycling
G0:0032525	7	somite rostral/caudal axis specification
G0:0015643	7	toxic substance binding
G0:0060687	7	regulation of branching involved in prostate gland morphogenesis
G0:0043596	7	nuclear replication fork
G0:0009620	7	response to fungus
G0:0003208	7	cardiac ventricle morphogenesis
G0:0042490	7	mechanoreceptor differentiation
G0:0042304	7	regulation of fatty acid biosynthetic process
G0:0050671	7	positive regulation of lymphocyte proliferation
G0:0043043	7	peptide biosynthetic process
G0:0009437	7	carnitine metabolic process
G0:0031065	7	positive regulation of histone deacetylation
G0:0055075	7	potassium ion homeostasis
G0:0030042	7	actin filament depolymerization
G0:0045410	7	positive regulation of interleukin-6 biosynthetic process
G0:0030948	7	negative regulation of vascular endothelial growth factor receptor signaling pathway
G0:0015937	7	coenzyme A biosynthetic process
G0:0006400	7	tRNA modification
G0:0090162	7	establishment of epithelial cell polarity
G0:0032229	7	negative regulation of synaptic transmission, GABAergic
G0:0019237	7	centromeric DNA binding
G0:0060231	7	mesenchymal to epithelial transition
G0:0002262	7	myeloid cell homeostasis
G0:0008499	7	UDP-galactose:beta-N-acetylglucosamine beta-1,3-galactosyltransferase activity
G0:0002726	7	positive regulation of T cell cytokine production
G0:0046903	7	secretion
G0:0060536	7	cartilage morphogenesis
G0:0035372	7	protein localization to microtubule
G0:0003417	7	growth plate cartilage development
G0:0085020	7	protein K6-linked ubiquitination
G0:0008395	7	steroid hydroxylase activity
G0:0051864	7	histone demethylase activity (H3-K36 specific)
G0:0002282	7	microglial cell activation involved in immune response
G0:0052689	7	carboxylic ester hydrolase activity
G0:0090051	7	negative regulation of cell migration involved in sprouting angiogenesis
G0:0031340	7	positive regulation of vesicle fusion
G0:0097320	7	membrane tubulation
G0:0008228	7	opsonization
G0:0014850	7	response to muscle activity
G0:0070244	7	negative regulation of thymocyte apoptotic process
G0:0044539	7	long-chain fatty acid import
G0:0007183	7	SMAD protein complex assembly
G0:0007184	7	SMAD protein import into nucleus
G0:0007185	7	transmembrane receptor protein tyrosine phosphatase signaling pathway
G0:0006584	7	catecholamine metabolic process

G0:0002116	7	semaphorin receptor complex
G0:0036310	7	annealing helicase activity
G0:0035005	7	1-phosphatidylinositol-4-phosphate 3-kinase activity
G0:0045475	7	locomotor rhythm
G0:0021513	7	spinal cord dorsal/ventral patterning
G0:0007216	7	G-protein coupled glutamate receptor signaling pathway
G0:0007217	7	tachykinin receptor signaling pathway
G0:0003181	7	atrioventricular valve morphogenesis
G0:0046415	7	urate metabolic process
G0:0060136	7	embryonic process involved in female pregnancy
G0:0060137	7	maternal process involved in parturition
G0:0005000	7	vasopressin receptor activity
G0:0002320	7	lymphoid progenitor cell differentiation
G0:0005229	7	intracellular calcium activated chloride channel activity
G0:0032930	7	positive regulation of superoxide anion generation
G0:0016614	7	oxidoreductase activity, acting on CH-OH group of donors
G0:0072643	7	interferon-gamma secretion
G0:0031659	7	positive regulation of cyclin-dependent protein serine/threonine kinase activity involved in G1/S transition of mitotic cell cycle
G0:0015077	7	monovalent inorganic cation transmembrane transporter activity
G0:0006491	7	N-glycan processing
G0:0004652	7	polynucleotide adenylyltransferase activity
G0:0090244	7	Wnt signaling pathway involved in somitogenesis
G0:0070166	7	enamel mineralization
G0:0014731	7	spectrin-associated cytoskeleton
G0:0014732	7	skeletal muscle atrophy
G0:0006333	7	chromatin assembly or disassembly
G0:0046470	7	phosphatidylcholine metabolic process
G0:0086064	7	cell communication by electrical coupling involved in cardiac conduction
G0:0005683	7	U7 snRNP
G0:0050966	7	detection of mechanical stimulus involved in sensory perception of pain
G0:0002161	7	aminoacyl-tRNA editing activity
G0:2001022	7	positive regulation of response to DNA damage stimulus
G0:0006544	7	glycine metabolic process
G0:0006929	7	substrate-dependent cell migration
G0:0000780	7	condensed nuclear chromosome, centromeric region
G0:0031573	7	intra-S DNA damage checkpoint
G0:0019068	7	virion assembly
G0:0031023	7	microtubule organizing center organization
G0:0001955	7	blood vessel maturation
G0:0061337	7	cardiac conduction
G0:0003143	7	embryonic heart tube morphogenesis
G0:0031960	7	response to corticosteroid
G0:0010873	7	positive regulation of cholesterol esterification
G0:0010870	7	positive regulation of receptor biosynthetic process
G0:0045348	7	positive regulation of MHC class II biosynthetic process
G0:0000046	7	autophagic vacuole fusion
G0:0070776	7	MOZ/MORF histone acetyltransferase complex
G0:0010518	7	positive regulation of phospholipase activity
G0:0006690	7	icosanoid metabolic process
G0:0004691	7	cAMP-dependent protein kinase activity
G0:0051156	7	glucose 6-phosphate metabolic process
G0:0060828	7	regulation of canonical Wnt signaling pathway
G0:0016763	7	transferase activity, transferring pentosyl groups
G0:0016004	7	phospholipase activator activity
G0:0035641	7	locomotory exploration behavior
G0:0060371	7	regulation of atrial cardiac muscle cell membrane depolarization
G0:0051963	7	regulation of synapse assembly
G0:0071420	7	cellular response to histamine
G0:0051988	7	regulation of attachment of spindle microtubules to kinetochore
G0:0046007	7	negative regulation of activated T cell proliferation
G0:0030371	7	translation repressor activity
G0:0030157	7	pancreatic juice secretion
G0:0043008	7	ATP-dependent protein binding
G0:0004908	7	interleukin-1 receptor activity
G0:0071850	7	mitotic cell cycle arrest
G0:0061072	7	iris morphogenesis
G0:0042693	7	muscle cell fate commitment
G0:0060426	7	lung vasculature development
G0:0060428	7	lung epithelium development
G0:0010838	7	positive regulation of keratinocyte proliferation
G0:0051901	7	positive regulation of mitochondrial depolarization
G0:0004571	7	mannosyl-oligosaccharide 1,2-alpha-mannosidase activity
G0:0004579	7	dolichyl-diphosphooligosaccharide-protein glycotransferase activity
G0:0009972	7	cytidine deamination

G0:0009156	7	ribonucleoside monophosphate biosynthetic process
G0:0071468	7	cellular response to acidity
G0:0038084	7	vascular endothelial growth factor signaling pathway
G0:0044598	7	doxorubicin metabolic process
G0:0061298	7	retina vasculature development in camera-type eye
G0:0045084	7	positive regulation of interleukin-12 biosynthetic process
G0:0045080	7	positive regulation of chemokine biosynthetic process
G0:0072341	7	modified amino acid binding
G0:0032099	7	negative regulation of appetite
G0:1901216	7	positive regulation of neuron death
G0:0033673	7	negative regulation of kinase activity
G0:0010955	7	negative regulation of protein processing
G0:0043270	7	positive regulation of ion transport
G0:0043279	7	response to alkaloid
G0:0034333	7	adherens junction assembly
G0:0005976	7	polysaccharide metabolic process
G0:0051923	7	sulfation
G0:0006776	7	vitamin A metabolic process
G0:0005548	7	phospholipid transporter activity
G0:0015271	7	outward rectifier potassium channel activity
G0:0010579	7	positive regulation of adenylate cyclase activity involved in G-protein coupled receptor signaling pathway
G0:0035748	7	myelin sheath abaxonal region
G0:0005222	7	intracellular cAMP activated cation channel activity
G0:0048806	7	genitalia development
G0:0045294	7	alpha-catenin binding
G0:0070679	7	inositol 1,4,5 trisphosphate binding
G0:0051444	7	negative regulation of ubiquitin-protein transferase activity
G0:1900017	7	positive regulation of cytokine production involved in inflammatory response
G0:0051492	7	regulation of stress fiber assembly
G0:0015844	7	monoamine transport
G0:0005021	7	vascular endothelial growth factor-activated receptor activity
G0:0030071	7	regulation of mitotic metaphase/anaphase transition
G0:0008528	7	G-protein coupled peptide receptor activity
G0:0004536	7	deoxyribonuclease activity
G0:0060287	7	epithelial cilium movement involved in determination of left/right asymmetry
G0:0019213	7	deacetylase activity
G0:0019217	7	regulation of fatty acid metabolic process
G0:2000020	7	positive regulation of male gonad development
G0:0031994	7	insulin-like growth factor I binding
G0:0045843	7	negative regulation of striated muscle tissue development
G0:0031005	7	filamin binding
G0:0036094	7	small molecule binding
G0:0090181	7	regulation of cholesterol metabolic process
G0:0040020	7	regulation of meiosis
G0:0005655	7	nucleolar ribonuclease P complex
G0:2000252	7	negative regulation of feeding behavior
G0:0045910	7	negative regulation of DNA recombination
G0:0034372	7	very-low-density lipoprotein particle remodeling
G0:0016175	7	superoxide-generating NADPH oxidase activity
G0:0006828	7	manganese ion transport
G0:0030274	7	LIM domain binding
G0:0051920	7	peroxiredoxin activity
G0:0060119	7	inner ear receptor cell development
G0:0060442	7	branching involved in prostate gland morphogenesis
G0:0006002	7	fructose 6-phosphate metabolic process
G0:0014050	7	negative regulation of glutamate secretion
G0:0031638	7	zymogen activation
G0:0038061	7	NIK/NF-kappaB signaling
G0:0019239	7	deaminase activity
G0:0000988	7	protein binding transcription factor activity
G0:0010831	7	positive regulation of myotube differentiation
G0:0060052	7	neurofilament cytoskeleton organization
G0:0060055	7	angiogenesis involved in wound healing
G0:0060710	7	chorio-allantoic fusion
G0:0060711	7	labyrinthine layer development
G0:0060712	7	spongiotrophoblast layer development
G0:2000270	7	negative regulation of fibroblast apoptotic process
G0:0051453	7	regulation of intracellular pH
G0:0005915	7	zonula adherens
G0:0030252	7	growth hormone secretion
G0:0009913	7	epidermal cell differentiation
G0:0006066	7	alcohol metabolic process

G0:0072112	7	glomerular visceral epithelial cell differentiation
G0:0033674	7	positive regulation of kinase activity
G0:0048608	7	reproductive structure development
G0:0019870	7	potassium channel inhibitor activity
G0:0035729	7	cellular response to hepatocyte growth factor stimulus
G0:0060039	7	pericardium development
G0:0035148	7	tube formation
G0:0034116	7	positive regulation of heterotypic cell-cell adhesion
G0:0006475	7	internal protein amino acid acetylation
G0:0038166	7	angiotensin-activated signaling pathway
G0:0048240	7	sperm capacitation
G0:0004303	7	estradiol 17-beta-dehydrogenase activity
G0:0032279	7	asymmetric synapse
G0:0010950	7	positive regulation of endopeptidase activity
G0:0032183	7	SUMO binding
G0:0032983	7	kainate selective glutamate receptor complex
G0:0030488	7	tRNA methylation
G0:0060770	7	negative regulation of epithelial cell proliferation involved in prostate gland development
G0:0050700	7	CARD domain binding
G0:0048642	7	negative regulation of skeletal muscle tissue development
G0:0006282	7	regulation of DNA repair
G0:0035242	7	protein-arginine omega-N asymmetric methyltransferase activity
G0:0008440	7	inositol-1,4,5-trisphosphate 3-kinase activity
G0:0030991	7	intraciliary transport particle A
G0:0000506	7	glycosylphosphatidylinositol-N-acetylglucosaminyltransferase (GPI-GnT) complex
G0:0030913	7	paranodal junction assembly
G0:0030916	7	otic vesicle formation
G0:0045824	7	negative regulation of innate immune response
G0:0008328	7	ionotropic glutamate receptor complex
G0:0017085	7	response to insecticide
G0:0070233	7	negative regulation of T cell apoptotic process
G0:0006739	7	NADP metabolic process
G0:0009313	7	oligosaccharide catabolic process
G0:0006208	7	pyrimidine nucleobase catabolic process
G0:0043303	7	mast cell degranulation
G0:0050891	7	multicellular organismal water homeostasis
G0:0050765	7	negative regulation of phagocytosis
G0:0051382	7	kinetochore assembly
G0:0010667	7	negative regulation of cardiac muscle cell apoptotic process
G0:0016307	7	phosphatidylinositol phosphate kinase activity
G0:0035590	7	purinergic nucleotide receptor signaling pathway
G0:0060561	7	apoptotic process involved in morphogenesis
G0:0022010	7	central nervous system myelination
G0:0001825	7	blastocyst formation
G0:0080008	7	Cul4-RING E3 ubiquitin ligase complex
G0:0006221	7	pyrimidine nucleotide biosynthetic process
G0:0046784	7	viral mRNA export from host cell nucleus
G0:0006082	7	organic acid metabolic process
G0:0030098	7	lymphocyte differentiation
G0:0005750	7	mitochondrial respiratory chain complex III
G0:0005579	7	membrane attack complex
G0:0000900	7	translation repressor activity, nucleic acid binding
G0:0042448	7	progesterone metabolic process
G0:0031462	7	Cul2-RING ubiquitin ligase complex
G0:0051024	7	positive regulation of immunoglobulin secretion
G0:0070273	7	phosphatidylinositol-4-phosphate binding
G0:0046541	7	saliva secretion
G0:0045617	7	negative regulation of keratinocyte differentiation
G0:0031123	7	RNA 3'-end processing
G0:0043254	7	regulation of protein complex assembly
G0:0031616	7	spindle pole centrosome
G0:0016641	7	oxidoreductase activity, acting on the CH-NH2 group of donors, oxygen as acceptor
G0:0048019	7	receptor antagonist activity
G0:0003382	7	epithelial cell morphogenesis
G0:0019787	7	small conjugating protein ligase activity
G0:0034501	7	protein localization to kinetochore
G0:0001961	7	positive regulation of cytokine-mediated signaling pathway
G0:0071313	7	cellular response to caffeine
G0:0060527	7	prostate epithelial cord arborization involved in prostate glandular acinus morphogenesis
G0:0046689	7	response to mercury ion
G0:0048188	7	Set1C/COMPASS complex

G0:0032780	7	negative regulation of ATPase activity
G0:0019992	6	diacylglycerol binding
G0:0030853	6	negative regulation of granulocyte differentiation
G0:0030851	6	granulocyte differentiation
G0:0030854	6	positive regulation of granulocyte differentiation
G0:0090344	6	negative regulation of cell aging
G0:0045359	6	positive regulation of interferon-beta biosynthetic process
G0:0055001	6	muscle cell development
G0:0055009	6	atrial cardiac muscle tissue morphogenesis
G0:0070063	6	RNA polymerase binding
G0:0051279	6	regulation of release of sequestered calcium ion into cytosol
G0:0003300	6	cardiac muscle hypertrophy
G0:0048554	6	positive regulation of metalloenzyme activity
G0:0042541	6	hemoglobin biosynthetic process
G0:0034382	6	chylomicron remnant clearance
G0:0034380	6	high-density lipoprotein particle assembly
G0:0034384	6	high-density lipoprotein particle clearance
G0:0006101	6	citrate metabolic process
G0:0006108	6	malate metabolic process
G0:0060261	6	positive regulation of transcription initiation from RNA polymerase II promoter
G0:0072015	6	glomerular visceral epithelial cell development
G0:0010907	6	positive regulation of glucose metabolic process
G0:0042167	6	heme catabolic process
G0:0001739	6	sex chromatin
G0:0008503	6	benzodiazepine receptor activity
G0:0015718	6	monocarboxylic acid transport
G0:0003916	6	DNA topoisomerase activity
G0:0030870	6	Mre11 complex
G0:0005138	6	interleukin-6 receptor binding
G0:0034715	6	pICln-Sm protein complex
G0:0002925	6	positive regulation of humoral immune response mediated by circulating immunoglobulin
G0:0007341	6	penetration of zona pellucida
G0:2000318	6	positive regulation of T-helper 17 type immune response
G0:0035051	6	cardiocyte differentiation
G0:0030020	6	extracellular matrix structural constituent conferring tensile strength
G0:0035634	6	response to stilbenoid
G0:0006346	6	methylation-dependent chromatin silencing
G0:0086013	6	membrane repolarization during cardiac muscle cell action potential
G0:0031730	6	CCR5 chemokine receptor binding
G0:0015893	6	drug transport
G0:0050667	6	homocysteine metabolic process
G0:0048539	6	bone marrow development
G0:0005697	6	telomerase holoenzyme complex
G0:0090080	6	positive regulation of MAPKKK cascade by fibroblast growth factor receptor signaling pathway
G0:0000405	6	bubble DNA binding
G0:0030816	6	positive regulation of cAMP metabolic process
G0:0030814	6	regulation of cAMP metabolic process
G0:0015923	6	mannosidase activity
G0:0007223	6	Wnt signaling pathway, calcium modulating pathway
G0:0046825	6	regulation of protein export from nucleus
G0:0001940	6	male pronucleus
G0:0016012	6	sarcoglycan complex
G0:0006323	6	DNA packaging
G0:0042582	6	azurophil granule
G0:0043190	6	ATP-binding cassette (ABC) transporter complex
G0:0043196	6	varicosity
G0:0005677	6	chromatin silencing complex
G0:0006531	6	aspartate metabolic process
G0:0001776	6	leukocyte homeostasis
G0:1902533	6	positive regulation of intracellular signal transduction
G0:0045347	6	negative regulation of MHC class II biosynthetic process
G0:0042805	6	actinin binding
G0:0070531	6	BRCA1-A complex
G0:0001574	6	ganglioside biosynthetic process
G0:0046581	6	intercellular canaliculus
G0:0071636	6	positive regulation of transforming growth factor beta production
G0:0035269	6	protein O-linked mannosylation
G0:0051896	6	regulation of protein kinase B signaling
G0:0030166	6	proteoglycan biosynthetic process
G0:2001223	6	negative regulation of neuron migration
G0:0006689	6	ganglioside catabolic process
G0:0036038	6	TCTN-B9D complex

G0:0045576	6	mast cell activation
G0:0048102	6	autophagic cell death
G0:0031957	6	very long-chain fatty acid-CoA ligase activity
G0:0050798	6	activated T cell proliferation
G0:0017076	6	purine nucleotide binding
G0:0017070	6	U6 snRNA binding
G0:0071380	6	cellular response to prostaglandin E stimulus
G0:0042797	6	tRNA transcription from RNA polymerase III promoter
G0:0008211	6	glucocorticoid metabolic process
G0:0032324	6	molybdopterin cofactor biosynthetic process
G0:1901380	6	negative regulation of potassium ion transmembrane transport
G0:0010656	6	negative regulation of muscle cell apoptotic process
G0:0061179	6	negative regulation of insulin secretion involved in cellular response to glucose stimulus
G0:0048304	6	positive regulation of isotype switching to IgG isotypes
G0:0005351	6	sugar:proton symporter activity
G0:0004000	6	adenosine deaminase activity
G0:0048739	6	cardiac muscle fiber development
G0:0006189	6	'de novo' IMP biosynthetic process
G0:0048732	6	gland development
G0:0006729	6	tetrahydrobiopterin biosynthetic process
G0:0000076	6	DNA replication checkpoint
G0:0032300	6	mismatch repair complex
G0:0001848	6	complement binding
G0:0015793	6	glycerol transport
G0:0006515	6	misfolded or incompletely synthesized protein catabolic process
G0:0038092	6	nodal signaling pathway
G0:0030314	6	junctional membrane complex
G0:0010042	6	response to manganese ion
G0:0032927	6	positive regulation of activin receptor signaling pathway
G0:0007289	6	spermatid nucleus differentiation
G0:0032790	6	ribosome disassembly
G0:0008641	6	small protein activating enzyme activity
G0:0000125	6	PCAF complex
G0:0045162	6	clustering of voltage-gated sodium channels
G0:0045955	6	negative regulation of calcium ion-dependent exocytosis
G0:0000014	6	single-stranded DNA endodeoxyribonuclease activity
G0:0000018	6	regulation of DNA recombination
G0:0004704	6	NF-kappaB-inducing kinase activity
G0:0018026	6	peptidyl-lysine monomethylation
G0:0032367	6	intracellular cholesterol transport
G0:0016790	6	thiolester hydrolase activity
G0:0043382	6	positive regulation of memory T cell differentiation
G0:0034405	6	response to fluid shear stress
G0:0030321	6	transepithelial chloride transport
G0:0030323	6	respiratory tube development
G0:0047617	6	acyl-CoA hydrolase activity
G0:0005372	6	water transmembrane transporter activity
G0:0000244	6	spliceosomal tri-snRNP complex assembly
G0:0060087	6	relaxation of vascular smooth muscle
G0:0002070	6	epithelial cell maturation
G0:0051103	6	DNA ligation involved in DNA repair
G0:0032809	6	neuronal cell body membrane
G0:0043615	6	astrocyte cell migration
G0:0043266	6	regulation of potassium ion transport
G0:0006356	6	regulation of transcription from RNA polymerase I promoter
G0:0007097	6	nuclear migration
G0:0050687	6	negative regulation of defense response to virus
G0:0030510	6	regulation of BMP signaling pathway
G0:0060416	6	response to growth hormone
G0:0043169	6	cation binding
G0:0016584	6	nucleosome positioning
G0:0014910	6	regulation of smooth muscle cell migration
G0:0019209	6	kinase activator activity
G0:0007019	6	microtubule depolymerization
G0:1901017	6	negative regulation of potassium ion transmembrane transporter activity
G0:0003091	6	renal water homeostasis
G0:0006573	6	valine metabolic process
G0:0032819	6	positive regulation of natural killer cell proliferation
G0:0000028	6	ribosomal small subunit assembly
G0:0031253	6	cell projection membrane
G0:0050291	6	sphingosine N-acyltransferase activity
G0:0032287	6	peripheral nervous system myelin maintenance
G0:0071204	6	histone pre-mRNA 3'end processing complex
G0:0030280	6	structural constituent of epidermis

G0:0071476	6	cellular hypotonic response
G0:0004523	6	RNA-DNA hybrid ribonuclease activity
G0:0042713	6	sperm ejaculation
G0:0022417	6	protein maturation by protein folding
G0:0032020	6	ISG15-protein conjugation
G0:0007176	6	regulation of epidermal growth factor-activated receptor activity
G0:0042158	6	lipoprotein biosynthetic process
G0:0016570	6	histone modification
G0:0009249	6	protein lipoylation
G0:0021591	6	ventricular system development
G0:0008195	6	phosphatidate phosphatase activity
G0:0004887	6	thyroid hormone receptor activity
G0:0033180	6	proton-transporting V-type ATPase, V1 domain
G0:2000480	6	negative regulation of cAMP-dependent protein kinase activity
G0:0033603	6	positive regulation of dopamine secretion
G0:0035036	6	sperm-egg recognition
G0:0003688	6	DNA replication origin binding
G0:0048660	6	regulation of smooth muscle cell proliferation
G0:0046920	6	alpha-(1->3)-fucosyltransferase activity
G0:0002829	6	negative regulation of type 2 immune response
G0:0010631	6	epithelial cell migration
G0:0001594	6	trace-amine receptor activity
G0:0045743	6	positive regulation of fibroblast growth factor receptor signaling pathway
G0:0060026	6	convergent extension
G0:0060022	6	hard palate development
G0:0045814	6	negative regulation of gene expression, epigenetic
G0:0035197	6	siRNA binding
G0:0032211	6	negative regulation of telomere maintenance via telomerase
G0:0070198	6	protein localization to chromosome, telomeric region
G0:0003376	6	sphingosine-1-phosphate signaling pathway
G0:0071546	6	pi-body
G0:0033629	6	negative regulation of cell adhesion mediated by integrin
G0:0043353	6	enucleate erythrocyte differentiation
G0:0005786	6	signal recognition particle, endoplasmic reticulum targeting
G0:0009838	6	abscission
G0:0003014	6	renal system process
G0:0004126	6	cytidine deaminase activity
G0:0006655	6	phosphatidylglycerol biosynthetic process
G0:0038036	6	sphingosine-1-phosphate receptor activity
G0:0032052	6	bile acid binding
G0:0048771	6	tissue remodeling
G0:0008432	6	JUN kinase binding
G0:0042118	6	endothelial cell activation
G0:0071383	6	cellular response to steroid hormone stimulus
G0:0030132	6	clathrin coat of coated pit
G0:0045760	6	positive regulation of action potential
G0:0030643	6	cellular phosphate ion homeostasis
G0:0070382	6	exocytic vesicle
G0:0060008	6	Sertoli cell differentiation
G0:0035315	6	hair cell differentiation
G0:0048251	6	elastic fiber assembly
G0:0051096	6	positive regulation of helicase activity
G0:0015450	6	P-P-bond-hydrolysis-driven protein transmembrane transporter activity
G0:0019104	6	DNA N-glycosylase activity
G0:0071732	6	cellular response to nitric oxide
G0:0034695	6	response to prostaglandin E
G0:0010887	6	negative regulation of cholesterol storage
G0:0010884	6	positive regulation of lipid storage
G0:1900119	6	positive regulation of execution phase of apoptosis
G0:0060762	6	regulation of branching involved in mammary gland duct morphogenesis
G0:0010269	6	response to selenium ion
G0:0009410	6	response to xenobiotic stimulus
G0:0031512	6	motile primary cilium
G0:0001882	6	nucleoside binding
G0:2000059	6	negative regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process
G0:0000930	6	gamma-tubulin complex
G0:0016593	6	Cdc73/Paf1 complex
G0:0016813	6	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides
G0:0008131	6	primary amine oxidase activity
G0:0072089	6	stem cell proliferation
G0:0050428	6	3'-phosphoadenosine 5'-phosphosulfate biosynthetic process
G0:0051569	6	regulation of histone H3-K4 methylation
G0:0051561	6	positive regulation of mitochondrial calcium ion concentration

G0:0042308	6	negative regulation of protein import into nucleus
G0:0006546	6	glycine catabolic process
G0:0050672	6	negative regulation of lymphocyte proliferation
G0:0050881	6	musculoskeletal movement
G0:0072583	6	clathrin-mediated endocytosis
G0:0060510	6	Type II pneumocyte differentiation
G0:0042471	6	ear morphogenesis
G0:0022027	6	interkinetic nuclear migration
G0:0022029	6	telencephalon cell migration
G0:0071514	6	genetic imprinting
G0:0060235	6	lens induction in camera-type eye
G0:0007614	6	short-term memory
G0:0002260	6	lymphocyte homeostasis
G0:0004630	6	phospholipase D activity
G0:0021884	6	forebrain neuron development
G0:0051247	6	positive regulation of protein metabolic process
G0:0010761	6	fibroblast migration
G0:0033210	6	leptin-mediated signaling pathway
G0:0016081	6	synaptic vesicle docking involved in exocytosis
G0:0043297	6	apical junction assembly
G0:0052033	6	pathogen-associated molecular pattern dependent induction by symbiont of
host innate immune response		
G0:0003416	6	endochondral bone growth
G0:0047372	6	acylglycerol lipase activity
G0:0070914	6	UV-damage excision repair
G0:0085029	6	extracellular matrix assembly
G0:2000288	6	positive regulation of myoblast proliferation
G0:0043312	6	neutrophil degranulation
G0:0097104	6	postsynaptic membrane assembly
G0:0060252	6	positive regulation of glial cell proliferation
G0:0007635	6	chemosensory behavior
G0:0048406	6	nerve growth factor binding
G0:0045046	6	protein import into peroxisome membrane
G0:0000729	6	DNA double-strand break processing
G0:0002446	6	neutrophil mediated immunity
G0:0050658	6	RNA transport
G0:0008020	6	G-protein coupled photoreceptor activity
G0:0031497	6	chromatin assembly
G0:0051014	6	actin filament severing
G0:0007406	6	negative regulation of neuroblast proliferation
G0:0033539	6	fatty acid beta-oxidation using acyl-CoA dehydrogenase
G0:0008517	6	folic acid transporter activity
G0:0007182	6	common-partner SMAD protein phosphorylation
G0:0005587	6	collagen type IV trimer
G0:0055013	6	cardiac muscle cell development
G0:0055012	6	ventricular cardiac muscle cell differentiation
G0:2000323	6	negative regulation of glucocorticoid receptor signaling pathway
G0:0051205	6	protein insertion into membrane
G0:0046870	6	cadmium ion binding
G0:0007379	6	segment specification
G0:0060539	6	diaphragm development
G0:0033130	6	acetylcholine receptor binding
G0:0050862	6	positive regulation of T cell receptor signaling pathway
G0:0015886	6	heme transport
G0:0097440	6	apical dendrite
G0:0018344	6	protein geranylgeranylation
G0:0008121	6	ubiquinol-cytochrome-c reductase activity
G0:0005223	6	intracellular cGMP activated cation channel activity
G0:1901379	6	regulation of potassium ion transmembrane transport
G0:0048024	6	regulation of mRNA splicing, via spliceosome
G0:0034144	6	negative regulation of toll-like receptor 4 signaling pathway
G0:0034145	6	positive regulation of toll-like receptor 4 signaling pathway
G0:0030867	6	rough endoplasmic reticulum membrane
G0:0042584	6	chromaffin granule membrane
G0:0046069	6	cGMP catabolic process
G0:0030130	6	clathrin coat of trans-Golgi network vesicle
G0:0043951	6	negative regulation of cAMP-mediated signaling
G0:0019082	6	viral protein processing
G0:0016461	6	unconventional myosin complex
G0:0031726	6	CCR1 chemokine receptor binding
G0:0005682	6	U5 snRNP
G0:0044292	6	dendrite terminus
G0:0044291	6	cell-cell contact zone
G0:2001020	6	regulation of response to DNA damage stimulus
G0:0008889	6	glycerophosphodiester phosphodiesterase activity

G0:0019215	6	intermediate filament binding
G0:0070087	6	chromo shadow domain binding
G0:0032593	6	insulin-responsive compartment
G0:0070286	6	axonemal dynein complex assembly
G0:0032400	6	melanosome localization
G0:0044458	6	motile cilium assembly
G0:0004415	6	hyaluronoglucosaminidase activity
G0:0034393	6	positive regulation of smooth muscle cell apoptotic process
G0:0032873	6	negative regulation of stress-activated MAPK cascade
G0:0072177	6	mesonephric duct development
G0:0001957	6	intramembranous ossification
G0:0003149	6	membranous septum morphogenesis
G0:0090279	6	regulation of calcium ion import
G0:0017069	6	snRNA binding
G0:0048505	6	regulation of timing of cell differentiation
G0:0060340	6	positive regulation of type I interferon-mediated signaling pathway
G0:0050847	6	progesterone receptor signaling pathway
G0:0050848	6	regulation of calcium-mediated signaling
G0:0001956	6	positive regulation of neurotransmitter secretion
G0:0046974	6	histone methyltransferase activity (H3-K9 specific)
G0:0060789	6	hair follicle placode formation
G0:0004439	6	phosphatidylinositol-4,5-bisphosphate 5-phosphatase activity
G0:0004438	6	phosphatidylinositol-3-phosphatase activity
G0:0051150	6	regulation of smooth muscle cell differentiation
G0:0021860	6	pyramidal neuron development
G0:0035640	6	exploration behavior
G0:0015824	6	proline transport
G0:0015825	6	L-serine transport
G0:0010535	6	positive regulation of activation of JAK2 kinase activity
G0:0035254	6	glutamate receptor binding
G0:0033178	6	proton-transporting two-sector ATPase complex, catalytic domain
G0:2001275	6	positive regulation of glucose import in response to insulin stimulus
G0:0031209	6	SCAR complex
G0:0034259	6	negative regulation of Rho GTPase activity
G0:0031402	6	sodium ion binding
G0:0055102	6	lipase inhibitor activity
G0:0005663	6	DNA replication factor C complex
G0:0016043	6	cellular component organization
G0:0010830	6	regulation of myotube differentiation
G0:0010839	6	negative regulation of keratinocyte proliferation
G0:0010614	6	negative regulation of cardiac muscle hypertrophy
G0:0005623	6	cell
G0:0071229	6	cellular response to acid
G0:0008064	6	regulation of actin polymerization or depolymerization
G0:0014033	6	neural crest cell differentiation
G0:0051347	6	positive regulation of transferase activity
G0:0051346	6	negative regulation of hydrolase activity
G0:0002523	6	leukocyte migration involved in inflammatory response
G0:0015074	6	DNA integration
G0:0046578	6	regulation of Ras protein signal transduction
G0:0038083	6	peptidyl-tyrosine autophosphorylation
G0:0035234	6	ectopic germ cell programmed cell death
G0:0016528	6	sarcoplasm
G0:0016255	6	attachment of GPI anchor to protein
G0:0017121	6	phospholipid scrambling
G0:0072205	6	metanephric collecting duct development
G0:0004969	6	histamine receptor activity
G0:0031264	6	death-inducing signaling complex
G0:0031265	6	CD95 death-inducing signaling complex
G0:0002064	6	epithelial cell development
G0:0004030	6	aldehyde dehydrogenase [NAD(P)+] activity
G0:0045499	6	chemorepellent activity
G0:0032811	6	negative regulation of epinephrine secretion
G0:0032813	6	tumor necrosis factor receptor superfamily binding
G0:0071875	6	adrenergic receptor signaling pathway
G0:0055123	6	digestive system development
G0:0000808	6	origin recognition complex
G0:0097345	6	mitochondrial outer membrane permeabilization
G0:0097208	6	alveolar lamellar body
G0:0061351	6	neural precursor cell proliferation
G0:0010818	6	T cell chemotaxis
G0:0060406	6	positive regulation of penile erection
G0:0005979	6	regulation of glycogen biosynthetic process
G0:0006777	6	Mo-molybdopterin cofactor biosynthetic process
G0:1902305	6	regulation of sodium ion transmembrane transport

G0:2000778	6	positive regulation of interleukin-6 secretion
G0:2000772	6	regulation of cellular senescence
G0:0001818	6	negative regulation of cytokine production
G0:0046512	6	sphingosine biosynthetic process
G0:0031466	6	Cul5-RING ubiquitin ligase complex
G0:0042608	6	T cell receptor binding
G0:0070670	6	response to interleukin-4
G0:0070419	6	nonhomologous end joining complex
G0:0034351	6	negative regulation of glial cell apoptotic process
G0:0015840	6	urea transport
G0:0035004	6	phosphatidylinositol 3-kinase activity
G0:0042923	6	neuropeptide binding
G0:0060463	6	lung lobe morphogenesis
G0:0072559	6	NLRP3 inflammasome complex
G0:0003158	6	endothelium development
G0:0008028	6	monocarboxylic acid transmembrane transporter activity
G0:0051302	6	regulation of cell division
G0:0021695	6	cerebellar cortex development
G0:0003085	6	negative regulation of systemic arterial blood pressure
G0:0003081	6	regulation of systemic arterial blood pressure by renin-angiotensin
G0:0045842	6	positive regulation of mitotic metaphase/anaphase transition
G0:0006563	6	L-serine metabolic process
G0:0035767	6	endothelial cell chemotaxis
G0:0009253	6	peptidoglycan catabolic process
G0:0002024	6	diet induced thermogenesis
G0:0033211	6	adiponectin-activated signaling pathway
G0:0004075	6	biotin carboxylase activity
G0:0032725	6	positive regulation of granulocyte macrophage colony-stimulating factor
production		
G0:0005851	6	eukaryotic translation initiation factor 2B complex
G0:0015232	6	heme transporter activity
G0:0035865	6	cellular response to potassium ion
G0:0006004	6	fucose metabolic process
G0:0048793	6	pronephros development
G0:0031639	6	plasminogen activation
G0:2000008	6	regulation of protein localization to cell surface
G0:2000009	6	negative regulation of protein localization to cell surface
G0:0019236	6	response to pheromone
G0:0043089	6	positive regulation of Cdc42 GTPase activity
G0:0060586	6	multicellular organismal iron ion homeostasis
G0:0097527	6	necroptotic signaling pathway
G0:0009584	6	detection of visible light
G0:0048261	6	negative regulation of receptor-mediated endocytosis
G0:0019534	6	toxin transporter activity
G0:0070182	6	DNA polymerase binding
G0:2000271	6	positive regulation of fibroblast apoptotic process
G0:2000279	6	negative regulation of DNA biosynthetic process
G0:0042791	6	5S class rRNA transcription from RNA polymerase III type 1 promoter
G0:0033619	6	membrane protein proteolysis
G0:0051983	6	regulation of chromosome segregation
G0:0061512	6	protein localization to cilium
G0:0006068	6	ethanol catabolic process
G0:0003956	6	NAD(P)+-protein-arginine ADP-ribosyltransferase activity
G0:0045630	6	positive regulation of T-helper 2 cell differentiation
G0:0043576	6	regulation of respiratory gaseous exchange
G0:0060054	6	positive regulation of epithelial cell proliferation involved in wound
healing		
G0:0006473	6	protein acetylation
G0:0046134	6	pyrimidine nucleoside biosynthetic process
G0:0048864	6	stem cell development
G0:2001300	6	lipoxin metabolic process
G0:0048247	6	lymphocyte chemotaxis
G0:0031643	6	positive regulation of myelination
G0:0045588	6	positive regulation of gamma-delta T cell differentiation
G0:0051552	6	flavone metabolic process
G0:0044183	6	protein binding involved in protein folding
G0:0048842	6	positive regulation of axon extension involved in axon guidance
G0:0006013	6	mannose metabolic process
G0:0006266	6	DNA ligation
G0:0043237	6	laminin-1 binding
G0:0006047	6	UDP-N-acetylglucosamine metabolic process
G0:0009792	6	embryo development ending in birth or egg hatching
G0:0010642	6	negative regulation of platelet-derived growth factor receptor signaling
pathway		
G0:0048643	6	positive regulation of skeletal muscle tissue development

G0:0007143	6	female meiotic division
G0:0048645	6	organ formation
G0:1901381	6	positive regulation of potassium ion transmembrane transport
G0:0016589	6	NURF complex
G0:0034214	6	protein hexamerization
G0:0030915	6	Smc5-Smc6 complex
G0:0060013	6	righting reflex
G0:0046487	6	glyoxylate metabolic process
G0:0046483	6	heterocycle metabolic process
G0:0045823	6	positive regulation of heart contraction
G0:0035965	6	cardiolipin acyl-chain remodeling
G0:0008140	6	cAMP response element binding protein binding
G0:0000127	6	transcription factor TFIIIC complex
G0:0008329	6	signaling pattern recognition receptor activity
G0:0045217	6	cell-cell junction maintenance
G0:2000188	6	regulation of cholesterol homeostasis
G0:0018401	6	peptidyl-proline hydroxylation to 4-hydroxy-L-proline
G0:0051573	6	negative regulation of histone H3-K9 methylation
G0:0010458	6	exit from mitosis
G0:0010457	6	centriole-centriole cohesion
G0:0030213	6	hyaluronan biosynthetic process
G0:0016447	6	somatic recombination of immunoglobulin gene segments
G0:0061003	6	positive regulation of dendritic spine morphogenesis
G0:0031167	6	rRNA methylation
G0:0004176	6	ATP-dependent peptidase activity
G0:0036302	6	atrioventricular canal development
G0:0006997	6	nucleus organization
G0:0003341	6	cilium movement
G0:0016308	6	1-phosphatidylinositol-4-phosphate 5-kinase activity
G0:0050957	6	equilibrioception
G0:0042788	6	polysomal ribosome
G0:0007064	6	mitotic sister chromatid cohesion
G0:0043497	6	regulation of protein heterodimerization activity
G0:0016462	6	pyrophosphatase activity
G0:0010941	6	regulation of cell death
G0:0002639	6	positive regulation of immunoglobulin production
G0:0030957	6	Tat protein binding
G0:0014808	6	release of sequestered calcium ion into cytosol by sarcoplasmic reticulum
G0:0032964	6	collagen biosynthetic process
G0:0007044	6	cell-substrate junction assembly
G0:0007041	6	lysosomal transport
G0:0045616	6	regulation of keratinocyte differentiation
G0:0015695	6	organic cation transport
G0:0016342	6	catenin complex
G0:0015833	6	peptide transport
G0:0042428	6	serotonin metabolic process
G0:0042423	6	catecholamine biosynthetic process
G0:0015194	6	L-serine transmembrane transporter activity
G0:0001561	6	fatty acid alpha-oxidation
G0:0031102	5	neuron projection regeneration
G0:0097178	5	ruffle assembly
G0:0020027	5	hemoglobin metabolic process
G0:0060267	5	positive regulation of respiratory burst
G0:0046654	5	tetrahydrofolate biosynthetic process
G0:0006620	5	posttranslational protein targeting to membrane
G0:0004445	5	inositol-polyphosphate 5-phosphatase activity
G0:0004994	5	somatostatin receptor activity
G0:0004668	5	protein-arginine deiminase activity
G0:0018101	5	protein citrullination
G0:0051271	5	negative regulation of cellular component movement
G0:0010757	5	negative regulation of plasminogen activation
G0:0010756	5	positive regulation of plasminogen activation
G0:0002903	5	negative regulation of B cell apoptotic process
G0:0006102	5	isocitrate metabolic process
G0:0090286	5	cytoskeletal anchoring at nuclear membrane
G0:0090281	5	negative regulation of calcium ion import
G0:0035860	5	glial cell-derived neurotrophic factor receptor signaling pathway
G0:0008200	5	ion channel inhibitor activity
G0:0048733	5	sebaceous gland development
G0:0005105	5	type 1 fibroblast growth factor receptor binding
G0:0009108	5	coenzyme biosynthetic process
G0:2000107	5	negative regulation of leukocyte apoptotic process
G0:0036159	5	inner dynein arm assembly
G0:0036158	5	outer dynein arm assembly
G0:0005865	5	striated muscle thin filament

G0:0016628	5	oxidoreductase activity, acting on the CH-CH group of donors, NAD or NADP as acceptor
G0:0008508	5	bile acid:sodium symporter activity
G0:0045653	5	negative regulation of megakaryocyte differentiation
G0:0070507	5	regulation of microtubule cytoskeleton organization
G0:0097153	5	cysteine-type endopeptidase activity involved in apoptotic process
G0:0007195	5	adenylate cyclase-inhibiting dopamine receptor signaling pathway
G0:0006642	5	triglyceride mobilization
G0:0072284	5	metanephric S-shaped body morphogenesis
G0:2001199	5	negative regulation of dendritic cell differentiation
G0:0006924	5	activation-induced cell death of T cells
G0:0004645	5	phosphorylase activity
G0:0019871	5	sodium channel inhibitor activity
G0:0010737	5	protein kinase A signaling
G0:0001696	5	gastric acid secretion
G0:0010739	5	positive regulation of protein kinase A signaling
G0:0021782	5	glial cell development
G0:1901800	5	positive regulation of proteasomal protein catabolic process
G0:0033265	5	choline binding
G0:0045077	5	negative regulation of interferon-gamma biosynthetic process
G0:0050916	5	sensory perception of sweet taste
G0:0086011	5	membrane repolarization during action potential
G0:0006122	5	mitochondrial electron transport, ubiquinol to cytochrome c
G0:0060122	5	inner ear receptor stereocilium organization
G0:0002318	5	myeloid progenitor cell differentiation
G0:0051047	5	positive regulation of secretion
G0:0001758	5	retinal dehydrogenase activity
G0:0032410	5	negative regulation of transporter activity
G0:0032411	5	positive regulation of transporter activity
G0:0046540	5	U4/U6 x U5 tri-snRNP complex
G0:0000403	5	Y-form DNA binding
G0:0070296	5	sarcoplasmic reticulum calcium ion transport
G0:0072584	5	caveolin-mediated endocytosis
G0:0071169	5	establishment of protein localization to chromatin
G0:0050878	5	regulation of body fluid levels
G0:0050871	5	positive regulation of B cell activation
G0:0006167	5	AMP biosynthetic process
G0:0030104	5	water homeostasis
G0:0006662	5	glycerol ether metabolic process
G0:0000796	5	condensin complex
G0:0044342	5	type B pancreatic cell proliferation
G0:0071374	5	cellular response to parathyroid hormone stimulus
G0:0008519	5	ammonium transmembrane transporter activity
G0:0050801	5	ion homeostasis
G0:0016015	5	morphogen activity
G0:0016019	5	peptidoglycan receptor activity
G0:0006497	5	protein lipidation
G0:0005672	5	transcription factor TFIIA complex
G0:0022900	5	electron transport chain
G0:2001014	5	regulation of skeletal muscle cell differentiation
G0:0001774	5	microglial cell activation
G0:0008090	5	retrograde axon cargo transport
G0:0070761	5	pre-snoRNP complex
G0:0071493	5	cellular response to UV-B
G0:0002573	5	myeloid leukocyte differentiation
G0:0050856	5	regulation of T cell receptor signaling pathway
G0:0033129	5	positive regulation of histone phosphorylation
G0:0047184	5	1-acylglycerophosphocholine O-acyltransferase activity
G0:0030346	5	protein phosphatase 2B binding
G0:0030345	5	structural constituent of tooth enamel
G0:0051891	5	positive regulation of cardioblast differentiation
G0:0061154	5	endothelial tube morphogenesis
G0:0045581	5	negative regulation of T cell differentiation
G0:0043031	5	negative regulation of macrophage activation
G0:0006686	5	sphingomyelin biosynthetic process
G0:0006684	5	sphingomyelin metabolic process
G0:0006685	5	sphingomyelin catabolic process
G0:1902017	5	regulation of cilium assembly
G0:0004689	5	phosphorylase kinase activity
G0:0032502	5	developmental process
G0:0045578	5	negative regulation of B cell differentiation
G0:0061304	5	retinal blood vessel morphogenesis
G0:0051971	5	positive regulation of transmission of nerve impulse
G0:0030579	5	ubiquitin-dependent SMAD protein catabolic process
G0:0005432	5	calcium:sodium antiporter activity

G0:0086036	5	regulation of cardiac muscle cell membrane potential
G0:0004749	5	ribose phosphate diphosphokinase activity
G0:0042795	5	snRNA transcription from RNA polymerase II promoter
G0:0006104	5	succinyl-CoA metabolic process
G0:0070700	5	BMP receptor binding
G0:0042866	5	pyruvate biosynthetic process
G0:0004024	5	alcohol dehydrogenase activity, zinc-dependent
G0:0051414	5	response to cortisol
G0:0000445	5	THO complex part of transcription export complex
G0:0051379	5	epinephrine binding
G0:0032452	5	histone demethylase activity
G0:0032454	5	histone demethylase activity (H3-K9 specific)
G0:0010694	5	positive regulation of alkaline phosphatase activity
G0:0019911	5	structural constituent of myelin sheath
G0:0016202	5	regulation of striated muscle tissue development
G0:0051707	5	response to other organism
G0:0042403	5	thyroid hormone metabolic process
G0:0048305	5	immunoglobulin secretion
G0:0007262	5	STAT protein import into nucleus
G0:0036016	5	cellular response to interleukin-3
G0:0006883	5	cellular sodium ion homeostasis
G0:0021853	5	cerebral cortex GABAergic interneuron migration
G0:0050920	5	regulation of chemotaxis
G0:0034656	5	nucleobase-containing small molecule catabolic process
G0:0060363	5	cranial suture morphogenesis
G0:0006725	5	cellular aromatic compound metabolic process
G0:2001054	5	negative regulation of mesenchymal cell apoptotic process
G0:0008054	5	cyclin catabolic process
G0:0008588	5	release of cytoplasmic sequestered NF-kappaB
G0:0008273	5	calcium, potassium:sodium antiporter activity
G0:0008278	5	cohesin complex
G0:2000727	5	positive regulation of cardiac muscle cell differentiation
G0:0000460	5	maturation of 5.8S rRNA
G0:0000462	5	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
G0:0032308	5	positive regulation of prostaglandin secretion
G0:0071985	5	multivesicular body sorting pathway
G0:0071458	5	integral component of cytoplasmic side of endoplasmic reticulum membrane
G0:0001842	5	neural fold formation
G0:0051764	5	actin crosslink formation
G0:0006534	5	cysteine metabolic process
G0:0006537	5	glutamate biosynthetic process
G0:0004977	5	melanocortin receptor activity
G0:0022626	5	cytosolic ribosome
G0:0018216	5	peptidyl-arginine methylation
G0:0005375	5	copper ion transmembrane transporter activity
G0:0004028	5	3-chloroallyl aldehyde dehydrogenase activity
G0:0006518	5	peptide metabolic process
G0:0016075	5	rRNA catabolic process
G0:0008504	5	monoamine transmembrane transporter activity
G0:0071248	5	cellular response to metal ion
G0:0060430	5	lung saccule development
G0:1900028	5	negative regulation of ruffle assembly
G0:1900029	5	positive regulation of ruffle assembly
G0:0015816	5	glycine transport
G0:0010828	5	positive regulation of glucose transport
G0:0051938	5	L-glutamate import
G0:0071455	5	cellular response to hyperoxia
G0:0072207	5	metanephric epithelium development
G0:0018027	5	peptidyl-lysine dimethylation
G0:0045322	5	unmethylated CpG binding
G0:0045657	5	positive regulation of monocyte differentiation
G0:0006705	5	mineralocorticoid biosynthetic process
G0:0032364	5	oxygen homeostasis
G0:0019957	5	C-C chemokine binding
G0:0010564	5	regulation of cell cycle process
G0:0071474	5	cellular hyperosmotic response
G0:0070300	5	phosphatidic acid binding
G0:0032585	5	multivesicular body membrane
G0:0043587	5	tongue morphogenesis
G0:0017111	5	nucleoside-triphosphatase activity
G0:0003708	5	retinoic acid receptor activity
G0:0006555	5	methionine metabolic process
G0:0006552	5	leucine catabolic process
G0:0004957	5	prostaglandin E receptor activity

G0:0031584	5	activation of phospholipase D activity
G0:0060665	5	regulation of branching involved in salivary gland morphogenesis by mesenchymal-epithelial signaling
G0:0060666	5	dichotomous subdivision of terminal units involved in salivary gland branching
G0:0060662	5	salivary gland cavitation
G0:0070842	5	aggresome assembly
G0:0022602	5	ovulation cycle process
G0:0034987	5	immunoglobulin receptor binding
G0:0018230	5	peptidyl-L-cysteine S-palmitoylation
G0:1990111	5	spermatoproteasome complex
G0:0004046	5	aminoacylase activity
G0:0004047	5	aminomethyltransferase activity
G0:1902430	5	negative regulation of beta-amyloid formation
G0:0010793	5	regulation of mRNA export from nucleus
G0:0007423	5	sensory organ development
G0:0008622	5	epsilon DNA polymerase complex
G0:1900181	5	negative regulation of protein localization to nucleus
G0:0000813	5	ESCRT I complex
G0:0003139	5	secondary heart field specification
G0:0006353	5	DNA-templated transcription, termination
G0:0051488	5	activation of anaphase-promoting complex activity
G0:0007098	5	centrosome cycle
G0:0050684	5	regulation of mRNA processing
G0:0001071	5	nucleic acid binding transcription factor activity
G0:0002666	5	positive regulation of T cell tolerance induction
G0:0016469	5	proton-transporting two-sector ATPase complex
G0:0015106	5	bicarbonate transmembrane transporter activity
G0:0030516	5	regulation of axon extension
G0:0030284	5	estrogen receptor activity
G0:0034392	5	negative regulation of smooth muscle cell apoptotic process
G0:0002862	5	negative regulation of inflammatory response to antigenic stimulus
G0:0002860	5	positive regulation of natural killer cell mediated cytotoxicity directed against tumor cell target
G0:0070097	5	delta-catenin binding
G0:0045329	5	carnitine biosynthetic process
G0:0030121	5	AP-1 adaptor complex
G0:0046500	5	S-adenosylmethionine metabolic process
G0:0017176	5	phosphatidylinositol N-acetylglucosaminyltransferase activity
G0:0006734	5	NADH metabolic process
G0:0015889	5	cobalamin transport
G0:0006572	5	tyrosine catabolic process
G0:0005007	5	fibroblast growth factor-activated receptor activity
G0:0030911	5	TPR domain binding
G0:0051122	5	hepoxilin biosynthetic process
G0:0018963	5	phthalate metabolic process
G0:0040012	5	regulation of locomotion
G0:0032754	5	positive regulation of interleukin-5 production
G0:0046339	5	diacylglycerol metabolic process
G0:0030297	5	transmembrane receptor protein tyrosine kinase activator activity
G0:0060850	5	regulation of transcription involved in cell fate commitment
G0:0051461	5	positive regulation of corticotropin secretion
G0:0005827	5	polar microtubule
G0:0005828	5	kinetochore microtubule
G0:0005927	5	muscle tendon junction
G0:0045820	5	negative regulation of glycolytic process
G0:0030061	5	mitochondrial crista
G0:0005219	5	ryanodine-sensitive calcium-release channel activity
G0:0008038	5	neuron recognition
G0:0014061	5	regulation of norepinephrine secretion
G0:0031622	5	positive regulation of fever generation
G0:0060290	5	transdifferentiation
G0:0042719	5	mitochondrial intermembrane space protein transporter complex
G0:0071253	5	connexin binding
G0:0048671	5	negative regulation of collateral sprouting
G0:0022414	5	reproductive process
G0:0009744	5	response to sucrose
G0:0019222	5	regulation of metabolic process
G0:0043546	5	molybdopterin cofactor binding
G0:1901522	5	positive regulation of transcription from RNA polymerase II promoter involved in cellular response to chemical stimulus
G0:0031013	5	troponin I binding
G0:0060046	5	regulation of acrosome reaction
G0:0060040	5	retinal bipolar neuron differentiation
G0:0060627	5	regulation of vesicle-mediated transport

G0:0001222	5	transcription corepressor binding
G0:1902475	5	L-alpha-amino acid transmembrane transport
G0:0000176	5	nuclear exosome (RNase complex)
G0:0045261	5	proton-transporting ATP synthase complex, catalytic core F(1)
G0:0016242	5	negative regulation of macroautophagy
G0:0032736	5	positive regulation of interleukin-13 production
G0:0072488	5	ammonium transmembrane transport
G0:0060831	5	smoothened signaling pathway involved in dorsal/ventral neural tube patterning
G0:0060830	5	ciliary receptor clustering involved in smoothened signaling pathway
G0:0033600	5	negative regulation of mammary gland epithelial cell proliferation
G0:0061133	5	endopeptidase activator activity
G0:0010738	5	regulation of protein kinase A signaling
G0:0002819	5	regulation of adaptive immune response
G0:0090315	5	negative regulation of protein targeting to membrane
G0:0046923	5	ER retention sequence binding
G0:0002821	5	positive regulation of adaptive immune response
G0:0050917	5	sensory perception of umami taste
G0:0071907	5	determination of digestive tract left/right asymmetry
G0:0042382	5	paraspeckles
G0:0035093	5	spermatogenesis, exchange of chromosomal proteins
G0:0016556	5	mRNA modification
G0:0042289	5	MHC class II protein binding
G0:0019863	5	IgE binding
G0:0060029	5	convergent extension involved in organogenesis
G0:0060023	5	soft palate development
G0:0001880	5	Mullerian duct regression
G0:0033119	5	negative regulation of RNA splicing
G0:0008171	5	O-methyltransferase activity
G0:0003831	5	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase activity
G0:0042908	5	xenobiotic transport
G0:0032714	5	negative regulation of interleukin-5 production
G0:0032713	5	negative regulation of interleukin-4 production
G0:0051525	5	NFAT protein binding
G0:0001783	5	B cell apoptotic process
G0:0007035	5	vacuolar acidification
G0:0030240	5	skeletal muscle thin filament assembly
G0:0097186	5	amelogenesis
G0:0004784	5	superoxide dismutase activity
G0:0045334	5	clathrin-coated endocytic vesicle
G0:0038031	5	non-canonical Wnt signaling pathway via JNK cascade
G0:0032057	5	negative regulation of translational initiation in response to stress
G0:0035881	5	amacrine cell differentiation
G0:0045762	5	positive regulation of adenylate cyclase activity
G0:0070389	5	chaperone cofactor-dependent protein refolding
G0:0045836	5	positive regulation of meiosis
G0:0045838	5	positive regulation of membrane potential
G0:2000601	5	positive regulation of Arp2/3 complex-mediated actin nucleation
G0:0065004	5	protein-DNA complex assembly
G0:0008158	5	hedgehog receptor activity
G0:0000137	5	Golgi cis cisterna
G0:0000138	5	Golgi trans cisterna
G0:0004331	5	fructose-2,6-bisphosphate 2-phosphatase activity
G0:0008628	5	hormone-mediated apoptotic signaling pathway
G0:0045591	5	positive regulation of regulatory T cell differentiation
G0:0051098	5	regulation of binding
G0:0051549	5	positive regulation of keratinocyte migration
G0:0010463	5	mesenchymal cell proliferation
G0:0051400	5	BH domain binding
G0:0019212	5	phosphatase inhibitor activity
G0:0000303	5	response to superoxide
G0:1900118	5	negative regulation of execution phase of apoptosis
G0:0060761	5	negative regulation of response to cytokine stimulus
G0:0060763	5	mammary duct terminal end bud growth
G0:0042609	5	CD4 receptor binding
G0:0050897	5	cobalt ion binding
G0:0032036	5	myosin heavy chain binding
G0:0060996	5	dendritic spine development
G0:0060575	5	intestinal epithelial cell differentiation
G0:0060576	5	intestinal epithelial cell development
G0:0046321	5	positive regulation of fatty acid oxidation
G0:0046323	5	glucose import
G0:0002768	5	immune response-regulating cell surface receptor signaling pathway
G0:0004952	5	dopamine neurotransmitter receptor activity

G0:0035336	5	long-chain fatty-acyl-CoA metabolic process
G0:0030033	5	microvillus assembly
G0:0060684	5	epithelial-mesenchymal cell signaling
G0:0002181	5	cytoplasmic translation
G0:0035562	5	negative regulation of chromatin binding
G0:0090141	5	positive regulation of mitochondrial fission
G0:0032205	5	negative regulation of telomere maintenance
G0:0044233	5	ER-mitochondrion membrane contact site
G0:0071539	5	protein localization to centrosome
G0:2000427	5	positive regulation of apoptotic cell clearance
G0:0070221	5	sulfide oxidation, using sulfide:quinone oxidoreductase
G0:0015871	5	choline transport
G0:0071280	5	cellular response to copper ion
G0:0033554	5	cellular response to stress
G0:0035925	5	mRNA 3'-UTR AU-rich region binding
G0:1903204	5	negative regulation of oxidative stress-induced neuron death
G0:0060744	5	mammary gland branching involved in thelarche
G0:0050774	5	negative regulation of dendrite morphogenesis
G0:0005742	5	mitochondrial outer membrane translocase complex
G0:0051823	5	regulation of synapse structural plasticity
G0:0070295	5	renal water absorption
G0:0046951	5	ketone body biosynthetic process
G0:0031904	5	endosome lumen
G0:0001539	5	cilium or flagellum-dependent cell motility
G0:0004559	5	alpha-mannosidase activity
G0:0005499	5	vitamin D binding
G0:0003357	5	noradrenergic neuron differentiation
G0:0019800	5	peptide cross-linking via chondroitin 4-sulfate glycosaminoglycan
G0:0055062	5	phosphate ion homeostasis
G0:0002740	5	negative regulation of cytokine secretion involved in immune response
G0:0060736	5	prostate gland growth
G0:0035356	5	cellular triglyceride homeostasis
G0:0035357	5	peroxisome proliferator activated receptor signaling pathway
G0:0048742	5	regulation of skeletal muscle fiber development
G0:0016709	5	oxidoreductase activity, acting on paired donors, with incorporation or
		reduction of molecular oxygen, NAD(P)H as one donor, and incorporation of one atom of oxygen
G0:0070937	5	CRD-mediated mRNA stability complex
G0:0051584	5	regulation of dopamine uptake involved in synaptic transmission
G0:0035902	5	response to immobilization stress
G0:0016671	5	oxidoreductase activity, acting on a sulfur group of donors, disulfide as
		acceptor
G0:0060236	5	regulation of mitotic spindle organization
G0:0042129	5	regulation of T cell proliferation
G0:0010954	5	positive regulation of protein processing
G0:0043535	5	regulation of blood vessel endothelial cell migration
G0:0097342	5	riposome
G0:0004499	5	N,N-dimethylaniline monooxygenase activity
G0:0001517	5	N-acetylglucosamine 6-O-sulfotransferase activity
G0:0001515	5	opioid peptide activity
G0:0060336	5	negative regulation of interferon-gamma-mediated signaling pathway
G0:0021554	5	optic nerve development
G0:0010764	5	negative regulation of fibroblast migration
G0:0038180	5	nerve growth factor signaling pathway
G0:0006398	5	histone mRNA 3'-end processing
G0:1902262	5	apoptotic process involved in patterning of blood vessels
G0:0042538	5	hyperosmotic salinity response
G0:0042536	5	negative regulation of tumor necrosis factor biosynthetic process
G0:0042531	5	positive regulation of tyrosine phosphorylation of STAT protein
G0:0044241	5	lipid digestion
G0:0042989	5	sequestering of actin monomers
G0:2000177	5	regulation of neural precursor cell proliferation
G0:2000178	5	negative regulation of neural precursor cell proliferation
G0:0003254	5	regulation of membrane depolarization
G0:0021960	5	anterior commissure morphogenesis
G0:0045606	5	positive regulation of epidermal cell differentiation
G0:0060259	5	regulation of feeding behavior
G0:0060706	5	cell differentiation involved in embryonic placenta development
G0:0090370	5	negative regulation of cholesterol efflux
G0:0060253	5	negative regulation of glial cell proliferation
G0:0033033	5	negative regulation of myeloid cell apoptotic process
G0:0048026	5	positive regulation of mRNA splicing, via spliceosome
G0:0004614	5	phosphoglucomutase activity
G0:2000344	5	positive regulation of acrosome reaction
G0:0001878	5	response to yeast
G0:0090331	5	negative regulation of platelet aggregation

G0:0071305	5	cellular response to vitamin D
G0:0033234	5	negative regulation of protein sumoylation
G0:0048562	5	embryonic organ morphogenesis
G0:0043140	5	ATP-dependent 3'-5' DNA helicase activity
G0:0005131	5	growth hormone receptor binding
G0:0050656	5	3'-phosphoadenosine 5'-phosphosulfate binding
G0:0005168	5	neurotrophin TRKA receptor binding
G0:0015057	5	thrombin receptor activity
G0:0051013	5	microtubule severing
G0:0032914	5	positive regulation of transforming growth factor beta1 production
G0:0070245	5	positive regulation of thymocyte apoptotic process
G0:0046085	5	adenosine metabolic process
G0:0097169	5	AIM2 inflammasome complex
G0:0050792	5	regulation of viral process
G0:0010917	5	negative regulation of mitochondrial membrane potential
G0:1902041	5	regulation of extrinsic apoptotic signaling pathway via death domain receptors
G0:0031394	5	positive regulation of prostaglandin biosynthetic process
G0:0045061	5	thymic T cell selection
G0:0004459	5	L-lactate dehydrogenase activity
G0:0043931	5	ossification involved in bone maturation
G0:0048048	5	embryonic eye morphogenesis
G0:0004185	5	serine-type carboxypeptidase activity
G0:0004679	5	AMP-activated protein kinase activity
G0:0021517	5	ventral spinal cord development
G0:0046873	5	metal ion transmembrane transporter activity
G0:0071321	5	cellular response to cGMP
G0:0003184	5	pulmonary valve morphogenesis
G0:0003180	5	aortic valve morphogenesis
G0:0042578	5	phosphoric ester hydrolase activity
G0:0050869	5	negative regulation of B cell activation
G0:0086006	5	voltage-gated sodium channel activity involved in cardiac muscle cell action potential
G0:0009804	5	coumarin metabolic process
G0:0004865	5	protein serine/threonine phosphatase inhibitor activity
G0:0097449	5	astrocyte projection
G0:0002328	5	pro-B cell differentiation
G0:0048729	5	tissue morphogenesis
G0:0002326	5	B cell lineage commitment
G0:0009113	5	purine nucleobase biosynthetic process
G0:0071156	5	regulation of cell cycle arrest
G0:0019439	5	aromatic compound catabolic process
G0:0043426	5	MRF binding
G0:0034498	5	early endosome to Golgi transport
G0:0034720	5	histone H3-K4 demethylation
G0:0050805	5	negative regulation of synaptic transmission
G0:0006657	5	CDP-choline pathway
G0:0030134	5	ER to Golgi transport vesicle
G0:0035456	5	response to interferon-beta
G0:0006900	5	membrane budding
G0:0033014	5	tetrapyrrole biosynthetic process
G0:0044351	5	macropinocytosis
G0:0019887	5	protein kinase regulator activity
G0:0071340	5	skeletal muscle acetylcholine-gated channel clustering
G0:1901741	5	positive regulation of myoblast fusion
G0:0021796	5	cerebral cortex regionalization
G0:0045927	5	positive regulation of growth
G0:0086067	5	AV node cell to bundle of His cell communication
G0:0043184	5	vascular endothelial growth factor receptor 2 binding
G0:0060485	5	mesenchyme development
G0:0006907	5	pinocytosis
G0:0002309	5	T cell proliferation involved in immune response
G0:2001028	5	positive regulation of endothelial cell chemotaxis
G0:0001768	5	establishment of T cell polarity
G0:0010666	5	positive regulation of cardiac muscle cell apoptotic process
G0:0035988	5	chondrocyte proliferation
G0:0008553	5	hydrogen-exporting ATPase activity, phosphorylative mechanism
G0:0014894	5	response to denervation involved in regulation of muscle adaptation
G0:0072669	5	tRNA-splicing ligase complex
G0:0071481	5	cellular response to X-ray
G0:0043405	5	regulation of MAP kinase activity
G0:0008762	5	UDP-N-acetylmuramate dehydrogenase activity
G0:0032405	5	MutLalpha complex binding
G0:0071421	5	manganese ion transmembrane transport
G0:0019695	5	choline metabolic process

G0:0016236	5	macroautophagy
G0:0033133	5	positive regulation of glucokinase activity
G0:0046599	5	regulation of centriole replication
G0:0043304	5	regulation of mast cell degranulation
G0:2001236	5	regulation of extrinsic apoptotic signaling pathway
G0:0006927	5	transformed cell apoptotic process
G0:0031579	5	membrane raft organization
G0:0019060	5	intracellular transport of viral protein in host cell
G0:0060956	5	endocardial cell differentiation
G0:0007256	5	activation of JNKK activity
G0:0007253	5	cytoplasmic sequestering of NF-kappaB
G0:0046834	5	lipid phosphorylation
G0:0032876	5	negative regulation of DNA endoreduplication
G0:0071813	5	lipoprotein particle binding
G0:2000675	5	negative regulation of type B pancreatic cell apoptotic process
G0:0060228	5	phosphatidylcholine-sterol O-acyltransferase activator activity
G0:0038170	5	somatostatin signaling pathway
G0:0003958	5	NADPH-hemoprotein reductase activity
G0:0048500	5	signal recognition particle
G0:0090184	5	positive regulation of kidney development
G0:0009157	5	deoxyribonucleoside monophosphate biosynthetic process
G0:0000439	5	core TFIIH complex
G0:0034452	5	dynactin binding
G0:0034105	5	positive regulation of tissue remodeling
G0:0034109	5	homotypic cell-cell adhesion
G0:0033153	5	T cell receptor V(D)J recombination
G0:0071817	5	MMXD complex
G0:0032962	5	positive regulation of inositol trisphosphate biosynthetic process
G0:0042255	5	ribosome assembly
G0:0043023	5	ribosomal large subunit binding
G0:0048318	5	axial mesoderm development
G0:0072383	5	plus-end-directed vesicle transport along microtubule
G0:2001259	5	positive regulation of cation channel activity
G0:2001256	5	regulation of store-operated calcium entry
G0:2001257	5	regulation of cation channel activity
G0:0035014	5	phosphatidylinositol 3-kinase regulator activity
G0:0031228	5	intrinsic component of Golgi membrane
G0:2000503	5	positive regulation of natural killer cell chemotaxis
G0:0050544	5	arachidonic acid binding
G0:0044319	5	wound healing, spreading of cells
G0:0060972	5	left/right pattern formation
G0:0070120	5	ciliary neurotrophic factor-mediated signaling pathway
G0:0032853	5	positive regulation of Ran GTPase activity
G0:0045542	5	positive regulation of cholesterol biosynthetic process
G0:0021861	5	forebrain radial glial cell differentiation
G0:1901998	5	toxin transport
G0:0045540	5	regulation of cholesterol biosynthetic process
G0:0019626	5	short-chain fatty acid catabolic process
G0:0098639	5	collagen binding involved in cell-matrix adhesion
G0:0032224	5	positive regulation of synaptic transmission, cholinergic
G0:0002385	5	mucosal immune response
G0:0060372	5	regulation of atrial cardiac muscle cell membrane repolarization
G0:0060373	5	regulation of ventricular cardiac muscle cell membrane depolarization
G0:0017081	5	chloride channel regulator activity
G0:0051964	5	negative regulation of synapse assembly
G0:0006312	5	mitotic recombination
G0:0043219	5	lateral loop
G0:0008048	5	calcium sensitive guanylate cyclase activator activity
G0:0006003	5	fructose 2,6-bisphosphate metabolic process
G0:2000737	5	negative regulation of stem cell differentiation
G0:0021631	5	optic nerve morphogenesis
G0:0019907	5	cyclin-dependent protein kinase activating kinase holoenzyme complex
G0:0033177	5	proton-transporting two-sector ATPase complex, proton-transporting domain
G0:0010991	5	negative regulation of SMAD protein complex assembly
G0:0044336	5	canonical Wnt signaling pathway involved in negative regulation of apoptotic process
G0:0090277	5	positive regulation of peptide hormone secretion
G0:0036006	5	cellular response to macrophage colony-stimulating factor stimulus
G0:0070100	5	negative regulation of chemokine-mediated signaling pathway
G0:0003105	5	negative regulation of glomerular filtration
G0:0003100	5	regulation of systemic arterial blood pressure by endothelin
G0:0060179	5	male mating behavior
G0:0034314	5	Arp2/3 complex-mediated actin nucleation
G0:0097225	5	sperm midpiece
G0:0008611	5	ether lipid biosynthetic process

G0:0043620	5	regulation of DNA-templated transcription in response to stress
G0:0061371	5	determination of heart left/right asymmetry
G0:0061370	5	testosterone biosynthetic process
G0:0010837	5	regulation of keratinocyte proliferation
G0:0010833	5	telomere maintenance via telomere lengthening
G0:0009374	5	biotin binding
G0:0015670	5	carbon dioxide transport
G0:1902188	5	positive regulation of viral release from host cell
G0:0070652	5	HAUS complex
G0:0004576	5	oligosaccharyl transferase activity
G0:0002360	5	T cell lineage commitment
G0:0003923	5	GPI-anchor transamidase activity
G0:0001875	5	lipopolysaccharide receptor activity
G0:0050863	5	regulation of T cell activation
G0:0031063	5	regulation of histone deacetylation
G0:0033194	5	response to hydroperoxide
G0:0006525	5	arginine metabolic process
G0:0005004	5	GPI-linked ephrin receptor activity
G0:0000276	5	mitochondrial proton-transporting ATP synthase complex, coupling factor F(o)
G0:0050996	5	positive regulation of lipid catabolic process
G0:0010314	5	phosphatidylinositol-5-phosphate binding
G0:0018206	5	peptidyl-methionine modification
G0:0004035	5	alkaline phosphatase activity
G0:0001609	5	G-protein coupled adenosine receptor activity
G0:0071870	5	cellular response to catecholamine stimulus
G0:0070695	5	FHF complex
G0:0051880	5	G-quadruplex DNA binding
G0:0043276	5	anoikis
G0:0046219	5	indolalkylamine biosynthetic process
G0:0016926	5	protein desumoylation
G0:0004551	5	nucleotide diphosphatase activity
G0:0016888	5	endodeoxyribonuclease activity, producing 5'-phosphomonoesters
G0:0014012	5	peripheral nervous system axon regeneration
G0:0070849	5	response to epidermal growth factor
G0:0015277	5	kainate selective glutamate receptor activity
G0:0014909	5	smooth muscle cell migration
G0:2000773	5	negative regulation of cellular senescence
G0:0032591	5	dendritic spine membrane
G0:0032592	5	integral component of mitochondrial membrane
G0:0035811	5	negative regulation of urine volume
G0:0035814	5	negative regulation of renal sodium excretion
G0:0035749	5	myelin sheath adaxonal region
G0:0016505	5	peptidase activator activity involved in apoptotic process
G0:0004945	5	angiotensin type II receptor activity
G0:0008420	5	CTD phosphatase activity
G0:0002043	5	blood vessel endothelial cell proliferation involved in sprouting
angiogenesis		
G0:0051135	5	positive regulation of NK T cell activation
G0:0034993	5	SUN-KASH complex
G0:0001667	5	ameboidal cell migration
G0:0001661	5	conditioned taste aversion
G0:0022612	5	gland morphogenesis
G0:0022614	5	membrane to membrane docking
G0:0032747	5	positive regulation of interleukin-23 production
G0:0018958	5	phenol-containing compound metabolic process
G0:0045292	5	mRNA cis splicing, via spliceosome
G0:0035999	5	tetrahydrofolate interconversion
G0:0044321	5	response to leptin
G0:0051005	5	negative regulation of lipoprotein lipase activity
G0:0048496	5	maintenance of organ identity
G0:0071504	5	cellular response to heparin
G0:0019218	5	regulation of steroid metabolic process
G0:0070083	5	clathrin-sculpted monoamine transport vesicle membrane
G0:0010591	5	regulation of lamellipodium assembly
G0:0071681	5	cellular response to indole-3-methanol
G0:0032963	5	collagen metabolic process
G0:0006561	5	proline biosynthetic process
G0:0060077	5	inhibitory synapse
G0:0090267	5	positive regulation of mitotic cell cycle spindle assembly checkpoint
G0:0017145	5	stem cell division
G0:0001642	5	group III metabotropic glutamate receptor activity
G0:0045008	5	depyrimidination
G0:0070431	5	nucleotide-binding oligomerization domain containing 2 signaling pathway
G0:0072498	5	embryonic skeletal joint development

G0:0016174	5	NAD(P)H oxidase activity
G0:0016298	5	lipase activity
G0:0005858	5	axonemal dynein complex
G0:0000710	5	meiotic mismatch repair
G0:0046703	5	natural killer cell lectin-like receptor binding
G0:0030275	5	LRR domain binding
G0:0035020	5	regulation of Rac protein signal transduction
G0:0015238	5	drug transmembrane transporter activity
G0:0003691	5	double-stranded telomeric DNA binding
G0:0072162	5	metanephric mesenchymal cell differentiation
G0:0005436	5	sodium:phosphate symporter activity
G0:0090383	5	phagosome acidification
G0:0003334	5	keratinocyte development
G0:0010608	5	posttranscriptional regulation of gene expression
G0:0001505	5	regulation of neurotransmitter levels
G0:0071910	5	determination of liver left/right asymmetry
G0:2000001	5	regulation of DNA damage checkpoint
G0:0042482	5	positive regulation of odontogenesis
G0:0060088	5	auditory receptor cell stereocilium organization
G0:0060056	5	mammary gland involution
G0:0044206	5	UMP salvage
G0:0060836	5	lymphatic endothelial cell differentiation
G0:0003840	5	gamma-glutamyltransferase activity
G0:0003846	5	2-acylglycerol O-acyltransferase activity
G0:0019530	5	taurine metabolic process
G0:0051451	5	myoblast migration
G0:0002686	5	negative regulation of leukocyte migration
G0:0006172	5	ADP biosynthetic process
G0:0048672	5	positive regulation of collateral sprouting
G0:0046813	5	receptor-mediated virion attachment to host cell
G0:0042765	5	GPI-anchor transamidase complex
G0:0030263	5	apoptotic chromosome condensation
G0:0031088	5	platelet dense granule membrane
G0:0030262	5	apoptotic nuclear changes
G0:0043985	5	histone H4-R3 methylation
G0:0032060	5	bleb assembly
G0:0043570	5	maintenance of DNA repeat elements
G0:0071028	5	nuclear mRNA surveillance
G0:0035721	5	intraciliary retrograde transport
G0:0060033	5	anatomical structure regression
G0:0050913	5	sensory perception of bitter taste
G0:0005078	5	MAP-kinase scaffold activity
G0:0048248	5	CXCR3 chemokine receptor binding
G0:0045110	5	intermediate filament bundle assembly
G0:0004300	5	enoyl-CoA hydratase activity
G0:0003828	5	alpha-N-acetylneuraminase alpha-2,8-sialyltransferase activity
G0:0033132	5	negative regulation of glucokinase activity
G0:0016500	5	protein-hormone receptor activity
G0:0048012	5	hepatocyte growth factor receptor signaling pathway
G0:0045545	5	syndecan binding
G0:0071569	5	protein ufmylation
G0:0016139	5	glycoside catabolic process
G0:0007021	5	tubulin complex assembly
G0:0007023	5	post-chaperonin tubulin folding pathway
G0:1901386	5	negative regulation of voltage-gated calcium channel activity
G0:0010572	5	positive regulation of platelet activation
G0:0035068	5	micro-ribonucleoprotein complex
G0:0010890	5	positive regulation of sequestering of triglyceride
G0:0010898	5	positive regulation of triglyceride catabolic process
G0:0006048	5	UDP-N-acetylglucosamine biosynthetic process
G0:0001520	5	outer dense fiber
G0:0036128	5	CatSper complex
G0:0010649	5	regulation of cell communication by electrical coupling
G0:0018095	5	protein polyglutamylation
G0:0018894	5	dibenzo-p-dioxin metabolic process
G0:2000049	5	positive regulation of cell-cell adhesion mediated by cadherin
G0:0090394	5	negative regulation of excitatory postsynaptic membrane potential
G0:0038027	5	apolipoprotein A-I-mediated signaling pathway
G0:0032049	5	cardiolipin biosynthetic process
G0:0042105	5	alpha-beta T cell receptor complex
G0:0021587	5	cerebellum morphogenesis
G0:0030917	5	midbrain-hindbrain boundary development
G0:0043619	5	regulation of transcription from RNA polymerase II promoter in response to oxidative stress
G0:0060541	5	respiratory system development

G0:0051256	5	spindle midzone assembly involved in mitosis
G0:0031053	5	primary miRNA processing
G0:0008142	5	oxysterol binding
G0:0004322	5	ferroxidase activity
G0:0045179	5	apical cortex
G0:0015355	5	secondary active monocarboxylate transmembrane transporter activity
G0:0043462	5	regulation of ATPase activity
G0:0007006	5	mitochondrial membrane organization
G0:0030210	5	heparin biosynthetic process
G0:0060206	5	estrous cycle phase
G0:0010216	5	maintenance of DNA methylation
G0:0050764	5	regulation of phagocytosis
G0:0003344	5	pericardium morphogenesis
G0:0008467	5	[heparan sulfate]-glucosamine 3-sulfotransferase 1 activity
G0:0046950	5	cellular ketone body metabolic process
G0:0002430	5	complement receptor mediated signaling pathway
G0:0030970	5	retrograde protein transport, ER to cytosol
G0:0051798	5	positive regulation of hair follicle development
G0:0006851	5	mitochondrial calcium ion transport
G0:0032233	5	positive regulation of actin filament bundle assembly
G0:0032426	5	stereocilium bundle tip
G0:0003407	5	neural retina development
G0:0035912	5	dorsal aorta morphogenesis
G0:0030893	5	meiotic cohesin complex
G0:0030891	5	VCB complex
G0:0008320	5	protein transmembrane transporter activity
G0:0045636	5	positive regulation of melanocyte differentiation
G0:0016907	5	G-protein coupled acetylcholine receptor activity
G0:0006220	5	pyrimidine nucleotide metabolic process
G0:0006222	5	UMP biosynthetic process
G0:0046785	5	microtubule polymerization
G0:0042421	5	norepinephrine biosynthetic process
G0:0060385	5	axonogenesis involved in innervation
G0:0007598	5	blood coagulation, extrinsic pathway
G0:0000712	5	resolution of meiotic recombination intermediates
G0:0031915	5	positive regulation of synaptic plasticity
G0:0045409	5	negative regulation of interleukin-6 biosynthetic process
G0:0021540	5	corpus callosum morphogenesis
G0:0016098	5	monoterpenoid metabolic process
G0:0046934	5	phosphatidylinositol-4,5-bisphosphate 3-kinase activity
G0:0060509	5	Type I pneumocyte differentiation
G0:0060501	5	positive regulation of epithelial cell proliferation involved in lung morphogenesis
G0:0042503	5	tyrosine phosphorylation of Stat3 protein
G0:0005143	5	interleukin-12 receptor binding
G0:0031465	5	Cul4B-RING E3 ubiquitin ligase complex
G0:0022038	5	corpus callosum development
G0:0051026	5	chiasma assembly
G0:0048515	5	spermatid differentiation
G0:0014807	5	regulation of somitogenesis
G0:2000146	5	negative regulation of cell motility
G0:0021955	5	central nervous system neuron axonogenesis
G0:0072520	5	seminiferous tubule development
G0:0097119	5	postsynaptic density protein 95 clustering
G0:0031694	5	alpha-2A adrenergic receptor binding
G0:0097371	5	MDM2/MDM4 family protein binding
G0:0030618	5	transforming growth factor beta receptor, pathway-specific cytoplasmic mediator activity
G0:1902231	5	positive regulation of intrinsic apoptotic signaling pathway in response to DNA damage
G0:0042761	5	very long-chain fatty acid biosynthetic process
G0:0045056	5	transcytosis
G0:0042760	5	very long-chain fatty acid catabolic process
G0:0051023	5	regulation of immunoglobulin secretion
G0:0000730	5	DNA recombinase assembly
G0:0052696	5	flavonoid glucuronidation
G0:0052697	5	xenobiotic glucuronidation
G0:0034969	5	histone arginine methylation
G0:0015696	5	ammonium transport
G0:1901844	5	regulation of cell communication by electrical coupling involved in cardiac conduction
G0:0006384	5	transcription initiation from RNA polymerase III promoter
G0:0071803	5	positive regulation of podosome assembly
G0:0005127	5	ciliary neurotrophic factor receptor binding
G0:0044245	5	polysaccharide digestion

G0:0002830	5	positive regulation of type 2 immune response
G0:0001711	5	endodermal cell fate commitment
G0:0001714	5	endodermal cell fate specification
G0:0071786	5	endoplasmic reticulum tubular network organization
G0:0043457	5	regulation of cellular respiration
G0:0034191	4	apolipoprotein A-I receptor binding
G0:0051782	4	negative regulation of cell division
G0:0003266	4	regulation of secondary heart field cardioblast proliferation
G0:0046651	4	lymphocyte proliferation
G0:1902219	4	negative regulation of intrinsic apoptotic signaling pathway in response to osmotic stress
G0:0048386	4	positive regulation of retinoic acid receptor signaling pathway
G0:0048039	4	ubiquinone binding
G0:0004663	4	Rab geranylgeranyltransferase activity
G0:0070061	4	fructose binding
G0:2000330	4	positive regulation of T-helper 17 cell lineage commitment
G0:0002906	4	negative regulation of mature B cell apoptotic process
G0:0033599	4	regulation of mammary gland epithelial cell proliferation
G0:0042093	4	T-helper cell differentiation
G0:0042092	4	type 2 immune response
G0:0016361	4	activin receptor activity, type I
G0:0009812	4	flavonoid metabolic process
G0:0070886	4	positive regulation of calcineurin-NFAT signaling cascade
G0:0001780	4	neutrophil homeostasis
G0:0010996	4	response to auditory stimulus
G0:0042168	4	heme metabolic process
G0:0009103	4	lipopolysaccharide biosynthetic process
G0:0003886	4	DNA (cytosine-5-)-methyltransferase activity
G0:0001738	4	morphogenesis of a polarized epithelium
G0:0001733	4	galactosylceramide sulfotransferase activity
G0:0001732	4	formation of translation initiation complex
G0:0001730	4	2'-5'-oligoadenylate synthetase activity
G0:0036155	4	acylglycerol acyl-chain remodeling
G0:0032387	4	negative regulation of intracellular transport
G0:0016624	4	oxidoreductase activity, acting on the aldehyde or oxo group of donors, disulfide as acceptor
G0:0014842	4	regulation of satellite cell proliferation
G0:0045656	4	negative regulation of monocyte differentiation
G0:1902236	4	negative regulation of intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress
G0:0003918	4	DNA topoisomerase type II (ATP-hydrolyzing) activity
G0:0036003	4	positive regulation of transcription from RNA polymerase II promoter in response to stress
G0:0050815	4	phosphoserine binding
G0:0030123	4	AP-3 adaptor complex
G0:0006910	4	phagocytosis, recognition
G0:0000778	4	condensed nuclear chromosome kinetochore
G0:0000779	4	condensed chromosome, centromeric region
G0:0000774	4	adenyl-nucleotide exchange factor activity
G0:0060903	4	positive regulation of meiosis I
G0:0010735	4	positive regulation of transcription via serum response element binding
G0:0046848	4	hydroxyapatite binding
G0:0004515	4	nicotinate-nucleotide adenyltransferase activity
G0:2000641	4	regulation of early endosome to late endosome transport
G0:0035502	4	metanephric part of ureteric bud development
G0:0034056	4	estrogen response element binding
G0:2000065	4	negative regulation of cortisol biosynthetic process
G0:0035630	4	bone mineralization involved in bone maturation
G0:0017034	4	Rap guanyl-nucleotide exchange factor activity
G0:0043171	4	peptide catabolic process
G0:0097452	4	GAIT complex
G0:0060129	4	thyroid-stimulating hormone-secreting cell differentiation
G0:0048280	4	vesicle fusion with Golgi apparatus
G0:0051048	4	negative regulation of secretion
G0:2001030	4	negative regulation of cellular glucuronidation
G0:0006474	4	N-terminal protein amino acid acetylation
G0:0001757	4	somite specification
G0:2000121	4	regulation of removal of superoxide radicals
G0:0032417	4	positive regulation of sodium:proton antiporter activity
G0:0046545	4	development of primary female sexual characteristics
G0:0016602	4	CCAAT-binding factor complex
G0:0008568	4	microtubule-severing ATPase activity
G0:0070741	4	response to interleukin-6
G0:0042063	4	gliogenesis
G0:2000785	4	regulation of autophagic vacuole assembly

G0:0070294	4	renal sodium ion absorption
G0:0070290	4	N-acylphosphatidylethanolamine-specific phospholipase D activity
G0:0002553	4	histamine secretion by mast cell
G0:0002125	4	maternal aggressive behavior
G0:0031698	4	beta-2 adrenergic receptor binding
G0:0019158	4	mannokinase activity
G0:0035469	4	determination of pancreatic left/right asymmetry
G0:0045039	4	protein import into mitochondrial inner membrane
G0:2000110	4	negative regulation of macrophage apoptotic process
G0:0006930	4	substrate-dependent cell migration, cell extension
G0:0006933	4	negative regulation of cell adhesion involved in substrate-bound cell migration
G0:0000791	4	euchromatin
G0:0031503	4	protein complex localization
G0:0044341	4	sodium-dependent phosphate transport
G0:0060923	4	cardiac muscle cell fate commitment
G0:0007221	4	positive regulation of transcription of Notch receptor target
G0:0010717	4	regulation of epithelial to mesenchymal transition
G0:0010716	4	negative regulation of extracellular matrix disassembly
G0:0019673	4	GDP-mannose metabolic process
G0:0002943	4	tRNA dihydrouridine synthesis
G0:0007320	4	insemination
G0:0016013	4	syntrophin complex
G0:0046449	4	creatinine metabolic process
G0:0017059	4	serine C-palmitoyltransferase complex
G0:0042587	4	glycogen granule
G0:0042588	4	zymogen granule
G0:0006499	4	N-terminal protein myristoylation
G0:0015807	4	L-amino acid transport
G0:0035613	4	RNA stem-loop binding
G0:0072050	4	S-shaped body morphogenesis
G0:0015722	4	canalicular bile acid transport
G0:0010664	4	negative regulation of striated muscle cell apoptotic process
G0:0035195	4	gene silencing by miRNA
G0:0009143	4	nucleoside triphosphate catabolic process
G0:0002455	4	humoral immune response mediated by circulating immunoglobulin
G0:0003720	4	telomerase activity
G0:0006533	4	aspartate catabolic process
G0:0001771	4	immunological synapse formation
G0:0097056	4	selenocysteinyl-tRNA(Sec) biosynthetic process
G0:0003229	4	ventricular cardiac muscle tissue development
G0:0008308	4	voltage-gated anion channel activity
G0:0042806	4	fucose binding
G0:0050851	4	antigen receptor-mediated signaling pathway
G0:0071141	4	SMAD protein complex
G0:0002142	4	stereocilia ankle link complex
G0:0097084	4	vascular smooth muscle cell development
G0:0030160	4	GKAP/Homer scaffold activity
G0:0005087	4	Ran guanyl-nucleotide exchange factor activity
G0:0000220	4	vacuolar proton-transporting V-type ATPase, V0 domain
G0:2001224	4	positive regulation of neuron migration
G0:0005332	4	gamma-aminobutyric acid:sodium symporter activity
G0:0005337	4	nucleoside transmembrane transporter activity
G0:0042634	4	regulation of hair cycle
G0:0031565	4	cytokinesis checkpoint
G0:0018879	4	biphenyl metabolic process
G0:0036033	4	mediator complex binding
G0:0032864	4	activation of Cdc42 GTPase activity
G0:0018685	4	alkane 1-monooxygenase activity
G0:0038110	4	interleukin-2-mediated signaling pathway
G0:0045577	4	regulation of B cell differentiation
G0:0061309	4	cardiac neural crest cell development involved in outflow tract morphogenesis
G0:0042035	4	regulation of cytokine biosynthetic process
G0:0042036	4	negative regulation of cytokine biosynthetic process
G0:0002682	4	regulation of immune system process
G0:0005652	4	nuclear lamina
G0:0060164	4	regulation of timing of neuron differentiation
G0:0048791	4	calcium ion-dependent exocytosis of neurotransmitter
G0:0016936	4	galactoside binding
G0:0000447	4	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)
G0:0000444	4	MIS12/MIND type complex
G0:0032451	4	demethylase activity
G0:0032455	4	nerve growth factor processing

G0:0010529	4	negative regulation of transposition
G0:0033146	4	regulation of intracellular estrogen receptor signaling pathway
G0:0046037	4	GMP metabolic process
G0:0046033	4	AMP metabolic process
G0:0042407	4	cristae formation
G0:0035799	4	ureter maturation
G0:0042992	4	negative regulation of transcription factor import into nucleus
G0:0035426	4	extracellular matrix-cell signaling
G0:0010989	4	negative regulation of low-density lipoprotein particle clearance
G0:0031545	4	peptidyl-proline 4-dioxygenase activity
G0:0090031	4	positive regulation of steroid hormone biosynthetic process
G0:0019788	4	NEDD8 ligase activity
G0:0044309	4	neuron spine
G0:0008649	4	rRNA methyltransferase activity
G0:0060100	4	positive regulation of phagocytosis, engulfment
G0:0060005	4	vestibular reflex
G0:0010940	4	positive regulation of necrotic cell death
G0:0007260	4	tyrosine phosphorylation of STAT protein
G0:0035650	4	AP-1 adaptor complex binding
G0:0031931	4	TORC1 complex
G0:0060364	4	frontal suture morphogenesis
G0:0005638	4	lamin filament
G0:0051919	4	positive regulation of fibrinolysis
G0:0006726	4	eye pigment biosynthetic process
G0:2001056	4	positive regulation of cysteine-type endopeptidase activity
G0:0015079	4	potassium ion transmembrane transporter activity
G0:0008582	4	regulation of synaptic growth at neuromuscular junction
G0:0003917	4	DNA topoisomerase type I activity
G0:0070728	4	leucine binding
G0:2000096	4	positive regulation of Wnt signaling pathway, planar cell polarity pathway
G0:0015245	4	fatty acid transporter activity
G0:0019932	4	second-messenger-mediated signaling
G0:0010543	4	regulation of platelet activation
G0:0030300	4	regulation of intestinal cholesterol absorption
G0:0047499	4	calcium-independent phospholipase A2 activity
G0:0003056	4	regulation of vascular smooth muscle contraction
G0:0072218	4	metanephric ascending thin limb development
G0:0006538	4	glutamate catabolic process
G0:0004974	4	leukotriene receptor activity
G0:0004971	4	alpha-amino-3-hydroxy-5-methyl-4-isoxazole propionate selective glutamate
receptor activity		
G0:0032432	4	actin filament bundle
G0:0004396	4	hexokinase activity
G0:0010040	4	response to iron(II) ion
G0:0044323	4	retinoic acid-responsive element binding
G0:0044320	4	cellular response to leptin stimulus
G0:0007288	4	sperm axoneme assembly
G0:0070213	4	protein auto-ADP-ribosylation
G0:0032827	4	negative regulation of natural killer cell differentiation involved in
immune response		
G0:0033522	4	histone H2A ubiquitination
G0:1901990	4	regulation of mitotic cell cycle phase transition
G0:0060439	4	trachea morphogenesis
G0:0015812	4	gamma-aminobutyric acid transport
G0:0010824	4	regulation of centrosome duplication
G0:0015811	4	L-cystine transport
G0:0010826	4	negative regulation of centrosome duplication
G0:0005964	4	phosphorylase kinase complex
G0:0030538	4	embryonic genitalia morphogenesis
G0:0005968	4	Rab-protein geranylgeranyltransferase complex
G0:0008330	4	protein tyrosine/threonine phosphatase activity
G0:0071459	4	protein localization to chromosome, centromeric region
G0:0003289	4	atrial septum primum morphogenesis
G0:0003283	4	atrial septum development
G0:0016199	4	axon midline choice point recognition
G0:0032369	4	negative regulation of lipid transport
G0:0019956	4	chemokine binding
G0:0071470	4	cellular response to osmotic stress
G0:0070309	4	lens fiber cell morphogenesis
G0:0046696	4	lipopolysaccharide receptor complex
G0:0004955	4	prostaglandin receptor activity
G0:0004958	4	prostaglandin F receptor activity
G0:0032269	4	negative regulation of cellular protein metabolic process
G0:0060669	4	embryonic placenta morphogenesis
G0:0031597	4	cytosolic proteasome complex

G0:0048341	4	paraxial mesoderm formation
G0:0022601	4	menstrual cycle phase
G0:0051101	4	regulation of DNA binding
G0:0051450	4	myoblast proliferation
G0:0034711	4	inhibin binding
G0:0032777	4	Piccolo NuA4 histone acetyltransferase complex
G0:0032808	4	lacrimal gland development
G0:0008626	4	granzyme-mediated apoptotic signaling pathway
G0:0000815	4	ESCRT III complex
G0:0070461	4	SAGA-type complex
G0:0042058	4	regulation of epidermal growth factor receptor signaling pathway
G0:1900004	4	negative regulation of serine-type endopeptidase activity
G0:0034618	4	arginine binding
G0:0034349	4	glial cell apoptotic process
G0:0005947	4	mitochondrial alpha-ketoglutarate dehydrogenase complex
G0:0071558	4	histone demethylase activity (H3-K27 specific)
G0:0014028	4	notochord formation
G0:0060415	4	muscle tissue morphogenesis
G0:0000389	4	mRNA 3'-splice site recognition
G0:0014009	4	glial cell proliferation
G0:0042731	4	PH domain binding
G0:0004720	4	protein-lysine 6-oxidase activity
G0:0086009	4	membrane repolarization
G0:0043515	4	kinetochore binding
G0:0030388	4	fructose 1,6-bisphosphate metabolic process
G0:0032348	4	negative regulation of aldosterone biosynthetic process
G0:0019208	4	phosphatase regulator activity
G0:0010586	4	miRNA metabolic process
G0:0003747	4	translation release factor activity
G0:0070324	4	thyroid hormone binding
G0:0070326	4	very-low-density lipoprotein particle receptor binding
G0:0042737	4	drug catabolic process
G0:0048859	4	formation of anatomical boundary
G0:0035771	4	interleukin-4-mediated signaling pathway
G0:0047631	4	ADP-ribose diphosphatase activity
G0:0042420	4	dopamine catabolic process
G0:0031077	4	post-embryonic camera-type eye development
G0:0031256	4	leading edge membrane
G0:0010002	4	cardioblast differentiation
G0:0007442	4	hindgut morphogenesis
G0:0046881	4	positive regulation of follicle-stimulating hormone secretion
G0:0043631	4	RNA polyadenylation
G0:0060011	4	Sertoli cell proliferation
G0:0060546	4	negative regulation of necroptotic process
G0:0004064	4	arylesterase activity
G0:0000836	4	Hrdlp ubiquitin ligase complex
G0:0019693	4	ribose phosphate metabolic process
G0:0033088	4	negative regulation of immature T cell proliferation in thymus
G0:0033081	4	regulation of T cell differentiation in thymus
G0:0033085	4	negative regulation of T cell differentiation in thymus
G0:0032137	4	guanine/thymine mispair binding
G0:0032133	4	chromosome passenger complex
G0:0034363	4	intermediate-density lipoprotein particle
G0:0005826	4	actomyosin contractile ring
G0:0051464	4	positive regulation of cortisol secretion
G0:0071208	4	histone pre-mRNA DCP binding
G0:0005111	4	type 2 fibroblast growth factor receptor binding
G0:0071205	4	protein localization to juxtaparanode region of axon
G0:0006290	4	pyrimidine dimer repair
G0:0072557	4	IPAF inflammasome complex
G0:0030289	4	protein phosphatase 4 complex
G0:0097491	4	sympathetic neuron projection guidance
G0:0043949	4	regulation of cAMP-mediated signaling
G0:0004528	4	phosphodiesterase I activity
G0:0014063	4	negative regulation of serotonin secretion
G0:0060298	4	positive regulation of sarcomere organization
G0:0015220	4	choline transmembrane transporter activity
G0:0007501	4	mesodermal cell fate specification
G0:0008298	4	intracellular mRNA localization
G0:0071922	4	regulation of cohesin localization to chromatin
G0:0010821	4	regulation of mitochondrion organization
G0:0001821	4	histamine secretion
G0:2000741	4	positive regulation of mesenchymal stem cell differentiation
G0:0035845	4	photoreceptor cell outer segment organization
G0:2000630	4	positive regulation of miRNA metabolic process

G0:0042159	4	lipoprotein catabolic process
G0:0016286	4	small conductance calcium-activated potassium channel activity
G0:0016576	4	histone dephosphorylation
G0:1901031	4	regulation of response to reactive oxygen species
G0:0031014	4	troponin T binding
G0:0003847	4	1-alkyl-2-acetylgllycerophosphocholine esterase activity
G0:0017150	4	tRNA dihydrouridine synthase activity
G0:0097029	4	mature dendritic cell differentiation
G0:0060628	4	regulation of ER to Golgi vesicle-mediated transport
G0:0030490	4	maturation of SSU-rRNA
G0:0005025	4	transforming growth factor beta receptor activity, type I
G0:0044387	4	negative regulation of protein kinase activity by regulation of protein phosphorylation
G0:0045123	4	cellular extravasation
G0:0008379	4	thioredoxin peroxidase activity
G0:0006824	4	cobalt ion transport
G0:0003854	4	3-beta-hydroxy-delta5-steroid dehydrogenase activity
G0:0033063	4	Rad51B-Rad51C-Rad51D-XRCC2 complex
G0:0003219	4	cardiac right ventricle formation
G0:0010424	4	DNA methylation on cytosine within a CG sequence
G0:0033601	4	positive regulation of mammary gland epithelial cell proliferation
G0:0050693	4	LBD domain binding
G0:0005849	4	mRNA cleavage factor complex
G0:0042481	4	regulation of odontogenesis
G0:0035520	4	monoubiquitinated protein deubiquitination
G0:0060455	4	negative regulation of gastric acid secretion
G0:0060452	4	positive regulation of cardiac muscle contraction
G0:0043372	4	positive regulation of CD4-positive, alpha-beta T cell differentiation
G0:0043374	4	CD8-positive, alpha-beta T cell differentiation
G0:0000347	4	TH0 complex
G0:0006015	4	5-phosphoribose 1-diphosphate biosynthetic process
G0:0072107	4	positive regulation of ureteric bud formation
G0:0006771	4	riboflavin metabolic process
G0:0010638	4	positive regulation of organelle organization
G0:0035869	4	ciliary transition zone
G0:0034497	4	protein localization to pre-autophagosomal structure
G0:0016776	4	phosphotransferase activity, phosphate group as acceptor
G0:0000974	4	Prp19 complex
G0:0016557	4	peroxisome membrane biogenesis
G0:0033299	4	secretion of lysosomal enzymes
G0:0019869	4	chloride channel inhibitor activity
G0:0035735	4	intraciliary transport involved in cilium morphogenesis
G0:0060028	4	convergent extension involved in axis elongation
G0:0002018	4	renin-angiotensin regulation of aldosterone production
G0:0048278	4	vesicle docking
G0:0008170	4	N-methyltransferase activity
G0:0048273	4	mitogen-activated protein kinase p38 binding
G0:0003836	4	beta-galactoside (CMP) alpha-2,3-sialyltransferase activity
G0:0070995	4	NADPH oxidation
G0:0030578	4	PML body organization
G0:0033591	4	response to L-ascorbic acid
G0:0044194	4	cytolytic granule
G0:0005862	4	muscle thin filament tropomyosin
G0:0003696	4	satellite DNA binding
G0:0033622	4	integrin activation
G0:0033625	4	positive regulation of integrin activation
G0:0030023	4	extracellular matrix constituent conferring elasticity
G0:0061030	4	epithelial cell differentiation involved in mammary gland alveolus development
G0:0061031	4	endodermal digestive tract morphogenesis
G0:0006072	4	glycerol-3-phosphate metabolic process
G0:0070231	4	T cell apoptotic process
G0:0000090	4	mitotic anaphase
G0:0038033	4	positive regulation of endothelial cell chemotaxis by VEGF-activated vascular endothelial growth factor receptor signaling pathway
G0:0016714	4	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced pteridine as one donor, and incorporation of one atom of oxygen
G0:0097066	4	response to thyroid hormone
G0:0045833	4	negative regulation of lipid metabolic process
G0:0006449	4	regulation of translational termination
G0:0034061	4	DNA polymerase activity
G0:0032264	4	IMP salvage
G0:0032190	4	acrosin binding
G0:0071557	4	histone H3-K27 demethylation

G0:0015101	4	organic cation transmembrane transporter activity
G0:0071559	4	response to transforming growth factor beta
G0:0051409	4	response to nitrosative stress
G0:0051045	4	negative regulation of membrane protein ectodomain proteolysis
G0:0008745	4	N-acetylmuramoyl-L-alanine amidase activity
G0:1901642	4	nucleoside transmembrane transport
G0:0072558	4	NLRP1 inflammasome complex
G0:0006273	4	lagging strand elongation
G0:0006054	4	N-acetylneuraminate metabolic process
G0:0060998	4	regulation of dendritic spine development
G0:0060992	4	response to fungicide
G0:0044782	4	cilium organization
G0:0046320	4	regulation of fatty acid oxidation
G0:0034340	4	response to type I interferon
G0:0034617	4	tetrahydrobiopterin binding
G0:0051973	4	positive regulation of telomerase activity
G0:0060688	4	regulation of morphogenesis of a branching structure
G0:0060686	4	negative regulation of prostatic bud formation
G0:0031782	4	type 4 melanocortin receptor binding
G0:0072086	4	specification of loop of Henle identity
G0:0008865	4	fructokinase activity
G0:0031433	4	telethonin binding
G0:0052848	4	inositol-3,5-bis(diphosphate)-2,3,4,6-tetrakisphosphate 5-diphosphatase activity
G0:0022009	4	central nervous system vasculogenesis
G0:0032206	4	positive regulation of telomere maintenance
G0:0032098	4	regulation of appetite
G0:0010193	4	response to ozone
G0:0016503	4	pheromone receptor activity
G0:0014832	4	urinary bladder smooth muscle contraction
G0:0050689	4	negative regulation of defense response to virus by host
G0:0051560	4	mitochondrial calcium ion homeostasis
G0:0071532	4	ankyrin repeat binding
G0:0046850	4	regulation of bone remodeling
G0:0006545	4	glycine biosynthetic process
G0:2000780	4	negative regulation of double-strand break repair
G0:0006547	4	histidine metabolic process
G0:0051387	4	negative regulation of neurotrophin TRK receptor signaling pathway
G0:0002669	4	positive regulation of T cell anergy
G0:0031848	4	protection from non-homologous end joining at telomere
G0:0060743	4	epithelial cell maturation involved in prostate gland development
G0:0005749	4	mitochondrial respiratory chain complex II
G0:1990381	4	ubiquitin-specific protease binding
G0:0010669	4	epithelial structure maintenance
G0:0004169	4	dolichyl-phosphate-mannose-protein mannosyltransferase activity
G0:2000651	4	positive regulation of sodium ion transmembrane transporter activity
G0:0031062	4	positive regulation of histone methylation
G0:0055077	4	gap junction hemi-channel activity
G0:0005497	4	androgen binding
G0:0045415	4	negative regulation of interleukin-8 biosynthetic process
G0:0032549	4	ribonucleoside binding
G0:0032543	4	mitochondrial translation
G0:0019805	4	quinolinate biosynthetic process
G0:0002551	4	mast cell chemotaxis
G0:0015936	4	coenzyme A metabolic process
G0:0021798	4	forebrain dorsal/ventral pattern formation
G0:0001839	4	neural plate morphogenesis
G0:0060512	4	prostate gland morphogenesis
G0:0015347	4	sodium-independent organic anion transmembrane transporter activity
G0:0042518	4	negative regulation of tyrosine phosphorylation of Stat3 protein
G0:0043103	4	hypoxanthine salvage
G0:0005176	4	ErbB-2 class receptor binding
G0:0070851	4	growth factor receptor binding
G0:0070938	4	contractile ring
G0:0070934	4	CRD-mediated mRNA stabilization
G0:0009605	4	response to external stimulus
G0:0015321	4	sodium-dependent phosphate transmembrane transporter activity
G0:0036101	4	leukotriene B4 catabolic process
G0:0032489	4	regulation of Cdc42 protein signal transduction
G0:0021943	4	formation of radial glial scaffolds
G0:0021940	4	positive regulation of cerebellar granule cell precursor proliferation
G0:0045627	4	positive regulation of T-helper 1 cell differentiation
G0:0043248	4	proteasome assembly
G0:0072513	4	positive regulation of secondary heart field cardioblast proliferation
G0:0097120	4	receptor localization to synapse

G0:0010957	4	negative regulation of vitamin D biosynthetic process
G0:0048144	4	fibroblast proliferation
G0:0043242	4	negative regulation of protein complex disassembly
G0:0033553	4	rDNA heterochromatin
G0:0004144	4	diacylglycerol 0-acyltransferase activity
G0:1903077	4	negative regulation of protein localization to plasma membrane
G0:0070053	4	thrombospondin receptor activity
G0:2000369	4	regulation of clathrin-mediated endocytosis
G0:0021555	4	midbrain-hindbrain boundary morphogenesis
G0:0021889	4	olfactory bulb interneuron differentiation
G0:0060486	4	Clara cell differentiation
G0:0010766	4	negative regulation of sodium ion transport
G0:0016080	4	synaptic vesicle targeting
G0:0090170	4	regulation of Golgi inheritance
G0:0060535	4	trachea cartilage morphogenesis
G0:0045986	4	negative regulation of smooth muscle contraction
G0:0045187	4	regulation of circadian sleep/wake cycle, sleep
G0:0045182	4	translation regulator activity
G0:0004826	4	phenylalanine-tRNA ligase activity
G0:0060393	4	regulation of pathway-restricted SMAD protein phosphorylation
G0:0042985	4	negative regulation of amyloid precursor protein biosynthetic process
G0:0042982	4	amyloid precursor protein metabolic process
G0:0010155	4	regulation of proton transport
G0:0032795	4	heterotrimeric G-protein binding
G0:0008392	4	arachidonic acid epoxygenase activity
G0:0044117	4	growth of symbiont in host
G0:0036120	4	cellular response to platelet-derived growth factor stimulus
G0:0032970	4	regulation of actin filament-based process
G0:0071797	4	LUBAC complex
G0:0003257	4	positive regulation of transcription from RNA polymerase II promoter
involved in myocardial precursor cell differentiation		
G0:0031117	4	positive regulation of microtubule depolymerization
G0:0060708	4	spongiotrophoblast differentiation
G0:0046642	4	negative regulation of alpha-beta T cell proliferation
G0:0007632	4	visual behavior
G0:0006610	4	ribosomal protein import into nucleus
G0:0002281	4	macrophage activation involved in immune response
G0:0045040	4	protein import into mitochondrial outer membrane
G0:0045047	4	protein targeting to ER
G0:0006949	4	syncytium formation
G0:0048027	4	mRNA 5'-UTR binding
G0:2000343	4	positive regulation of chemokine (C-X-C motif) ligand 2 production
G0:0010748	4	negative regulation of plasma membrane long-chain fatty acid transport
G0:0035174	4	histone serine kinase activity
G0:0061428	4	negative regulation of transcription from RNA polymerase II promoter in response to hypoxia
G0:0042089	4	cytokine biosynthetic process
G0:0005134	4	interleukin-2 receptor binding
G0:0048702	4	embryonic neurocranium morphogenesis
G0:0004849	4	uridine kinase activity
G0:0004844	4	uracil DNA N-glycosylase activity
G0:0071986	4	Regulator complex
G0:0003945	4	N-acetyllactosamine synthase activity
G0:0009649	4	entrainment of circadian clock
G0:0009648	4	photoperiodism
G0:0003896	4	DNA primase activity
G0:0010715	4	regulation of extracellular matrix disassembly
G0:0000109	4	nucleotide-excision repair complex
G0:0015184	4	L-cystine transmembrane transporter activity
G0:0003279	4	cardiac septum development
G0:0019896	4	axon transport of mitochondrion
G0:0005955	4	calcineurin complex
G0:0097167	4	circadian regulation of translation
G0:0050793	4	regulation of developmental process
G0:0010916	4	negative regulation of very-low-density lipoprotein particle clearance
G0:0002118	4	aggressive behavior
G0:0001537	4	N-acetylgalactosamine 4-O-sulfotransferase activity
G0:0031821	4	G-protein coupled serotonin receptor binding
G0:0045063	4	T-helper 1 cell differentiation
G0:0045064	4	T-helper 2 cell differentiation
G0:0045069	4	regulation of viral genome replication
G0:0031536	4	positive regulation of exit from mitosis
G0:0030072	4	peptide hormone secretion
G0:0045472	4	response to ether
G0:0021516	4	dorsal spinal cord development

G0:0051208	4	sequestering of calcium ion
G0:0046878	4	positive regulation of saliva secretion
G0:0010724	4	regulation of definitive erythrocyte differentiation
G0:0055070	4	copper ion homeostasis
G0:0001915	4	negative regulation of T cell mediated cytotoxicity
G0:0001919	4	regulation of receptor recycling
G0:0032925	4	regulation of activin receptor signaling pathway
G0:0035625	4	epidermal growth factor-activated receptor transactivation by G-protein coupled receptor signaling pathway
G0:0032237	4	activation of store-operated calcium channel activity
G0:0003183	4	mitral valve morphogenesis
G0:0086008	4	voltage-gated potassium channel activity involved in cardiac muscle cell action potential repolarization
G0:0002051	4	osteoblast fate commitment
G0:0014826	4	vein smooth muscle contraction
G0:0051599	4	response to hydrostatic pressure
G0:2000138	4	positive regulation of cell proliferation involved in heart morphogenesis
G0:0003211	4	cardiac ventricle formation
G0:0015705	4	iodide transport
G0:0032642	4	regulation of chemokine production
G0:0070513	4	death domain binding
G0:0010803	4	regulation of tumor necrosis factor-mediated signaling pathway
G0:0071174	4	mitotic spindle checkpoint
G0:0042723	4	thiamine-containing compound metabolic process
G0:0030868	4	smooth endoplasmic reticulum membrane
G0:0006163	4	purine nucleotide metabolic process
G0:0010936	4	negative regulation of macrophage cytokine production
G0:0006651	4	diacylglycerol biosynthetic process
G0:0006650	4	glycerophospholipid metabolic process
G0:0006659	4	phosphatidylserine biosynthetic process
G0:0006658	4	phosphatidylserine metabolic process
G0:0035459	4	cargo loading into vesicle
G0:0030644	4	cellular chloride ion homeostasis
G0:0004470	4	malic enzyme activity
G0:0046882	4	negative regulation of follicle-stimulating hormone secretion
G0:0035615	4	clathrin adaptor activity
G0:0006489	4	dolichyl diphosphate biosynthetic process
G0:0019210	4	kinase inhibitor activity
G0:0080154	4	regulation of fertilization
G0:0021533	4	cell differentiation in hindbrain
G0:0051222	4	positive regulation of protein transport
G0:0051224	4	negative regulation of protein transport
G0:0050051	4	leukotriene-B4 20-monooxygenase activity
G0:0019885	4	antigen processing and presentation of endogenous peptide antigen via MHC class I
G0:0038127	4	ERBB signaling pathway
G0:0021797	4	forebrain anterior/posterior pattern specification
G0:0006482	4	protein demethylation
G0:0045639	4	positive regulation of myeloid cell differentiation
G0:0005686	4	U2 snRNP
G0:0060157	4	urinary bladder development
G0:0051057	4	positive regulation of small GTPase mediated signal transduction
G0:0051054	4	positive regulation of DNA metabolic process
G0:0044294	4	dendritic growth cone
G0:0019966	4	interleukin-1 binding
G0:0051970	4	negative regulation of transmission of nerve impulse
G0:0006549	4	isoleucine metabolic process
G0:0032407	4	MutSalpha complex binding
G0:2000510	4	positive regulation of dendritic cell chemotaxis
G0:0046626	4	regulation of insulin receptor signaling pathway
G0:0002159	4	desmosome assembly
G0:0097418	4	neurofibrillary tangle
G0:0035473	4	lipase binding
G0:1902004	4	positive regulation of beta-amyloid formation
G0:0006670	4	sphingosine metabolic process
G0:0005326	4	neurotransmitter transporter activity
G0:0000788	4	nuclear nucleosome
G0:0031577	4	spindle checkpoint
G0:0007258	4	JUN phosphorylation
G0:0070141	4	response to UV-A
G0:0071816	4	tail-anchored membrane protein insertion into ER membrane
G0:0008063	4	Toll signaling pathway
G0:0045569	4	TRAIL binding
G0:0061333	4	renal tubule morphogenesis
G0:0047057	4	vitamin-K-epoxide reductase (warfarin-sensitive) activity

G0:0043218	4	compact myelin
G0:0048845	4	venous blood vessel morphogenesis
G0:0045906	4	negative regulation of vasoconstriction
G0:0097264	4	self proteolysis
G0:0035662	4	Toll-like receptor 4 binding
G0:0060318	4	definitive erythrocyte differentiation
G0:0006405	4	RNA export from nucleus
G0:0035088	4	establishment or maintenance of apical/basal cell polarity
G0:0035082	4	axoneme assembly
G0:0046533	4	negative regulation of photoreceptor cell differentiation
G0:0015872	4	dopamine transport
G0:0045345	4	positive regulation of MHC class I biosynthetic process
G0:0030686	4	90S preribosome
G0:0060732	4	positive regulation of inositol phosphate biosynthetic process
G0:0004758	4	serine C-palmitoyltransferase activity
G0:0003960	4	NADPH:quinone reductase activity
G0:0045351	4	type I interferon biosynthetic process
G0:0045356	4	positive regulation of interferon-alpha biosynthetic process
G0:0072602	4	interleukin-4 secretion
G0:0097490	4	sympathetic neuron projection extension
G0:0032463	4	negative regulation of protein homooligomerization
G0:0034454	4	microtubule anchoring at centrosome
G0:0071498	4	cellular response to fluid shear stress
G0:0021612	4	facial nerve structural organization
G0:0016600	4	flotillin complex
G0:0010513	4	positive regulation of phosphatidylinositol biosynthetic process
G0:0033152	4	immunoglobulin V(D)J recombination
G0:0051716	4	cellular response to stimulus
G0:0016482	4	cytoplasmic transport
G0:0035276	4	ethanol binding
G0:0046976	4	histone methyltransferase activity (H3-K27 specific)
G0:0042256	4	mature ribosome assembly
G0:0004694	4	eukaryotic translation initiation factor 2alpha kinase activity
G0:1902285	4	semaphorin-plexin signaling pathway involved in neuron projection guidance
G0:1902282	4	voltage-gated potassium channel activity involved in ventricular cardiac muscle cell action potential repolarization
G0:0051152	4	positive regulation of smooth muscle cell differentiation
G0:0051151	4	negative regulation of smooth muscle cell differentiation
G0:0051155	4	positive regulation of striated muscle cell differentiation
G0:0018243	4	protein O-linked glycosylation via threonine
G0:0060971	4	embryonic heart tube left/right pattern formation
G0:0036021	4	endolysosome lumen
G0:0036020	4	endolysosome membrane
G0:0008540	4	proteasome regulatory particle, base subcomplex
G0:0003161	4	cardiac conduction system development
G0:0070242	4	thymocyte apoptotic process
G0:0004522	4	pancreatic ribonuclease activity
G0:0002029	4	desensitization of G-protein coupled receptor protein signaling pathway
G0:2000738	4	positive regulation of stem cell differentiation
G0:0002503	4	peptide antigen assembly with MHC class II protein complex
G0:0016274	4	protein-arginine N-methyltransferase activity
G0:0051771	4	negative regulation of nitric-oxide synthase biosynthetic process
G0:0030151	4	molybdenum ion binding
G0:0071547	4	piP-body
G0:0000212	4	meiotic spindle organization
G0:0090330	4	regulation of platelet aggregation
G0:0009052	4	pentose-phosphate shunt, non-oxidative branch
G0:0044332	4	Wnt signaling pathway involved in dorsal/ventral axis specification
G0:0051286	4	cell tip
G0:0036002	4	pre-mRNA binding
G0:0015467	4	G-protein activated inward rectifier potassium channel activity
G0:0003104	4	positive regulation of glomerular filtration
G0:0090231	4	regulation of spindle checkpoint
G0:0015809	4	arginine transport
G0:0045943	4	positive regulation of transcription from RNA polymerase I promoter
G0:1903237	4	negative regulation of leukocyte tethering or rolling
G0:0050974	4	detection of mechanical stimulus involved in sensory perception
G0:0032389	4	MutLalpha complex
G0:2001046	4	positive regulation of integrin-mediated signaling pathway
G0:0008061	4	chitin binding
G0:0014031	4	mesenchymal cell development
G0:0004711	4	ribosomal protein S6 kinase activity
G0:0052796	4	exo-alpha-(2->8)-sialidase activity
G0:0070734	4	histone H3-K27 methylation
G0:0051345	4	positive regulation of hydrolase activity

G0:0051344	4	negative regulation of cyclic-nucleotide phosphodiesterase activity
G0:0016783	4	sulfurtransferase activity
G0:0016780	4	phosphotransferase activity, for other substituted phosphate groups
G0:0007412	4	axon target recognition
G0:0038085	4	vascular endothelial growth factor binding
G0:0033192	4	calmodulin-dependent protein phosphatase activity
G0:0017128	4	phospholipid scramblase activity
G0:0006526	4	arginine biosynthetic process
G0:0046684	4	response to pyrethroid
G0:0045085	4	negative regulation of interleukin-2 biosynthetic process
G0:0031404	4	chloride ion binding
G0:0031262	4	Ndc80 complex
G0:0090003	4	regulation of establishment of protein localization to plasma membrane
G0:0050501	4	hyaluronan synthase activity
G0:0005384	4	manganese ion transmembrane transporter activity
G0:0001601	4	peptide YY receptor activity
G0:1901214	4	regulation of neuron death
G0:0055129	4	L-proline biosynthetic process
G0:0042045	4	epithelial fluid transport
G0:0042048	4	olfactory behavior
G0:0097209	4	epidermal lamellar body
G0:0015867	4	ATP transport
G0:0010815	4	bradykinin catabolic process
G0:0005853	4	eukaryotic translation elongation factor 1 complex
G0:0006772	4	thiamine metabolic process
G0:0031905	4	early endosome lumen
G0:1990023	4	mitotic spindle midzone
G0:0000395	4	mRNA 5'-splice site recognition
G0:0004558	4	alpha-glucosidase activity
G0:0019470	4	4-hydroxyproline catabolic process
G0:0051321	4	meiotic cell cycle
G0:0032375	4	negative regulation of cholesterol transport
G0:0019941	4	modification-dependent protein catabolic process
G0:0010574	4	regulation of vascular endothelial growth factor production
G0:0070318	4	positive regulation of G0 to G1 transition
G0:0070314	4	G1 to G0 transition
G0:0070317	4	negative regulation of G0 to G1 transition
G0:0045682	4	regulation of epidermis development
G0:1900747	4	negative regulation of vascular endothelial growth factor signaling pathway
G0:0050807	4	regulation of synapse organization
G0:0035813	4	regulation of renal sodium excretion
G0:1901029	4	negative regulation of mitochondrial outer membrane permeabilization
involved in	apoptotic signaling pathway	
G0:0090385	4	phagosome-lysosome fusion
G0:0001514	4	selenocysteine incorporation
G0:0042997	4	negative regulation of Golgi to plasma membrane protein transport
G0:0072221	4	metanephric distal convoluted tubule development
G0:0070857	4	regulation of bile acid biosynthetic process
G0:0006548	4	histidine catabolic process
G0:0006543	4	glutamine catabolic process
G0:0060596	4	mammary placode formation
G0:0032466	4	negative regulation of cytokinesis
G0:0070852	4	cell body fiber
G0:0060591	4	chondroblast differentiation
G0:0060676	4	ureteric bud formation
G0:0051138	4	positive regulation of NK T cell differentiation
G0:0034991	4	nuclear meiotic cohesin complex
G0:0021615	4	glossopharyngeal nerve morphogenesis
G0:0032680	4	regulation of tumor necrosis factor production
G0:0000290	4	deadenylation-dependent decapping of nuclear-transcribed mRNA
G0:0060841	4	venous blood vessel development
G0:0060842	4	arterial endothelial cell differentiation
G0:0034354	4	'de novo' NAD biosynthetic process from tryptophan
G0:0006287	4	base-excision repair, gap-filling
G0:0030291	4	protein serine/threonine kinase inhibitor activity
G0:0005954	4	calcium- and calmodulin-dependent protein kinase complex
G0:0030492	4	hemoglobin binding
G0:0043201	4	response to leucine
G0:0003150	4	muscular septum morphogenesis
G0:0008024	4	positive transcription elongation factor complex b
G0:0060285	4	cilium-dependent cell motility
G0:0010499	4	proteasomal ubiquitin-independent protein catabolic process
G0:0022405	4	hair cycle process
G0:0032354	4	response to follicle-stimulating hormone

G0:0019211	4	phosphatase activator activity
G0:0010594	4	regulation of endothelial cell migration
G0:0001835	4	blastocyst hatching
G0:0002175	4	protein localization to paranode region of axon
G0:0052658	4	inositol-1,4,5-trisphosphate 5-phosphatase activity
G0:0016742	4	hydroxymethyl-, formyl- and related transferase activity
G0:0021696	4	cerebellar cortex morphogenesis
G0:0045716	4	positive regulation of low-density lipoprotein particle receptor
biosynthetic process		
G0:0006564	4	L-serine biosynthetic process
G0:0060075	4	regulation of resting membrane potential
G0:0060074	4	synapse maturation
G0:0060078	4	regulation of postsynaptic membrane potential
G0:0035497	4	cAMP response element binding
G0:0060613	4	fat pad development
G0:0033564	4	anterior/posterior axon guidance
G0:0030718	4	germ-line stem cell maintenance
G0:0060214	4	endocardium formation
G0:0008612	4	peptidyl-lysine modification to peptidyl-hypusine
G0:0019511	4	peptidyl-proline hydroxylation
G0:0052795	4	exo-alpha-(2->6)-sialidase activity
G0:0052794	4	exo-alpha-(2->3)-sialidase activity
G0:0070836	4	caveola assembly
G0:0045919	4	positive regulation of cytolysis
G0:0016101	4	diterpenoid metabolic process
G0:0045916	4	negative regulation of complement activation
G0:0090191	4	negative regulation of branching involved in ureteric bud morphogenesis
G0:0009301	4	snRNA transcription
G0:0035021	4	negative regulation of Rac protein signal transduction
G0:0035022	4	positive regulation of Rac protein signal transduction
G0:0060447	4	bud outgrowth involved in lung branching
G0:0006007	4	glucose catabolic process
G0:0048619	4	embryonic hindgut morphogenesis
G0:0071218	4	cellular response to misfolded protein
G0:0014051	4	gamma-aminobutyric acid secretion
G0:0014054	4	positive regulation of gamma-aminobutyric acid secretion
G0:0001504	4	neurotransmitter uptake
G0:0003988	4	acetyl-CoA C-acyltransferase activity
G0:0044020	4	histone methyltransferase activity (H4-R3 specific)
G0:2000002	4	negative regulation of DNA damage checkpoint
G0:0043559	4	insulin binding
G0:0043084	4	penile erection
G0:0009582	4	detection of abiotic stimulus
G0:0097113	4	alpha-amino-3-hydroxy-5-methyl-4-isoxazole propionate selective glutamate
receptor clustering		
G0:0036089	4	cleavage furrow formation
G0:0008186	4	RNA-dependent ATPase activity
G0:0033158	4	regulation of protein import into nucleus, translocation
G0:0045132	4	meiotic chromosome segregation
G0:0045134	4	uridine-diphosphatase activity
G0:0035412	4	regulation of catenin import into nucleus
G0:0004897	4	ciliary neurotrophic factor receptor activity
G0:0005610	4	laminin-5 complex
G0:0044314	4	protein K27-linked ubiquitination
G0:0004090	4	carbonyl reductase (NADPH) activity
G0:0004095	4	carnitine O-palmitoyltransferase activity
G0:0000052	4	citruilline metabolic process
G0:0004740	4	pyruvate dehydrogenase (acetyl-transferring) kinase activity
G0:0051534	4	negative regulation of NFAT protein import into nucleus
G0:0015179	4	L-amino acid transmembrane transporter activity
G0:0016151	4	nickel cation binding
G0:0090266	4	regulation of mitotic cell cycle spindle assembly checkpoint
G0:0051454	4	intracellular pH elevation
G0:0044615	4	nuclear pore nuclear basket
G0:0031428	4	box C/D snoRNP complex
G0:0002634	4	regulation of germinal center formation
G0:0043125	4	ErbB-3 class receptor binding
G0:0030259	4	lipid glycosylation
G0:0061041	4	regulation of wound healing
G0:0016934	4	extracellular-glycine-gated chloride channel activity
G0:0032393	4	MHC class I receptor activity
G0:0000085	4	mitotic G2 phase
G0:0030260	4	entry into host cell
G0:0017160	4	Ral GTPase binding
G0:0010626	4	negative regulation of Schwann cell proliferation

G0:0003309	4	type B pancreatic cell differentiation
G0:0035877	4	death effector domain binding
G0:0042165	4	neurotransmitter binding
G0:0071395	4	cellular response to jasmonic acid stimulus
G0:0042297	4	vocal learning
G0:0042296	4	ISG15 ligase activity
G0:0072289	4	metanephric nephron tubule formation
G0:0032453	4	histone demethylase activity (H3-K4 specific)
G0:0050915	4	sensory perception of sour taste
G0:0006477	4	protein sulfation
G0:0048861	4	leukemia inhibitory factor signaling pathway
G0:0035189	4	Rb-E2F complex
G0:1902711	4	GABA-A receptor complex
G0:0033136	4	serine phosphorylation of STAT3 protein
G0:0045869	4	negative regulation of single stranded viral RNA replication via double stranded DNA intermediate
G0:0004301	4	epoxide hydrolase activity
G0:0004305	4	ethanolamine kinase activity
G0:0004308	4	exo-alpha-sialidase activity
G0:0018393	4	internal peptidyl-lysine acetylation
G0:0003873	4	6-phosphofructo-2-kinase activity
G0:0015379	4	potassium:chloride symporter activity
G0:2000210	4	positive regulation of anoikis
G0:0032184	4	SUMO polymer binding
G0:0051431	4	corticotropin-releasing hormone receptor 2 binding
G0:0051430	4	corticotropin-releasing hormone receptor 1 binding
G0:1901385	4	regulation of voltage-gated calcium channel activity
G0:0047035	4	testosterone dehydrogenase (NAD+) activity
G0:0033634	4	positive regulation of cell-cell adhesion mediated by integrin
G0:0033631	4	cell-cell adhesion mediated by integrin
G0:0035065	4	regulation of histone acetylation
G0:0010891	4	negative regulation of sequestering of triglyceride
G0:0010894	4	negative regulation of steroid biosynthetic process
G0:0006269	4	DNA replication, synthesis of RNA primer
G0:0042743	4	hydrogen peroxide metabolic process
G0:0050702	4	interleukin-1 beta secretion
G0:0004111	4	creatine kinase activity
G0:0004112	4	cyclic-nucleotide phosphodiesterase activity
G0:0014049	4	positive regulation of glutamate secretion
G0:0072108	4	positive regulation of mesenchymal to epithelial transition involved in metanephros morphogenesis
G0:0032045	4	guanyl-nucleotide exchange factor complex
G0:0038028	4	insulin receptor signaling pathway via phosphatidylinositol 3-kinase
G0:0031781	4	type 3 melanocortin receptor binding
G0:0060018	4	astrocyte fate commitment
G0:0017183	4	peptidyl-diphthamide biosynthetic process from peptidyl-histidine
G0:0048263	4	determination of dorsal identity
G0:0035308	4	negative regulation of protein dephosphorylation
G0:0072091	4	regulation of stem cell proliferation
G0:0006875	4	cellular metal ion homeostasis
G0:0006873	4	cellular ion homeostasis
G0:0034123	4	positive regulation of toll-like receptor signaling pathway
G0:2000189	4	positive regulation of cholesterol homeostasis
G0:0070492	4	oligosaccharide binding
G0:2000821	4	regulation of grooming behavior
G0:0051574	4	positive regulation of histone H3-K9 methylation
G0:0051575	4	5'-deoxyribose-5-phosphate lyase activity
G0:0010452	4	histone H3-K36 methylation
G0:0010453	4	regulation of cell fate commitment
G0:0070234	4	positive regulation of T cell apoptotic process
G0:0007000	4	nucleolus organization
G0:2000987	4	positive regulation of behavioral fear response
G0:0001920	4	negative regulation of receptor recycling
G0:0060754	4	positive regulation of mast cell chemotaxis
G0:0060750	4	epithelial cell proliferation involved in mammary gland duct elongation
G0:0002189	4	ribose phosphate diphosphokinase complex
G0:0051385	4	response to mineralocorticoid
G0:0051380	4	norepinephrine binding
G0:0046952	4	ketone body catabolic process
G0:0006999	4	nuclear pore organization
G0:0032025	4	response to cobalt ion
G0:0032021	4	NELF complex
G0:0031233	4	intrinsic component of external side of plasma membrane
G0:0070006	4	metalloaminopeptidase activity
G0:0032374	4	regulation of cholesterol transport

G0:0060982	4	coronary artery morphogenesis
G0:0019834	4	phospholipase A2 inhibitor activity
G0:0050955	4	thermoception
G0:0002752	4	cell surface pattern recognition receptor signaling pathway
G0:0060693	4	regulation of branching involved in salivary gland morphogenesis
G0:0048755	4	branching morphogenesis of a nerve
G0:0004340	4	glucokinase activity
G0:0031442	4	positive regulation of mRNA 3'-end processing
G0:0033617	4	mitochondrial respiratory chain complex IV assembly
G0:0032232	4	negative regulation of actin filament bundle assembly
G0:0014829	4	vascular smooth muscle contraction
G0:0052840	4	inositol diphosphate tetrakisphosphate diphosphatase activity
G0:0021938	4	smoothened signaling pathway involved in regulation of cerebellar granule
cell precursor cell		proliferation
G0:0033010	4	paranodal junction
G0:0043496	4	regulation of protein homodimerization activity
G0:0016460	4	myosin II complex
G0:0045637	4	regulation of myeloid cell differentiation
G0:0008599	4	protein phosphatase type 1 regulator activity
G0:0015858	4	nucleoside transport
G0:0006084	4	acetyl-CoA metabolic process
G0:0030091	4	protein repair
G0:0005751	4	mitochondrial respiratory chain complex IV
G0:0002636	4	positive regulation of germinal center formation
G0:0046978	4	TAP1 binding
G0:0042699	4	follicle-stimulating hormone signaling pathway
G0:0008486	4	diphosphoinositol-polyphosphate diphosphatase activity
G0:0070022	4	transforming growth factor beta receptor homodimeric complex
G0:0021544	4	subpallium development
G0:0021545	4	cranial nerve development
G0:0021891	4	olfactory bulb interneuron development
G0:0021892	4	cerebral cortex GABAergic interneuron differentiation
G0:0032009	4	early phagosome
G0:0035519	4	protein K29-linked ubiquitination
G0:0048592	4	eye morphogenesis
G0:0031467	4	Cul7-RING ubiquitin ligase complex
G0:0090175	4	regulation of establishment of planar polarity
G0:0022037	4	metencephalon development
G0:0014802	4	terminal cisterna
G0:0019318	4	hexose metabolic process
G0:0032966	4	negative regulation of collagen biosynthetic process
G0:0007042	4	lysosomal lumen acidification
G0:0033563	4	dorsal/ventral axon guidance
G0:0021957	4	corticospinal tract morphogenesis
G0:0032611	4	interleukin-1 beta production
G0:0045619	4	regulation of lymphocyte differentiation
G0:0005047	4	signal recognition particle binding
G0:0034755	4	iron ion transmembrane transport
G0:0097114	4	N-methyl-D-aspartate receptor clustering
G0:0060713	4	labyrinthine layer morphogenesis
G0:0030375	4	thyroid hormone receptor coactivator activity
G0:0003383	4	apical constriction
G0:0021569	4	rhombomere 3 development
G0:0007386	4	compartment pattern specification
G0:0046425	4	regulation of JAK-STAT cascade
G0:0051645	4	Golgi localization
G0:0033504	4	floor plate development
G0:0061088	4	regulation of sequestering of zinc ion
G0:0060528	4	secretory columnar luminal epithelial cell differentiation involved in
prostate glandular acinus		development
G0:0048570	4	notochord morphogenesis
G0:0035434	4	copper ion transmembrane transport
G0:0042520	4	positive regulation of tyrosine phosphorylation of Stat4 protein
G0:0052845	4	inositol-5-diphosphate-1,2,3,4,6-pentakisphosphate diphosphatase activity
G0:0052844	4	inositol-3-diphosphate-1,2,4,5,6-pentakisphosphate diphosphatase activity
G0:0052847	4	inositol-1,5-bisdiphosphate-2,3,4,6-tetrakisphosphate 5-diphosphatase
activity		
G0:0052846	4	inositol-1,5-bisdiphosphate-2,3,4,6-tetrakisphosphate 1-diphosphatase
activity		
G0:0052841	4	inositol bisdiphosphate tetrakisphosphate diphosphatase activity
G0:0052843	4	inositol-1-diphosphate-2,3,4,5,6-pentakisphosphate diphosphatase activity
G0:0052842	4	inositol diphosphate pentakisphosphate diphosphatase activity
G0:0006166	4	purine ribonucleoside salvage
G0:0004839	4	ubiquitin activating enzyme activity
G0:0031489	4	myosin V binding

G0:0090116	4	C-5 methylation of cytosine
G0:0046683	4	response to organophosphorus
G0:0045922	4	negative regulation of fatty acid metabolic process
G0:0032909	4	regulation of transforming growth factor beta2 production
G0:0033503	4	HULC complex
G0:0008526	4	phosphatidylinositol transporter activity
G0:0021978	4	telencephalon regionalization
G0:0070257	4	positive regulation of mucus secretion
G0:0034190	3	apolipoprotein receptor binding
G0:0050833	3	pyruvate transmembrane transporter activity
G0:0034776	3	response to histamine
G0:1900165	3	negative regulation of interleukin-6 secretion
G0:1900164	3	nodal signaling pathway involved in determination of lateral mesoderm
left/right asymmetry		
G0:0051788	3	response to misfolded protein
G0:0006598	3	polyamine catabolic process
G0:0060266	3	negative regulation of respiratory burst involved in inflammatory response
G0:0006591	3	ornithine metabolic process
G0:0010903	3	negative regulation of very-low-density lipoprotein particle remodeling
G0:0051877	3	pigment granule aggregation in cell center
G0:0007621	3	negative regulation of female receptivity
G0:0006627	3	protein processing involved in protein targeting to mitochondrion
G0:0048388	3	endosomal lumen acidification
G0:0004995	3	tachykinin receptor activity
G0:0004449	3	isocitrate dehydrogenase (NAD+) activity
G0:0004992	3	platelet activating factor receptor activity
G0:0055005	3	ventricular cardiac myofibril assembly
G0:0043987	3	histone H3-S10 phosphorylation
G0:0004802	3	transketolase activity
G0:0031324	3	negative regulation of cellular metabolic process
G0:0002902	3	regulation of B cell apoptotic process
G0:0032933	3	SREBP signaling pathway
G0:0004800	3	thyroxine 5'-deiodinase activity
G0:0051668	3	localization within membrane
G0:0035166	3	post-embryonic hemopoiesis
G0:0061419	3	positive regulation of transcription from RNA polymerase II promoter in
response to hypoxia		
G0:0042094	3	interleukin-2 biosynthetic process
G0:0048550	3	negative regulation of pinocytosis
G0:0048553	3	negative regulation of metalloenzyme activity
G0:0072012	3	glomerulus vasculature development
G0:0008207	3	C21-steroid hormone metabolic process
G0:0050254	3	rhodopsin kinase activity
G0:2000105	3	positive regulation of DNA-dependent DNA replication
G0:0008502	3	melatonin receptor activity
G0:0032651	3	regulation of interleukin-1 beta production
G0:0008274	3	gamma-tubulin ring complex
G0:0070508	3	cholesterol import
G0:0003910	3	DNA ligase (ATP) activity
G0:0071107	3	response to parathyroid hormone
G0:0050819	3	negative regulation of coagulation
G0:0097155	3	fasciculation of sensory neuron axon
G0:0097159	3	organic cyclic compound binding
G0:0061084	3	negative regulation of protein refolding
G0:0072282	3	metanephric nephron tubule morphogenesis
G0:0031838	3	haptoglobin-hemoglobin complex
G0:0034584	3	piRNA binding
G0:0015015	3	heparan sulfate proteoglycan biosynthetic process, enzymatic modification
G0:0004464	3	leukotriene-C4 synthase activity
G0:0004465	3	lipoprotein lipase activity
G0:0004466	3	long-chain-acyl-CoA dehydrogenase activity
G0:0004461	3	lactose synthase activity
G0:0008970	3	phosphatidylcholine 1-acylhydrolase activity
G0:0001996	3	positive regulation of heart rate by epinephrine-norepinephrine
G0:0021521	3	ventral spinal cord interneuron specification
G0:0021524	3	visceral motor neuron differentiation
G0:0021834	3	chemorepulsion involved in embryonic olfactory bulb interneuron precursor
migration		
G0:0021529	3	spinal cord oligodendrocyte cell differentiation
G0:0046600	3	negative regulation of centriole replication
G0:0007207	3	phospholipase C-activating G-protein coupled acetylcholine receptor
signaling pathway		
G0:0018125	3	peptidyl-cysteine methylation
G0:0021781	3	glial cell fate commitment
G0:0002922	3	positive regulation of humoral immune response

G0:0045079	3	negative regulation of chemokine biosynthetic process
G0:0033260	3	nuclear cell cycle DNA replication
G0:0050912	3	detection of chemical stimulus involved in sensory perception of taste
G0:0033269	3	internode region of axon
G0:0006344	3	maintenance of chromatin silencing
G0:0003199	3	endocardial cushion to mesenchymal transition involved in heart valve formation
G0:0004999	3	vasoactive intestinal polypeptide receptor activity
G0:0042345	3	regulation of NF-kappaB import into nucleus
G0:0000189	3	MAPK import into nucleus
G0:0031735	3	CCR10 chemokine receptor binding
G0:0060126	3	somatotropin secreting cell differentiation
G0:0060128	3	corticotropin hormone secreting cell differentiation
G0:0016048	3	detection of temperature stimulus
G0:0009166	3	nucleotide catabolic process
G0:0050220	3	prostaglandin-E synthase activity
G0:0071453	3	cellular response to oxygen levels
G0:0035995	3	detection of muscle stretch
G0:0046546	3	development of primary male sexual characteristics
G0:0042825	3	TAP complex
G0:0043415	3	positive regulation of skeletal muscle tissue regeneration
G0:0072673	3	lamellipodium morphogenesis
G0:0000404	3	heteroduplex DNA loop binding
G0:0070569	3	uridylyltransferase activity
G0:0071168	3	protein localization to chromatin
G0:0043256	3	laminin complex
G0:0002554	3	serotonin secretion by platelet
G0:0032675	3	regulation of interleukin-6 production
G0:0035282	3	segmentation
G0:0035284	3	brain segmentation
G0:0042759	3	long-chain fatty acid biosynthetic process
G0:0006663	3	platelet activating factor biosynthetic process
G0:0006931	3	substrate-dependent cell migration, cell attachment to substrate
G0:0090074	3	negative regulation of protein homodimerization activity
G0:0098519	3	nucleotide phosphatase activity, acting on free nucleotides
G0:0051180	3	vitamin transport
G0:0090400	3	stress-induced premature senescence
G0:0007228	3	positive regulation of hh target transcription factor activity
G0:0070172	3	positive regulation of tooth mineralization
G0:2000669	3	negative regulation of dendritic cell apoptotic process
G0:0061458	3	reproductive system development
G0:0014706	3	striated muscle tissue development
G0:0014707	3	branchiomer skeletal muscle development
G0:0003273	3	cell migration involved in endocardial cushion formation
G0:0086070	3	SA node cell to atrial cardiac muscle cell communication
G0:0033829	3	O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase activity
G0:0031752	3	D5 dopamine receptor binding
G0:0031750	3	D3 dopamine receptor binding
G0:0060492	3	lung induction
G0:0047756	3	chondroitin 4-sulfotransferase activity
G0:0005250	3	A-type (transient outward) potassium channel activity
G0:0001306	3	age-dependent response to oxidative stress
G0:0001302	3	replicative cell aging
G0:2001016	3	positive regulation of skeletal muscle cell differentiation
G0:0003726	3	double-stranded RNA adenosine deaminase activity
G0:0008898	3	S-adenosylmethionine-homocysteine S-methyltransferase activity
G0:0018394	3	peptidyl-lysine acetylation
G0:0008097	3	5S rRNA binding
G0:0010659	3	cardiac muscle cell apoptotic process
G0:0008238	3	exopeptidase activity
G0:0001573	3	ganglioside metabolic process
G0:0016480	3	negative regulation of transcription from RNA polymerase III promoter
G0:0070545	3	PeBoW complex
G0:0031401	3	positive regulation of protein modification process
G0:0019287	3	isopentenyl diphosphate biosynthetic process, mevalonate pathway
G0:0032696	3	negative regulation of interleukin-13 production
G0:0010501	3	RNA secondary structure unwinding
G0:0050855	3	regulation of B cell receptor signaling pathway
G0:0033128	3	negative regulation of histone phosphorylation
G0:0046582	3	Rap GTPase activator activity
G0:0071639	3	positive regulation of monocyte chemotactic protein-1 production
G0:0071638	3	negative regulation of monocyte chemotactic protein-1 production
G0:0046639	3	negative regulation of alpha-beta T cell differentiation
G0:0035404	3	histone-serine phosphorylation
G0:0061153	3	trachea gland development

G0:0004937	3	alpha1-adrenergic receptor activity
G0:0004938	3	alpha2-adrenergic receptor activity
G0:0005338	3	nucleotide-sugar transmembrane transporter activity
G0:0042631	3	cellular response to water deprivation
G0:0098536	3	deuterosome
G0:0019076	3	viral release from host cell
G0:0045198	3	establishment of epithelial cell apical/basal polarity
G0:0060948	3	cardiac vascular smooth muscle cell development
G0:0015562	3	efflux transmembrane transporter activity
G0:0060012	3	synaptic transmission, glycinergic
G0:0046649	3	lymphocyte activation
G0:0021877	3	forebrain neuron fate commitment
G0:0021871	3	forebrain regionalization
G0:0047045	3	testosterone 17-beta-dehydrogenase (NADP+) activity
G0:0072429	3	response to intra-S DNA damage checkpoint signaling
G0:0008431	3	vitamin E binding
G0:0034673	3	inhibin-betaglycan-ActRII complex
G0:0035385	3	Roundabout signaling pathway
G0:0010866	3	regulation of triglyceride biosynthetic process
G0:0019262	3	N-acetylneuraminase catabolic process
G0:0060160	3	negative regulation of dopamine receptor signaling pathway
G0:0046661	3	male sex differentiation
G0:0046058	3	cAMP metabolic process
G0:0048133	3	male germ-line stem cell asymmetric division
G0:0072193	3	ureter smooth muscle cell differentiation
G0:0016857	3	racemase and epimerase activity, acting on carbohydrates and derivatives
G0:0000056	3	ribosomal small subunit export from nucleus
G0:0033864	3	positive regulation of NAD(P)H oxidase activity
G0:0051434	3	BH3 domain binding
G0:0019448	3	L-cysteine catabolic process
G0:0008241	3	peptidyl-dipeptidase activity
G0:0051373	3	FAT2 binding
G0:0006562	3	proline catabolic process
G0:0032450	3	maltose alpha-glucosidase activity
G0:0034445	3	negative regulation of plasma lipoprotein particle oxidation
G0:0034112	3	positive regulation of homotypic cell-cell adhesion
G0:0033326	3	cerebrospinal fluid secretion
G0:0016615	3	malate dehydrogenase activity
G0:0002513	3	tolerance induction to self antigen
G0:0010521	3	telomerase inhibitor activity
G0:0010523	3	negative regulation of calcium ion transport into cytosol
G0:0070885	3	negative regulation of calcineurin-NFAT signaling cascade
G0:1901077	3	regulation of relaxation of muscle
G0:0001159	3	core promoter proximal region DNA binding
G0:0035246	3	peptidyl-arginine N-methylation
G0:0072011	3	glomerular endothelium development
G0:0010988	3	regulation of low-density lipoprotein particle clearance
G0:0010980	3	positive regulation of vitamin D 24-hydroxylase activity
G0:0048302	3	regulation of isotype switching to IgG isotypes
G0:2000286	3	receptor internalization involved in canonical Wnt signaling pathway
G0:2001242	3	regulation of intrinsic apoptotic signaling pathway
G0:2000021	3	regulation of ion homeostasis
G0:0090036	3	regulation of protein kinase C signaling
G0:0051142	3	positive regulation of NK T cell proliferation
G0:0044300	3	cerebellar mossy fiber
G0:0032849	3	positive regulation of cellular pH reduction
G0:0043652	3	engulfment of apoptotic cell
G0:0019054	3	modulation by virus of host process
G0:0038171	3	cannabinoid signaling pathway
G0:0055118	3	negative regulation of cardiac muscle contraction
G0:0052723	3	inositol hexakisphosphate 1-kinase activity
G0:0052724	3	inositol hexakisphosphate 3-kinase activity
G0:0045066	3	regulatory T cell differentiation
G0:0043227	3	membrane-bounded organelle
G0:0004980	3	melanocyte-stimulating hormone receptor activity
G0:0002331	3	pre-B cell allelic exclusion
G0:0061364	3	apoptotic process involved in luteolysis
G0:0031937	3	positive regulation of chromatin silencing
G0:0097431	3	mitotic spindle pole
G0:0009988	3	cell-cell recognition
G0:0009187	3	cyclic nucleotide metabolic process
G0:2001055	3	positive regulation of mesenchymal cell apoptotic process
G0:0050252	3	retinol O-fatty-acyltransferase activity
G0:0004582	3	dolichyl-phosphate beta-D-mannosyltransferase activity
G0:0002677	3	negative regulation of chronic inflammatory response

G0:0072189	3	ureter development
G0:0004769	3	steroid delta-isomerase activity
G0:0045309	3	protein phosphorylated amino acid binding
G0:2000729	3	positive regulation of mesenchymal cell proliferation involved in ureter development
G0:0006354	3	DNA-templated transcription, elongation
G0:0000463	3	maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
G0:0000466	3	maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
G0:0070585	3	protein localization to mitochondrion
G0:0051351	3	positive regulation of ligase activity
G0:0001845	3	phagolysosome assembly
G0:0001846	3	opsonin binding
G0:0046543	3	development of secondary female sexual characteristics
G0:0046544	3	development of secondary male sexual characteristics
G0:0046010	3	positive regulation of circadian sleep/wake cycle, non-REM sleep
G0:0007113	3	endomitotic cell cycle
G0:0038091	3	positive regulation of cell proliferation by VEGF-activated platelet derived growth factor receptor signaling pathway
G0:0071674	3	mononuclear cell migration
G0:0033300	3	dehydroascorbic acid transporter activity
G0:0034465	3	response to carbon monoxide
G0:0015697	3	quaternary ammonium group transport
G0:0017136	3	NAD-dependent histone deacetylase activity
G0:0045899	3	positive regulation of RNA polymerase II transcriptional preinitiation complex assembly
G0:0000268	3	peroxisome targeting sequence binding
G0:0072136	3	metanephric mesenchymal cell proliferation involved in metanephros development
G0:0009048	3	dosage compensation by inactivation of X chromosome
G0:0036289	3	peptidyl-serine autophosphorylation
G0:0032792	3	negative regulation of CREB transcription factor activity
G0:0019031	3	viral envelope
G0:2000974	3	negative regulation of pro-B cell differentiation
G0:0043243	3	positive regulation of protein complex disassembly
G0:0045163	3	clustering of voltage-gated potassium channels
G0:0060438	3	trachea development
G0:0015810	3	aspartate transport
G0:0010829	3	negative regulation of glucose transport
G0:0051932	3	synaptic transmission, GABAergic
G0:0045959	3	negative regulation of complement activation, classical pathway
G0:0006706	3	steroid catabolic process
G0:1902175	3	regulation of oxidative stress-induced intrinsic apoptotic signaling pathway
G0:0005967	3	mitochondrial pyruvate dehydrogenase complex
G0:0004563	3	beta-N-acetylhexosaminidase activity
G0:0008073	3	ornithine decarboxylase inhibitor activity
G0:0016891	3	endoribonuclease activity, producing 5'-phosphomonoesters
G0:0000015	3	phosphopyruvate hydratase complex
G0:0031664	3	regulation of lipopolysaccharide-mediated signaling pathway
G0:0004705	3	JUN kinase activity
G0:0004706	3	JUN kinase kinase kinase activity
G0:0018023	3	peptidyl-lysine trimethylation
G0:0045321	3	leukocyte activation
G0:0045323	3	interleukin-1 receptor complex
G0:0000275	3	mitochondrial proton-transporting ATP synthase complex, catalytic core F(1)
G0:0070971	3	endoplasmic reticulum exit site
G0:0019959	3	interleukin-8 binding
G0:0010560	3	positive regulation of glycoprotein biosynthetic process
G0:0072345	3	NAADP-sensitive calcium-release channel activity
G0:0033363	3	secretory granule organization
G0:0035754	3	B cell chemotaxis
G0:0002074	3	extraocular skeletal muscle development
G0:0033185	3	dolichol-phosphate-mannose synthase complex
G0:0033186	3	CAF-1 complex
G0:0016533	3	cyclin-dependent protein kinase 5 holoenzyme complex
G0:0030185	3	nitric oxide transport
G0:0046691	3	intracellular canaliculus
G0:0072350	3	tricarboxylic acid metabolic process
G0:0060084	3	synaptic transmission involved in micturition
G0:0031301	3	integral component of organelle membrane
G0:0031587	3	positive regulation of inositol 1,4,5-trisphosphate-sensitive calcium-release channel activity

G0:0009299	3	mRNA transcription
G0:0051106	3	positive regulation of DNA ligation
G0:0051100	3	negative regulation of binding
G0:0004045	3	aminoacyl-tRNA hydrolase activity
G0:0032800	3	receptor biosynthetic process
G0:0010159	3	specification of organ position
G0:0019012	3	virion
G0:0070682	3	proteasome regulatory particle assembly
G0:0032119	3	sequestering of zinc ion
G0:1900182	3	positive regulation of protein localization to nucleus
G0:0000819	3	sister chromatid segregation
G0:0007506	3	gonadal mesoderm development
G0:0071224	3	cellular response to peptidoglycan
G0:0071221	3	cellular response to bacterial lipopeptide
G0:0043260	3	laminin-11 complex
G0:0061087	3	positive regulation of histone H3-K27 methylation
G0:0061086	3	negative regulation of histone H3-K27 methylation
G0:0097211	3	cellular response to gonadotropin-releasing hormone
G0:0000942	3	condensed nuclear chromosome outer kinetochore
G0:0015879	3	carnitine transport
G0:0010807	3	regulation of synaptic vesicle priming
G0:0007500	3	mesodermal cell fate determination
G0:0005944	3	1-phosphatidylinositol-4-phosphate 3-kinase, class IB complex
G0:1903208	3	negative regulation of hydrogen peroxide-induced neuron death
G0:0036265	3	RNA (guanine-N7)-methylation
G0:0048483	3	autonomic nervous system development
G0:1990050	3	phosphatidic acid transporter activity
G0:0002016	3	regulation of blood volume by renin-angiotensin
G0:0048625	3	myoblast fate commitment
G0:0000033	3	alpha-1,3-mannosyltransferase activity
G0:0034391	3	regulation of smooth muscle cell apoptotic process
G0:0018022	3	peptidyl-lysine methylation
G0:0051310	3	metaphase plate congression
G0:0032342	3	aldosterone biosynthetic process
G0:0019976	3	interleukin-2 binding
G0:0010587	3	miRNA catabolic process
G0:0071417	3	cellular response to organonitrogen compound
G0:2000768	3	positive regulation of nephron tubule epithelial cell differentiation
G0:0070325	3	lipoprotein particle receptor binding
G0:0070327	3	thyroid hormone transport
G0:0004013	3	adenosylhomocysteinase activity
G0:0042415	3	norepinephrine metabolic process
G0:0035773	3	insulin secretion involved in cellular response to glucose stimulus
G0:0048808	3	male genitalia morphogenesis
G0:0003095	3	pressure natriuresis
G0:0005594	3	collagen type IX trimer
G0:0046501	3	protoporphyrinogen IX metabolic process
G0:0045851	3	pH reduction
G0:0006574	3	valine catabolic process
G0:0006576	3	cellular biogenic amine metabolic process
G0:0015746	3	citrate transport
G0:0060066	3	oviduct development
G0:0097009	3	energy homeostasis
G0:0009263	3	deoxyribonucleotide biosynthetic process
G0:0051123	3	RNA polymerase II transcriptional preinitiation complex assembly
G0:0051128	3	regulation of cellular component organization
G0:0009008	3	DNA-methyltransferase activity
G0:0001652	3	granular component
G0:0032289	3	central nervous system myelin formation
G0:1901223	3	negative regulation of NIK/NF-kappaB signaling
G0:0003876	3	AMP deaminase activity
G0:0019563	3	glycerol catabolic process
G0:0070669	3	response to interleukin-2
G0:0004062	3	aryl sulfotransferase activity
G0:0019557	3	histidine catabolic process to glutamate and formate
G0:0040013	3	negative regulation of locomotion
G0:0032139	3	dinucleotide insertion or deletion binding
G0:0016167	3	glial cell-derived neurotrophic factor receptor activity
G0:0034447	3	very-low-density lipoprotein particle clearance
G0:0006296	3	nucleotide-excision repair, DNA incision, 5'-to lesion
G0:0015853	3	adenine transport
G0:0001012	3	RNA polymerase II regulatory region DNA binding
G0:0032446	3	protein modification by small protein conjugation
G0:0043331	3	response to dsRNA
G0:0004525	3	ribonuclease III activity

G0:0005218	3	intracellular ligand-gated calcium channel activity
G0:0004647	3	phosphoserine phosphatase activity
G0:0008295	3	spermidine biosynthetic process
G0:0008294	3	calcium- and calmodulin-responsive adenylate cyclase activity
G0:0015081	3	sodium ion transmembrane transporter activity
G0:0001826	3	inner cell mass cell differentiation
G0:0045726	3	positive regulation of integrin biosynthetic process
G0:0072278	3	metanephric comma-shaped body morphogenesis
G0:0072277	3	metanephric glomerular capillary formation
G0:1900744	3	regulation of p38MAPK cascade
G0:1900748	3	positive regulation of vascular endothelial growth factor signaling pathway
G0:0060043	3	regulation of cardiac muscle cell proliferation
G0:0072144	3	glomerular mesangial cell development
G0:0017159	3	pantetheine hydrolase activity
G0:0017151	3	DEAD/H-box RNA helicase binding
G0:0002035	3	brain renin-angiotensin system
G0:0002034	3	regulation of blood vessel size by renin-angiotensin
G0:0002032	3	desensitization of G-protein coupled receptor protein signaling pathway by arrestin
G0:0071008	3	U2-type post-mRNA release spliceosomal complex
G0:0036091	3	positive regulation of transcription from RNA polymerase II promoter in response to oxidative stress
G0:0000179	3	rRNA (adenine-N6,N6-)-dimethyltransferase activity
G0:0000177	3	cytoplasmic exosome (RNase complex)
G0:0004882	3	androgen receptor activity
G0:0004886	3	9-cis retinoic acid receptor activity
G0:0070644	3	vitamin D response element binding
G0:0004082	3	bisphosphoglycerate mutase activity
G0:0004083	3	bisphosphoglycerate 2-phosphatase activity
G0:0048852	3	diencephalon morphogenesis
G0:0070424	3	regulation of nucleotide-binding oligomerization domain containing signaling pathway
G0:0060401	3	cytosolic calcium ion transport
G0:0050698	3	proteoglycan sulfotransferase activity
G0:0033602	3	negative regulation of dopamine secretion
G0:0050691	3	regulation of defense response to virus by host
G0:0051447	3	negative regulation of meiotic cell cycle
G0:0071774	3	response to fibroblast growth factor
G0:0035033	3	histone deacetylase regulator activity
G0:0035524	3	proline transmembrane transport
G0:0035526	3	retrograde transport, plasma membrane to Golgi
G0:0035522	3	monoubiquitinated histone H2A deubiquitination
G0:0035529	3	NADH pyrophosphatase activity
G0:0030008	3	TRAPP complex
G0:0042369	3	vitamin D catabolic process
G0:0042360	3	vitamin E metabolic process
G0:0000340	3	RNA 7-methylguanosine cap binding
G0:0004505	3	phenylalanine 4-monooxygenase activity
G0:0042775	3	mitochondrial ATP synthesis coupled electron transport
G0:0042773	3	ATP synthesis coupled electron transport
G0:0046929	3	negative regulation of neurotransmitter secretion
G0:0050473	3	arachidonate 15-lipoxygenase activity
G0:1902513	3	regulation of organelle transport along microtubule
G0:0002826	3	negative regulation of T-helper 1 type immune response
G0:0002820	3	negative regulation of adaptive immune response
G0:0007529	3	establishment of synaptic specificity at neuromuscular junction
G0:0010637	3	negative regulation of mitochondrial fusion
G0:0036374	3	glutathione hydrolase activity
G0:0001591	3	dopamine neurotransmitter receptor activity, coupled via Gi/Go
G0:0003997	3	acyl-CoA oxidase activity
G0:0044030	3	regulation of DNA methylation
G0:0060083	3	smooth muscle contraction involved in micturition
G0:2000017	3	positive regulation of determination of dorsal identity
G0:0030505	3	inorganic diphosphate transport
G0:0010841	3	positive regulation of circadian sleep/wake cycle, wakefulness
G0:0019240	3	citrulline biosynthetic process
G0:0042175	3	nuclear outer membrane-endoplasmic reticulum membrane network
G0:0003051	3	angiotensin-mediated drinking behavior
G0:0043398	3	HLH domain binding
G0:0044211	3	CTP salvage
G0:0019862	3	IgA binding
G0:0019867	3	outer membrane
G0:0071942	3	XPC complex
G0:0060027	3	convergent extension involved in gastrulation

G0:0060024	3	rhythmic synaptic transmission
G0:0060020	3	Bergmann glial cell differentiation
G0:0097513	3	myosin II filament
G0:0061198	3	fungiform papilla formation
G0:0046103	3	inosine biosynthetic process
G0:0009597	3	detection of virus
G0:0009595	3	detection of biotic stimulus
G0:0050803	3	regulation of synapse structure and activity
G0:0031296	3	B cell costimulation
G0:1902495	3	transmembrane transporter complex
G0:0004311	3	farnesyltransferase activity
G0:0070996	3	type 1 melanocortin receptor binding
G0:0042904	3	9-cis-retinoic acid biosynthetic process
G0:2000466	3	negative regulation of glycogen (starch) synthase activity
G0:2000467	3	positive regulation of glycogen (starch) synthase activity
G0:0033596	3	TSC1-TSC2 complex
G0:0033590	3	response to cobalamin
G0:0001781	3	neutrophil apoptotic process
G0:0051425	3	PTB domain binding
G0:0005863	3	striated muscle myosin thick filament
G0:0007033	3	vacuole organization
G0:0000938	3	GARP complex
G0:0047086	3	ketosteroid monooxygenase activity
G0:0016884	3	carbon-nitrogen ligase activity, with glutamine as amido-N-donor
G0:0030241	3	skeletal muscle myosin thick filament assembly
G0:0033623	3	regulation of integrin activation
G0:0004739	3	pyruvate dehydrogenase (acetyl-transferring) activity
G0:0035054	3	embryonic heart tube anterior/posterior pattern specification
G0:0061038	3	uterus morphogenesis
G0:0031995	3	insulin-like growth factor II binding
G0:0005784	3	Sec61 translocon complex
G0:0005785	3	signal recognition particle receptor complex
G0:0003941	3	L-serine ammonia-lyase activity
G0:0042758	3	long-chain fatty acid catabolic process
G0:0072709	3	cellular response to sorbitol
G0:0072138	3	mesenchymal cell proliferation involved in ureteric bud development
G0:0004128	3	cytochrome-b5 reductase activity, acting on NAD(P)H
G0:0004127	3	cytidylate kinase activity
G0:0032507	3	maintenance of protein location in cell
G0:0032050	3	clathrin heavy chain binding
G0:0032051	3	clathrin light chain binding
G0:2000984	3	negative regulation of ATP citrate synthase activity
G0:0016715	3	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced ascorbate as one donor, and incorporation of one atom of oxygen
G0:0004873	3	asialoglycoprotein receptor activity
G0:0043506	3	regulation of JUN kinase activity
G0:0043504	3	mitochondrial DNA repair
G0:0070383	3	DNA cytosine deamination
G0:0071034	3	CUT catabolic process
G0:0061205	3	paramesonephric duct development
G0:0060559	3	positive regulation of caldiol 1-monooxygenase activity
G0:0097062	3	dendritic spine maintenance
G0:0065002	3	intracellular protein transmembrane transport
G0:0004332	3	fructose-bisphosphate aldolase activity
G0:0006868	3	glutamine transport
G0:0045226	3	extracellular polysaccharide biosynthetic process
G0:0070972	3	protein localization to endoplasmic reticulum
G0:0070602	3	regulation of centromeric sister chromatid cohesion
G0:0031415	3	NatA complex
G0:2000195	3	negative regulation of female gonad development
G0:0045007	3	depurination
G0:0045006	3	DNA deamination
G0:0045590	3	negative regulation of regulatory T cell differentiation
G0:0051097	3	negative regulation of helicase activity
G0:0051546	3	keratinocyte migration
G0:0002317	3	plasma cell differentiation
G0:0032991	3	macromolecular complex
G0:0071731	3	response to nitric oxide
G0:0071733	3	transcriptional activation by promoter-enhancer looping
G0:0033026	3	negative regulation of mast cell apoptotic process
G0:0030229	3	very-low-density lipoprotein particle receptor activity
G0:0000104	3	succinate dehydrogenase activity
G0:0061010	3	gall bladder development
G0:0061014	3	positive regulation of mRNA catabolic process

G0:0006278	3	RNA-dependent DNA replication
G0:0010883	3	regulation of lipid storage
G0:0000309	3	nicotinamide-nucleotide adenylyltransferase activity
G0:1901727	3	positive regulation of histone deacetylase activity
G0:0031313	3	extrinsic component of endosome membrane
G0:0072148	3	epithelial cell fate commitment
G0:0048408	3	epidermal growth factor binding
G0:0004656	3	procollagen-proline 4-dioxygenase activity
G0:0002192	3	IRES-dependent translational initiation
G0:0002193	3	MAML1-RBP-Jkappa- ICN1 complex
G0:0048641	3	regulation of skeletal muscle tissue development
G0:0009414	3	response to water deprivation
G0:0004104	3	cholinesterase activity
G0:0036336	3	dendritic cell migration
G0:0003136	3	negative regulation of heart induction by canonical Wnt signaling pathway
G0:0003130	3	BMP signaling pathway involved in heart induction
G0:0055098	3	response to low-density lipoprotein particle
G0:0001885	3	endothelial cell development
G0:0055092	3	sterol homeostasis
G0:0032527	3	protein exit from endoplasmic reticulum
G0:0042133	3	neurotransmitter metabolic process
G0:1901897	3	regulation of relaxation of cardiac muscle
G0:1901020	3	negative regulation of calcium ion transmembrane transporter activity
G0:0034201	3	response to oleic acid
G0:0019826	3	oxygen sensor activity
G0:0060574	3	intestinal epithelial cell maturation
G0:0060571	3	morphogenesis of an epithelial fold
G0:0015918	3	sterol transport
G0:0060579	3	ventral spinal cord interneuron fate commitment
G0:0046322	3	negative regulation of fatty acid oxidation
G0:0046498	3	S-adenosylhomocysteine metabolic process
G0:0002767	3	immune response-inhibiting cell surface receptor signaling pathway
G0:0045408	3	regulation of interleukin-6 biosynthetic process
G0:0030984	3	kininogen binding
G0:0021536	3	diencephalon development
G0:0035330	3	regulation of hippo signaling
G0:0035331	3	negative regulation of hippo signaling
G0:0086080	3	protein binding involved in heterotypic cell-cell adhesion
G0:0045143	3	homologous chromosome segregation
G0:0004351	3	glutamate decarboxylase activity
G0:0045200	3	establishment of neuroblast polarity
G0:0016972	3	thiol oxidase activity
G0:0035990	3	tendon cell differentiation
G0:0009624	3	response to nematode
G0:0032203	3	telomere formation via telomerase
G0:0019254	3	carnitine metabolic process, CoA-linked
G0:0014834	3	skeletal muscle satellite cell maintenance involved in skeletal muscle regeneration
G0:0044154	3	histone H3-K14 acetylation
G0:0015125	3	bile acid transmembrane transporter activity
G0:0071535	3	RING-like zinc finger domain binding
G0:0030035	3	microspike assembly
G0:0007079	3	mitotic chromosome movement towards spindle pole
G0:0050682	3	AF-2 domain binding
G0:0071288	3	cellular response to mercury ion
G0:0033003	3	regulation of mast cell activation
G0:0070837	3	dehydroascorbic acid transport
G0:0030201	3	heparan sulfate proteoglycan metabolic process
G0:0072577	3	endothelial cell apoptotic process
G0:0006210	3	thymine catabolic process
G0:0006213	3	pyrimidine nucleoside metabolic process
G0:0072672	3	neutrophil extravasation
G0:0000320	3	re-entry into mitotic cell cycle
G0:0050883	3	musculoskeletal movement, spinal reflex action
G0:1900135	3	positive regulation of renin secretion into blood stream
G0:0031849	3	olfactory receptor binding
G0:0060742	3	epithelial cell differentiation involved in prostate gland development
G0:0060741	3	prostate gland stromal morphogenesis
G0:0009436	3	glyoxylate catabolic process
G0:0070562	3	regulation of vitamin D receptor signaling pathway
G0:0002248	3	connective tissue replacement involved in inflammatory response wound healing
G0:0004165	3	dodecenoyl-CoA delta-isomerase activity
G0:0004167	3	dopachrome isomerase activity
G0:0070293	3	renal absorption

G0:0031064	3	negative regulation of histone deacetylation
G0:0006982	3	response to lipid hydroperoxide
G0:0003358	3	noradrenergic neuron development
G0:0008475	3	procollagen-lysine 5-dioxygenase activity
G0:0008474	3	palmitoyl-(protein) hydrolase activity
G0:0003350	3	pulmonary myocardium development
G0:0070032	3	synaptobrevin 2-SNAP-25-syntaxin-1a-complexin I complex
G0:0032010	3	phagolysosome
G0:0034261	3	negative regulation of Ras GTPase activity
G0:0030942	3	endoplasmic reticulum signal peptide binding
G0:0002408	3	myeloid dendritic cell chemotaxis
G0:0030947	3	regulation of vascular endothelial growth factor receptor signaling pathway
G0:0022007	3	convergent extension involved in neural plate elongation
G0:0034088	3	maintenance of mitotic sister chromatid cohesion
G0:0002741	3	positive regulation of cytokine secretion involved in immune response
G0:0070487	3	monocyte aggregation
G0:0051612	3	negative regulation of serotonin uptake
G0:0060513	3	prostatic bud formation
G0:0009279	3	cell outer membrane
G0:0042510	3	regulation of tyrosine phosphorylation of Stat1 protein
G0:0006154	3	adenosine catabolic process
G0:0016939	3	kinesin II complex
G0:0070858	3	negative regulation of bile acid biosynthetic process
G0:0090161	3	Golgi ribbon formation
G0:0048807	3	female genitalia morphogenesis
G0:0022028	3	tangential migration from the subventricular zone to the olfactory bulb
G0:0032226	3	positive regulation of synaptic transmission, dopaminergic
G0:0051586	3	positive regulation of dopamine uptake involved in synaptic transmission
G0:0032437	3	cuticular plate
G0:0070201	3	regulation of establishment of protein localization
G0:0032959	3	inositol trisphosphate biosynthetic process
G0:0032958	3	inositol phosphate biosynthetic process
G0:0030886	3	negative regulation of myeloid dendritic cell activation
G0:0030881	3	beta-2-microglobulin binding
G0:0033687	3	osteoblast proliferation
G0:0033683	3	nucleotide-excision repair, DNA incision
G0:0045621	3	positive regulation of lymphocyte differentiation
G0:0045626	3	negative regulation of T-helper 1 cell differentiation
G0:0031649	3	heat generation
G0:0006235	3	dTTP biosynthetic process
G0:0004723	3	calcium-dependent protein serine/threonine phosphatase activity
G0:0031133	3	regulation of axon diameter
G0:0090310	3	negative regulation of methylation-dependent chromatin silencing
G0:0010956	3	negative regulation of calcidiol 1-monooxygenase activity
G0:1902083	3	negative regulation of peptidyl-cysteine S-nitrosylation
G0:0055056	3	D-glucose transmembrane transporter activity
G0:0036042	3	long-chain fatty acyl-CoA binding
G0:0004634	3	phosphopyruvate hydratase activity
G0:0018158	3	protein oxidation
G0:0070052	3	collagen V binding
G0:0070050	3	neuron cellular homeostasis
G0:0070051	3	fibrinogen binding
G0:2000360	3	negative regulation of binding of sperm to zona pellucida
G0:2000366	3	positive regulation of STAT protein import into nucleus
G0:0021559	3	trigeminal nerve development
G0:0032564	3	dATP binding
G0:0010762	3	regulation of fibroblast migration
G0:0016082	3	synaptic vesicle priming
G0:0021775	3	smoothed signaling pathway involved in ventral spinal cord interneuron specification
G0:0021776	3	smoothed signaling pathway involved in spinal cord motor neuron cell fate specification
G0:0071899	3	negative regulation of estrogen receptor binding
G0:0048340	3	paraxial mesoderm morphogenesis
G0:0047374	3	methylumbelliferyl-acetate deacetylase activity
G0:0046185	3	aldehyde catabolic process
G0:0002438	3	acute inflammatory response to antigenic stimulus
G0:0002091	3	negative regulation of receptor internalization
G0:0002098	3	tRNA wobble uridine modification
G0:0006391	3	transcription initiation from mitochondrial promoter
G0:0035374	3	chondroitin sulfate binding
G0:0070915	3	lysophosphatidic acid receptor activity
G0:0036297	3	interstrand cross-link repair
G0:0008821	3	crossover junction endodeoxyribonuclease activity

G0:0014878	3	response to electrical stimulus involved in regulation of muscle adaptation
G0:0010482	3	regulation of epidermal cell division
G0:0036124	3	histone H3-K9 trimethylation
G0:0048295	3	positive regulation of isotype switching to IgE isotypes
G0:0036122	3	BMP binding
G0:0036123	3	histone H3-K9 dimethylation
G0:2000171	3	negative regulation of dendrite development
G0:0070093	3	negative regulation of glucagon secretion
G0:0070269	3	pyroptosis
G0:0070095	3	fructose-6-phosphate binding
G0:0042625	3	ATPase activity, coupled to transmembrane movement of ions
G0:0044299	3	C-fiber
G0:0045602	3	negative regulation of endothelial cell differentiation
G0:0019166	3	trans-2-enoyl-CoA reductase (NADPH) activity
G0:0047115	3	trans-1,2-dihydrobenzene-1,2-diol dehydrogenase activity
G0:0072539	3	T-helper 17 cell differentiation
G0:0043159	3	acrosomal matrix
G0:0034186	3	apolipoprotein A-I binding
G0:0031113	3	regulation of microtubule polymerization
G0:0097109	3	neurologin family protein binding
G0:0097108	3	hedgehog family protein binding
G0:0035583	3	sequestering of TGFbeta in extracellular matrix
G0:0035582	3	sequestering of BMP in extracellular matrix
G0:0051795	3	positive regulation of catagen
G0:0061630	3	ubiquitin protein ligase activity
G0:0097361	3	CIA complex
G0:0051861	3	glycolipid binding
G0:0007638	3	mechanosensory behavior
G0:0036462	3	TRAIL-activated apoptotic signaling pathway
G0:0002283	3	neutrophil activation involved in immune response
G0:0000720	3	pyrimidine dimer repair by nucleotide-excision repair
G0:0004619	3	phosphoglycerate mutase activity
G0:0034979	3	NAD-dependent protein deacetylase activity
G0:0021571	3	rhombomere 5 development
G0:0021575	3	hindbrain morphogenesis
G0:0010742	3	macrophage derived foam cell differentiation
G0:0021754	3	facial nucleus development
G0:0001936	3	regulation of endothelial cell proliferation
G0:0060745	3	mammary gland branching involved in pregnancy
G0:0046340	3	diacylglycerol catabolic process
G0:0051653	3	spindle localization
G0:1901164	3	negative regulation of trophoblast cell migration
G0:1901166	3	neural crest cell migration involved in autonomic nervous system development
G0:0035173	3	histone kinase activity
G0:0006116	3	NADH oxidation
G0:0043142	3	single-stranded DNA-dependent ATPase activity
G0:0043141	3	ATP-dependent 5'-3' DNA helicase activity
G0:0048936	3	peripheral nervous system neuron axonogenesis
G0:0070891	3	lipoteichoic acid binding
G0:0090292	3	nuclear matrix anchoring at nuclear membrane
G0:0050650	3	chondroitin sulfate proteoglycan biosynthetic process
G0:0031493	3	nucleosomal histone binding
G0:0060112	3	generation of ovulation cycle rhythm
G0:0060117	3	auditory receptor cell development
G0:0009396	3	folic acid-containing compound biosynthetic process
G0:0007403	3	glial cell fate determination
G0:0015187	3	glycine transmembrane transporter activity
G0:0015186	3	L-glutamine transmembrane transporter activity
G0:0015181	3	arginine transmembrane transporter activity
G0:0015180	3	L-alanine transmembrane transporter activity
G0:0015183	3	L-aspartate transmembrane transporter activity
G0:0001727	3	lipid kinase activity
G0:2000117	3	negative regulation of cysteine-type endopeptidase activity
G0:0070820	3	tertiary granule
G0:1901313	3	positive regulation of gene expression involved in extracellular matrix organization
G0:1901315	3	negative regulation of histone H2A K63-linked ubiquitination
G0:0003278	3	apoptotic process involved in heart morphogenesis
G0:0005958	3	DNA-dependent protein kinase-DNA ligase 4 complex
G0:0019367	3	fatty acid elongation, saturated fatty acid
G0:0070537	3	histone H2A K63-linked deubiquitination
G0:0044530	3	supraspliceosomal complex
G0:0006582	3	melanin metabolic process

G0:0060279	3	positive regulation of ovulation
G0:0046668	3	regulation of retinal cell programmed cell death
G0:0005588	3	collagen type V trimer
G0:0005589	3	collagen type VI trimer
G0:0031826	3	type 2A serotonin receptor binding
G0:2001180	3	negative regulation of interleukin-10 secretion
G0:2001181	3	positive regulation of interleukin-10 secretion
G0:0070579	3	methylcytosine dioxygenase activity
G0:0004982	3	N-formyl peptide receptor activity
G0:0043932	3	ossification involved in bone remodeling
G0:0004677	3	DNA-dependent protein kinase activity
G0:0018119	3	peptidyl-cysteine S-nitrosylation
G0:0072592	3	oxygen metabolic process
G0:0060913	3	cardiac cell fate determination
G0:0060916	3	mesenchymal cell proliferation involved in lung development
G0:0046874	3	quinolinate metabolic process
G0:0002934	3	desmosome organization
G0:0001913	3	T cell mediated cytotoxicity
G0:0033256	3	I-kappaB/NF-kappaB complex
G0:0030478	3	actin cap
G0:0009264	3	deoxyribonucleotide catabolic process
G0:0042577	3	lipid phosphatase activity
G0:0086001	3	cardiac muscle cell action potential
G0:0097443	3	sorting endosome
G0:0045918	3	negative regulation of cytolysis
G0:0015137	3	citrate transmembrane transporter activity
G0:0018343	3	protein farnesylation
G0:0001740	3	Barr body
G0:0090543	3	Flemming body
G0:0005220	3	inositol 1,4,5-trisphosphate-sensitive calcium-release channel activity
G0:0048143	3	astrocyte activation
G0:0019344	3	cysteine biosynthetic process
G0:0009056	3	catabolic process
G0:0019348	3	dolichol metabolic process
G0:0032649	3	regulation of interferon-gamma production
G0:0032648	3	regulation of interferon-beta production
G0:0043420	3	anthranilate metabolic process
G0:0045646	3	regulation of erythrocyte differentiation
G0:0071173	3	spindle assembly checkpoint
G0:0034141	3	positive regulation of toll-like receptor 3 signaling pathway
G0:0002158	3	osteoclast proliferation
G0:0046060	3	dATP metabolic process
G0:0046061	3	dATP catabolic process
G0:0046068	3	cGMP metabolic process
G0:0097149	3	centralspindlin complex
G0:0004117	3	calmodulin-dependent cyclic-nucleotide phosphodiesterase activity
G0:0002138	3	retinoic acid biosynthetic process
G0:0032946	3	positive regulation of mononuclear cell proliferation
G0:0030135	3	coated vesicle
G0:0032497	3	detection of lipopolysaccharide
G0:0004471	3	malate dehydrogenase (decarboxylating) (NAD+) activity
G0:0047894	3	flavonol 3-sulfotransferase activity
G0:0046883	3	regulation of hormone secretion
G0:0048069	3	eye pigmentation
G0:0046886	3	positive regulation of hormone biosynthetic process
G0:0021535	3	cell migration in hindbrain
G0:0021532	3	neural tube patterning
G0:0021530	3	spinal cord oligodendrocyte cell fate specification
G0:0051220	3	cytoplasmic sequestering of protein
G0:0003256	3	regulation of transcription from RNA polymerase II promoter involved in myocardial precursor cell differentiation
G0:0051223	3	regulation of protein transport
G0:0032095	3	regulation of response to food
G0:2000304	3	positive regulation of ceramide biosynthetic process
G0:0097477	3	lateral motor column neuron migration
G0:0046477	3	glycosylceramide catabolic process
G0:0045925	3	positive regulation of female receptivity
G0:0008356	3	asymmetric cell division
G0:0031727	3	CCR2 chemokine receptor binding
G0:0060335	3	positive regulation of interferon-gamma-mediated signaling pathway
G0:0060480	3	lung goblet cell differentiation
G0:0048525	3	negative regulation of viral process
G0:0060154	3	cellular process regulating host cell cycle in response to virus
G0:0048294	3	negative regulation of isotype switching to IgE isotypes
G0:0050265	3	RNA uridylyltransferase activity

G0:0070668	3	positive regulation of mast cell proliferation
G0:0001765	3	membrane raft assembly
G0:0001766	3	membrane raft polarization
G0:0008559	3	xenobiotic-transporting ATPase activity
G0:0016941	3	natriuretic peptide receptor activity
G0:0016942	3	insulin-like growth factor binding protein complex
G0:0000154	3	rRNA modification
G0:0015760	3	glucose-6-phosphate transport
G0:0006925	3	inflammatory cell apoptotic process
G0:0047718	3	indanol dehydrogenase activity
G0:0070574	3	cadmium ion transmembrane transport
G0:0072594	3	establishment of protein localization to organelle
G0:0034121	3	regulation of toll-like receptor signaling pathway
G0:0000832	3	inositol hexakisphosphate 5-kinase activity
G0:0046596	3	regulation of viral entry into host cell
G0:0046598	3	positive regulation of viral entry into host cell
G0:0090068	3	positive regulation of cell cycle process
G0:0035295	3	tube development
G0:0002151	3	G-quadruplex RNA binding
G0:0061146	3	Peyer's patch morphogenesis
G0:0048880	3	sensory system development
G0:0005094	3	Rho GDP-dissociation inhibitor activity
G0:0008948	3	oxaloacetate decarboxylase activity
G0:0052659	3	inositol-1,3,4,5-tetrakisphosphate 5-phosphatase activity
G0:0044375	3	regulation of peroxisome size
G0:0080130	3	L-phenylalanine:2-oxoglutarate aminotransferase activity
G0:0005726	3	perichromatin fibrils
G0:0032878	3	regulation of establishment or maintenance of cell polarity
G0:0071818	3	BAT3 complex
G0:0021801	3	cerebral cortex radial glia guided migration
G0:0021800	3	cerebral cortex tangential migration
G0:0038108	3	negative regulation of appetite by leptin-mediated signaling pathway
G0:0090403	3	oxidative stress-induced premature senescence
G0:0045900	3	negative regulation of translational elongation
G0:0045901	3	positive regulation of translational elongation
G0:0045908	3	negative regulation of vasodilation
G0:0086046	3	membrane depolarization during SA node cell action potential
G0:0019064	3	fusion of virus membrane with host plasma membrane
G0:0004719	3	protein-L-isoaspartate (D-aspartate) O-methyltransferase activity
G0:0090276	3	regulation of peptide hormone secretion
G0:0010871	3	negative regulation of receptor biosynthetic process
G0:0017060	3	3-galactosyl-N-acetylglucosaminide 4-alpha-L-fucosyltransferase activity
G0:0090188	3	negative regulation of pancreatic juice secretion
G0:0003953	3	NAD+ nucleosidase activity
G0:0035089	3	establishment of apical/basal cell polarity
G0:0002361	3	CD4-positive, CD25-positive, alpha-beta regulatory T cell differentiation
G0:0005173	3	stem cell factor receptor binding
G0:0035196	3	production of miRNAs involved in gene silencing by miRNA
G0:0005172	3	vascular endothelial growth factor receptor binding
G0:0009642	3	response to light intensity
G0:0006295	3	nucleotide-excision repair, DNA incision, 3'-to lesion
G0:0004803	3	transposase activity
G0:0016929	3	SUMO-specific protease activity
G0:0070779	3	D-aspartate import
G0:0060263	3	regulation of respiratory burst
G0:0019478	3	D-amino acid catabolic process
G0:0042816	3	vitamin B6 metabolic process
G0:1990393	3	3M complex
G0:0000432	3	positive regulation of transcription from RNA polymerase II promoter by glucose
G0:0071492	3	cellular response to UV-A
G0:0070552	3	BRISC complex
G0:0032460	3	negative regulation of protein oligomerization
G0:0030823	3	regulation of cGMP metabolic process
G0:0015036	3	disulfide oxidoreductase activity
G0:0033150	3	cytoskeletal calyx
G0:0016212	3	kynurenine-oxoglutarate transaminase activity
G0:0051712	3	positive regulation of killing of cells of other organism
G0:0047192	3	1-alkylglycerophosphocholine O-acetyltransferase activity
G0:0002176	3	male germ cell proliferation
G0:0030687	3	preribosome, large subunit precursor
G0:0097094	3	craniofacial suture morphogenesis
G0:0030172	3	troponin C binding
G0:0048311	3	mitochondrion distribution
G0:2001258	3	negative regulation of cation channel activity

G0:0004698	3	calcium-dependent protein kinase C activity
G0:0090043	3	regulation of tubulin deacetylation
G0:0090045	3	positive regulation of deacetylase activity
G0:0034136	3	negative regulation of toll-like receptor 2 signaling pathway
G0:0051153	3	regulation of striated muscle cell differentiation
G0:0051154	3	negative regulation of striated muscle cell differentiation
G0:0018242	3	protein O-linked glycosylation via serine
G0:0036023	3	embryonic skeletal limb joint morphogenesis
G0:0070125	3	mitochondrial translational elongation
G0:0060339	3	negative regulation of type I interferon-mediated signaling pathway
G0:0070129	3	regulation of mitochondrial translation
G0:0032859	3	activation of Ral GTPase activity
G0:0032142	3	single guanine insertion binding
G0:0038165	3	oncostatin-M-mediated signaling pathway
G0:0038161	3	prolactin signaling pathway
G0:0045541	3	negative regulation of cholesterol biosynthetic process
G0:0032225	3	regulation of synaptic transmission, dopaminergic
G0:0003162	3	atrioventricular node development
G0:0071322	3	cellular response to carbohydrate stimulus
G0:0030055	3	cell-substrate junction
G0:0033120	3	positive regulation of RNA splicing
G0:0060379	3	cardiac muscle cell myoblast differentiation
G0:0060374	3	mast cell differentiation
G0:0060192	3	negative regulation of lipase activity
G0:0060197	3	cloacal septation
G0:0001959	3	regulation of cytokine-mediated signaling pathway
G0:0005030	3	neurotrophin receptor activity
G0:0006311	3	meiotic gene conversion
G0:0004594	3	pantothenate kinase activity
G0:0004596	3	peptide alpha-N-acetyltransferase activity
G0:0048609	3	multicellular organismal reproductive process
G0:0004775	3	succinate-CoA ligase (ADP-forming) activity
G0:0003909	3	DNA ligase activity
G0:0018193	3	peptidyl-amino acid modification
G0:0032444	3	activin responsive factor complex
G0:0032449	3	CBM complex
G0:0019908	3	nuclear cyclin-dependent protein kinase holoenzyme complex
G0:0015016	3	[heparan sulfate]-glucosamine N-sulfotransferase activity
G0:0015018	3	galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase activity
G0:0046005	3	positive regulation of circadian sleep/wake cycle, REM sleep
G0:0060296	3	regulation of cilium beat frequency involved in ciliary motility
G0:0007109	3	cytokinesis, completion of separation
G0:0060205	3	cytoplasmic membrane-bounded vesicle lumen
G0:0030150	3	protein import into mitochondrial matrix
G0:0042272	3	nuclear RNA export factor complex
G0:0043009	3	chordate embryonic development
G0:0000213	3	tRNA-intron endonuclease activity
G0:0000214	3	tRNA-intron endonuclease complex
G0:2001271	3	negative regulation of cysteine-type endopeptidase activity involved in execution phase of apoptosis
G0:0042660	3	positive regulation of cell fate specification
G0:0042662	3	negative regulation of mesodermal cell fate specification
G0:0042663	3	regulation of endodermal cell fate specification
G0:0042668	3	auditory receptor cell fate determination
G0:0031205	3	endoplasmic reticulum Sec complex
G0:0090027	3	negative regulation of monocyte chemotaxis
G0:0090022	3	regulation of neutrophil chemotaxis
G0:0046040	3	IMP metabolic process
G0:0044331	3	cell-cell adhesion mediated by cadherin
G0:0009051	3	pentose-phosphate shunt, oxidative branch
G0:0042427	3	serotonin biosynthetic process
G0:0021942	3	radial glia guided migration of Purkinje cell
G0:0008900	3	hydrogen:potassium-exchanging ATPase activity
G0:0051280	3	negative regulation of release of sequestered calcium ion into cytosol
G0:0061156	3	pulmonary artery morphogenesis
G0:0001992	3	regulation of systemic arterial blood pressure by vasopressin
G0:0001997	3	positive regulation of the force of heart contraction by epinephrine-norepinephrine
G0:0001994	3	norepinephrine-epinephrine vasoconstriction involved in regulation of systemic arterial blood pressure
G0:0043648	3	dicarboxylic acid metabolic process
G0:0008670	3	2,4-dienoyl-CoA reductase (NADPH) activity
G0:0021847	3	ventricular zone neuroblast division
G0:0055106	3	ubiquitin-protein transferase regulator activity
G0:0070458	3	cellular detoxification of nitrogen compound

G0:0021769	3	orbitofrontal cortex development
G0:0043259	3	laminin-10 complex
G0:0016701	3	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen
G0:0033688	3	regulation of osteoblast proliferation
G0:0043486	3	histone exchange
G0:0033685	3	negative regulation of luteinizing hormone secretion
G0:0060421	3	positive regulation of heart growth
G0:0090238	3	positive regulation of arachidonic acid secretion
G0:0010834	3	telomere maintenance via telomere shortening
G0:0015808	3	L-alanine transport
G0:0051902	3	negative regulation of mitochondrial depolarization
G0:0009992	3	cellular water homeostasis
G0:0009991	3	response to extracellular stimulus
G0:1902186	3	regulation of viral release from host cell
G0:2001044	3	regulation of integrin-mediated signaling pathway
G0:1990000	3	amyloid fibril formation
G0:0042977	3	activation of JAK2 kinase activity
G0:0016866	3	intramolecular transferase activity
G0:0002366	3	leukocyte activation involved in immune response
G0:0072197	3	ureter morphogenesis
G0:0003872	3	6-phosphofructokinase activity
G0:0010044	3	response to aluminum ion
G0:0042853	3	L-alanine catabolic process
G0:0051343	3	positive regulation of cyclic-nucleotide phosphodiesterase activity
G0:0032318	3	regulation of Ras GTPase activity
G0:0032317	3	regulation of Rap GTPase activity
G0:0015254	3	glycerol channel activity
G0:0050861	3	positive regulation of B cell receptor signaling pathway
G0:0002521	3	leukocyte differentiation
G0:0015780	3	nucleotide-sugar transport
G0:0071464	3	cellular response to hydrostatic pressure
G0:0071467	3	cellular response to pH
G0:0003406	3	retinal pigment epithelium development
G0:0071439	3	clathrin complex
G0:0071438	3	invadopodium membrane
G0:0070243	3	regulation of thymocyte apoptotic process
G0:0007127	3	meiosis I
G0:0047484	3	regulation of response to osmotic stress
G0:0016520	3	growth hormone-releasing hormone receptor activity
G0:0005787	3	signal peptidase complex
G0:0035694	3	mitochondrial protein catabolic process
G0:0031701	3	angiotensin receptor binding
G0:0072201	3	negative regulation of mesenchymal cell proliferation
G0:0004965	3	G-protein coupled GABA receptor activity
G0:0004967	3	glucagon receptor activity
G0:0004966	3	galanin receptor activity
G0:0009298	3	GDP-mannose biosynthetic process
G0:0003338	3	metanephros morphogenesis
G0:0010310	3	regulation of hydrogen peroxide metabolic process
G0:0050508	3	glucuronosyl-N-acetylglucosaminyl-proteoglycan 4-alpha-N-acetylglucosaminyltransferase activity
G0:0005381	3	iron ion transmembrane transporter activity
G0:0001602	3	pancreatic polypeptide receptor activity
G0:0036066	3	protein O-linked fucosylation
G0:0090311	3	regulation of protein deacetylation
G0:0032767	3	copper-dependent protein binding
G0:2000381	3	negative regulation of mesoderm development
G0:0070699	3	type II activin receptor binding
G0:0019556	3	histidine catabolic process to glutamate and formamide
G0:0032100	3	positive regulation of appetite
G0:0045505	3	dynein intermediate chain binding
G0:0000801	3	central element
G0:0043271	3	negative regulation of ion transport
G0:2000969	3	positive regulation of alpha-amino-3-hydroxy-5-methyl-4-isoxazole propionate selective glutamate receptor activity
G0:0034620	3	cellular response to unfolded protein
G0:0034629	3	cellular protein complex localization
G0:0042447	3	hormone catabolic process
G0:0005148	3	prolactin receptor binding
G0:0071447	3	cellular response to hydroperoxide
G0:0004556	3	alpha-amylase activity
G0:0031670	3	cellular response to nutrient
G0:0004735	3	pyrroline-5-carboxylate reductase activity
G0:0014827	3	intestine smooth muscle contraction

G0:0002891	3	positive regulation of immunoglobulin mediated immune response
G0:0032376	3	positive regulation of cholesterol transport
G0:0044065	3	regulation of respiratory system process
G0:0010573	3	vascular endothelial growth factor production
G0:2000774	3	positive regulation of cellular senescence
G0:0007144	3	female meiosis I
G0:0034436	3	glycoprotein transport
G0:2000599	3	negative regulation of cyclin catabolic process
G0:0016508	3	long-chain-enoyl-CoA hydratase activity
G0:0017101	3	aminoacyl-tRNA synthetase multienzyme complex
G0:0017108	3	5'-flap endonuclease activity
G0:0043047	3	single-stranded telomeric DNA binding
G0:0046968	3	peptide antigen transport
G0:0000255	3	allantoin metabolic process
G0:0000253	3	3-keto sterol reductase activity
G0:0004946	3	bombesin receptor activity
G0:0060090	3	binding, bridging
G0:0060594	3	mammary gland specification
G0:0060675	3	ureteric bud morphogenesis
G0:0005010	3	insulin-like growth factor-activated receptor activity
G0:0044804	3	nucleophagy
G0:0004052	3	arachidonate 12-lipoxygenase activity
G0:0001660	3	fever generation
G0:0032741	3	positive regulation of interleukin-18 production
G0:0004566	3	beta-glucuronidase activity
G0:0032299	3	ribonuclease H2 complex
G0:0045298	3	tubulin complex
G0:0070672	3	response to interleukin-15
G0:0044327	3	dendritic spine head
G0:0040009	3	regulation of growth rate
G0:0040023	3	establishment of nucleus localization
G0:0032688	3	negative regulation of interferon-beta production
G0:0051495	3	positive regulation of cytoskeleton organization
G0:0007089	3	traversing start control point of mitotic cell cycle
G0:0006288	3	base-excision repair, DNA ligation
G0:0002679	3	respiratory burst involved in defense response
G0:0050849	3	negative regulation of calcium-mediated signaling
G0:0033159	3	negative regulation of protein import into nucleus, translocation
G0:0060468	3	prevention of polyspermy
G0:0048495	3	Roundabout binding
G0:0003157	3	endocardium development
G0:0048639	3	positive regulation of developmental growth
G0:0048630	3	skeletal muscle tissue growth
G0:0014074	3	response to purine-containing compound
G0:0008282	3	ATP-sensitive potassium channel complex
G0:0019797	3	procollagen-proline 3-dioxygenase activity
G0:0071603	3	endothelial cell-cell adhesion
G0:0002005	3	angiotensin catabolic process in blood
G0:0051304	3	chromosome separation
G0:0032357	3	oxidized purine DNA binding
G0:0071933	3	Arp2/3 complex binding
G0:0010593	3	negative regulation of lamellipodium assembly
G0:0071934	3	thiamine transmembrane transport
G0:0030350	3	iron-responsive element binding
G0:0001831	3	trophectodermal cellular morphogenesis
G0:0001832	3	blastocyst growth
G0:0007161	3	calcium-independent cell-matrix adhesion
G0:0043305	3	negative regulation of mast cell degranulation
G0:0016560	3	protein import into peroxisome matrix, docking
G0:0016561	3	protein import into peroxisome matrix, translocation
G0:0045715	3	negative regulation of low-density lipoprotein particle receptor
biosynthetic process		
G0:0017162	3	aryl hydrocarbon receptor binding
G0:0006565	3	L-serine catabolic process
G0:0006568	3	tryptophan metabolic process
G0:0043625	3	delta DNA polymerase complex
G0:0072307	3	regulation of metanephric nephron tubule epithelial cell differentiation
G0:0097011	3	cellular response to granulocyte macrophage colony-stimulating factor stimulus
G0:0097016	3	L27 domain binding
G0:0030688	3	preribosome, small subunit precursor
G0:0002025	3	vasodilation by norepinephrine-epinephrine involved in regulation of systemic arterial blood pressure
G0:0030174	3	regulation of DNA-dependent DNA replication initiation
G0:0042978	3	ornithine decarboxylase activator activity

G0:0070653	3	high-density lipoprotein particle receptor binding
G0:0072044	3	collecting duct development
G0:0005658	3	alpha DNA polymerase:primase complex
G0:0034371	3	chylomicron remodeling
G0:0034370	3	triglyceride-rich lipoprotein particle remodeling
G0:0016176	3	superoxide-generating NADPH oxidase activator activity
G0:0071219	3	cellular response to molecule of bacterial origin
G0:0060166	3	olfactory pit development
G0:0015403	3	thiamine uptake transmembrane transporter activity
G0:0048680	3	positive regulation of axon regeneration
G0:0010606	3	positive regulation of cytoplasmic mRNA processing body assembly
G0:0042373	3	vitamin K metabolic process
G0:0042371	3	vitamin K biosynthetic process
G0:0060440	3	trachea formation
G0:0043367	3	CD4-positive, alpha-beta T cell differentiation
G0:0004924	3	oncostatin-M receptor activity
G0:0004517	3	nitric-oxide synthase activity
G0:0072049	3	comma-shaped body morphogenesis
G0:0035092	3	sperm chromatin condensation
G0:0018636	3	phenanthrene 9,10-monooxygenase activity
G0:0015272	3	ATP-activated inward rectifier potassium channel activity
G0:0001883	3	purine nucleoside binding
G0:0009750	3	response to fructose
G0:0003985	3	acetyl-CoA C-acetyltransferase activity
G0:0019724	3	B cell mediated immunity
G0:0044027	3	hypermethylation of CpG island
G0:0003408	3	optic cup formation involved in camera-type eye development
G0:0071918	3	urea transmembrane transport
G0:0004699	3	calcium-independent protein kinase C activity
G0:0030292	3	protein tyrosine kinase inhibitor activity
G0:0008401	3	retinoic acid 4-hydroxylase activity
G0:0043550	3	regulation of lipid kinase activity
G0:0044265	3	cellular macromolecule catabolic process
G0:0002090	3	regulation of receptor internalization
G0:0043083	3	synaptic cleft
G0:1900222	3	negative regulation of beta-amyloid clearance
G0:0060058	3	positive regulation of apoptotic process involved in mammary gland involution
G0:0060585	3	positive regulation of prostaglandin-endoperoxide synthase activity
G0:0097039	3	protein linear polyubiquitination
G0:0061184	3	positive regulation of dermatome development
G0:0072300	3	positive regulation of metanephric glomerulus development
G0:0060638	3	mesenchymal-epithelial cell signaling
G0:0009236	3	cobalamin biosynthetic process
G0:0060632	3	regulation of microtubule-based movement
G0:0035591	3	signaling adaptor activity
G0:0048841	3	regulation of axon extension involved in axon guidance
G0:0009583	3	detection of light stimulus
G0:0043293	3	apoptosome
G0:0030730	3	sequestering of triglyceride
G0:0071598	3	neuronal ribonucleoprotein granule
G0:0016765	3	transferase activity, transferring alkyl or aryl (other than methyl) groups
G0:0018916	3	nitrobenzene metabolic process
G0:0070633	3	transepithelial transport
G0:0045988	3	negative regulation of striated muscle contraction
G0:0004748	3	ribonucleoside-diphosphate reductase activity, thioredoxin disulfide as acceptor
G0:0070189	3	kynurenine metabolic process
G0:0050294	3	steroid sulfotransferase activity
G0:0033076	3	isoquinoline alkaloid metabolic process
G0:2000278	3	regulation of DNA biosynthetic process
G0:0042796	3	snRNA transcription from RNA polymerase III promoter
G0:0015174	3	basic amino acid transmembrane transporter activity
G0:0031084	3	BLOC-2 complex
G0:0047429	3	nucleoside-triphosphate diphosphatase activity
G0:0051987	3	positive regulation of attachment of spindle microtubules to kinetochore
G0:0070814	3	hydrogen sulfide biosynthetic process
G0:0030573	3	bile acid catabolic process
G0:0006177	3	GMP biosynthetic process
G0:0018076	3	N-terminal peptidyl-lysine acetylation
G0:0043121	3	neurotrophin binding
G0:0048763	3	calcium-induced calcium release activity
G0:0061049	3	cell growth involved in cardiac muscle cell development
G0:0009448	3	gamma-aminobutyric acid metabolic process

G0:0072017	3	distal tubule development
G0:1990086	3	lens fiber cell apoptotic process
G0:0009912	3	auditory receptor cell fate commitment
G0:0006065	3	UDP-glucuronate biosynthetic process
G0:0031618	3	nuclear centromeric heterochromatin
G0:0004792	3	thiosulfate sulfurtransferase activity
G0:0071001	3	U4/U6 snRNP
G0:0060399	3	positive regulation of growth hormone receptor signaling pathway
G0:0005900	3	oncostatin-M receptor complex
G0:0051900	3	regulation of mitochondrial depolarization
G0:0010621	3	negative regulation of transcription by transcription factor localization
G0:0046914	3	transition metal ion binding
G0:0043988	3	histone H3-S28 phosphorylation
G0:0038007	3	netrin-activated signaling pathway
G0:0032066	3	nucleolus to nucleoplasm transport
G0:0003308	3	negative regulation of Wnt signaling pathway involved in heart development
G0:0035878	3	nail development
G0:0008426	3	protein kinase C inhibitor activity
G0:0035873	3	lactate transmembrane transport
G0:0034103	3	regulation of tissue remodeling
G0:0045759	3	negative regulation of action potential
G0:0070370	3	cellular heat acclimation
G0:1900246	3	positive regulation of RIG-I signaling pathway
G0:0035722	3	interleukin-12-mediated signaling pathway
G0:0010693	3	negative regulation of alkaline phosphatase activity
G0:0097058	3	CRLF-CLCF1 complex
G0:0044406	3	adhesion of symbiont to host
G0:0044205	3	'de novo' UMP biosynthetic process
G0:0070613	3	regulation of protein processing
G0:0070966	3	nuclear-transcribed mRNA catabolic process, no-go decay
G0:0070969	3	ULK1-ATG13-FIP200 complex
G0:0051088	3	PMA-inducible membrane protein ectodomain proteolysis
G0:0032275	3	luteinizing hormone secretion
G0:0033588	3	Elongator holoenzyme complex
G0:0030485	3	smooth muscle contractile fiber
G0:0010470	3	regulation of gastrulation
G0:0033144	3	negative regulation of intracellular steroid hormone receptor signaling pathway
G0:0005896	3	interleukin-6 receptor complex
G0:0005899	3	insulin receptor complex
G0:0007028	3	cytoplasm organization
G0:0033058	3	directional locomotion
G0:0033632	3	regulation of cell-cell adhesion mediated by integrin
G0:1990247	3	N6-methyladenosine-containing RNA binding
G0:1990246	3	uniplex complex
G0:0031987	3	locomotion involved in locomotory behavior
G0:0072540	3	T-helper 17 cell lineage commitment
G0:0031989	3	bombesin receptor signaling pathway
G0:0043320	3	natural killer cell degranulation
G0:0010897	3	negative regulation of triglyceride catabolic process
G0:0005797	3	Golgi medial cisterna
G0:0035791	3	platelet-derived growth factor receptor-beta signaling pathway
G0:0003166	3	bundle of His development
G0:0048194	3	Golgi vesicle budding
G0:0031365	3	N-terminal protein amino acid modification
G0:0072133	3	metanephric mesenchyme morphogenesis
G0:0048478	3	replication fork protection
G0:0090245	3	axis elongation involved in somitogenesis
G0:0005534	3	galactose binding
G0:0004118	3	cGMP-stimulated cyclic-nucleotide phosphodiesterase activity
G0:0010644	3	cell communication by electrical coupling
G0:0046935	3	1-phosphatidylinositol-3-kinase regulator activity
G0:0001547	3	antral ovarian follicle growth
G0:0071953	3	elastic fiber
G0:0055087	3	Ski complex
G0:2000041	3	negative regulation of planar cell polarity pathway involved in axis elongation
G0:2000048	3	negative regulation of cell-cell adhesion mediated by cadherin
G0:0035793	3	positive regulation of metanephric mesenchymal cell migration by platelet-derived growth factor receptor-beta signaling pathway
G0:0038026	3	reelin-mediated signaling pathway
G0:0008449	3	N-acetylglucosamine-6-sulfatase activity
G0:0034666	3	integrin alpha2-beta1 complex
G0:0030910	3	olfactory placode formation
G0:0060544	3	regulation of necroptotic process

G0:0046486	3	glycerolipid metabolic process
G0:0002774	3	Fc receptor mediated inhibitory signaling pathway
G0:0097070	3	ductus arteriosus closure
G0:0003253	3	cardiac neural crest cell migration involved in outflow tract morphogenesis
G0:0033512	3	L-lysine catabolic process to acetyl-CoA via saccharopine
G0:0006458	3	'de novo' protein folding
G0:0008537	3	proteasome activator complex
G0:0008184	3	glycogen phosphorylase activity
G0:0035303	3	regulation of dephosphorylation
G0:0032608	3	interferon-beta production
G0:0000164	3	protein phosphatase type 1 complex
G0:0072095	3	regulation of branch elongation involved in ureteric bud branching
G0:0008853	3	exodeoxyribonuclease III activity
G0:0031427	3	response to methotrexate
G0:0032218	3	riboflavin transport
G0:0032217	3	riboflavin transporter activity
G0:0032212	3	positive regulation of telomere maintenance via telomerase
G0:0002693	3	positive regulation of cellular extravasation
G0:0010454	3	negative regulation of cell fate commitment
G0:0004949	3	cannabinoid receptor activity
G0:0070236	3	negative regulation of activation-induced cell death of T cells
G0:0017040	3	ceramidase activity
G0:0004948	3	calcitonin receptor activity
G0:0071723	3	lipopeptide binding
G0:0070988	3	demethylation
G0:0036378	3	calcitriol biosynthetic process from calciol
G0:0045604	3	regulation of epidermal cell differentiation
G0:0015698	3	inorganic anion transport
G0:1901679	3	nucleotide transmembrane transport
G0:0061009	3	common bile duct development
G0:0061002	3	negative regulation of dendritic spine morphogenesis
G0:0006207	3	'de novo' pyrimidine nucleobase biosynthetic process
G0:0006203	3	dGTP catabolic process
G0:0031094	3	platelet dense tubular network
G0:0000338	3	protein deneddylation
G0:0004911	3	interleukin-2 receptor activity
G0:0035928	3	rRNA import into mitochondrion
G0:1900103	3	positive regulation of endoplasmic reticulum unfolded protein response
G0:0030546	3	receptor activator activity
G0:1900106	3	positive regulation of hyaluronan cable assembly
G0:0051649	3	establishment of localization in cell
G0:0060203	3	clathrin-sculpted glutamate transport vesicle membrane
G0:0060201	3	clathrin-sculpted acetylcholine transport vesicle membrane
G0:0022824	3	transmitter-gated ion channel activity
G0:0034875	3	caffeine oxidase activity
G0:0044770	3	cell cycle phase transition
G0:0051383	3	kinetochore organization
G0:0046959	3	habituation
G0:0010668	3	ectodermal cell differentiation
G0:0060564	3	negative regulation of mitotic anaphase-promoting complex activity
G0:0055069	3	zinc ion homeostasis
G0:0006995	3	cellular response to nitrogen starvation
G0:0032027	3	myosin light chain binding
G0:0032252	3	secretory granule localization
G0:0070008	3	serine-type exopeptidase activity
G0:0015651	3	quaternary ammonium group transmembrane transporter activity
G0:1901888	3	regulation of cell junction assembly
G0:0003006	3	developmental process involved in reproduction
G0:0043533	3	inositol 1,3,4,5 tetrakisphosphate binding
G0:0016233	3	telomere capping
G0:0034273	3	Atg1p signaling complex
G0:0060230	3	lipoprotein lipase activator activity
G0:0050951	3	sensory perception of temperature stimulus
G0:0071062	3	alpha-v-beta3 integrin-vitronectin complex
G0:0006432	3	phenylalanyl-tRNA aminoacylation
G0:0060563	3	neuroepithelial cell differentiation
G0:0006382	3	adenosine to inosine editing
G0:0051533	3	positive regulation of NFAT protein import into nucleus
G0:0000103	3	sulfate assimilation
G0:0042461	3	photoreceptor cell development
G0:0006857	3	oligopeptide transport
G0:0090150	3	establishment of protein localization to membrane
G0:0044208	3	'de novo' AMP biosynthetic process
G0:0080009	3	mRNA methylation

G0:0035574	3	histone H4-K20 demethylation
G0:0003340	3	negative regulation of mesenchymal to epithelial transition involved in
metanephros		morphogenesis
G0:0035575	3	histone demethylase activity (H4-K20 specific)
G0:0070212	3	protein poly-ADP-ribosylation
G0:1901475	3	pyruvate transmembrane transport
G0:0021930	3	cerebellar granule cell precursor proliferation
G0:0035910	3	ascending aorta morphogenesis
G0:0030896	3	checkpoint clamp complex
G0:0043567	3	regulation of insulin-like growth factor receptor signaling pathway
G0:0043139	3	5'-3' DNA helicase activity
G0:0061574	3	ASAP complex
G0:0048713	3	regulation of oligodendrocyte differentiation
G0:0006085	3	acetyl-CoA biosynthetic process
G0:0006089	3	lactate metabolic process
G0:1900127	3	positive regulation of hyaluronan biosynthetic process
G0:1900126	3	negative regulation of hyaluronan biosynthetic process
G0:0031852	3	mu-type opioid receptor binding
G0:0072179	3	nephric duct formation
G0:0051835	3	positive regulation of synapse structural plasticity
G0:2001137	3	positive regulation of endocytic recycling
G0:0046975	3	histone methyltransferase activity (H3-K36 specific)
G0:0046979	3	TAP2 binding
G0:0045404	3	positive regulation of interleukin-4 biosynthetic process
G0:2000370	3	positive regulation of clathrin-mediated endocytosis
G0:0021543	3	pallium development
G0:0032002	3	interleukin-28 receptor complex
G0:0015085	3	calcium ion transmembrane transporter activity
G0:0019815	3	B cell receptor complex
G0:0071883	3	activation of MAPK activity by adrenergic receptor signaling pathway
G0:0097197	3	tetraspanin-enriched microdomain
G0:0061042	3	vascular wound healing
G0:0002084	3	protein depalmitoylation
G0:1900212	3	negative regulation of mesenchymal cell apoptotic process involved in
metanephros		development
G0:0016553	3	base conversion or substitution editing
G0:0034435	3	cholesterol esterification
G0:0042500	3	aspartic endopeptidase activity, intramembrane cleaving
G0:0042506	3	tyrosine phosphorylation of Stat5 protein
G0:0006419	3	alanyl-tRNA aminoacylation
G0:0008107	3	galactoside 2-alpha-L-fucosyltransferase activity
G0:0008105	3	asymmetric protein localization
G0:0035241	3	protein-arginine omega-N monomethyltransferase activity
G0:0004813	3	alanine-tRNA ligase activity
G0:0046523	3	S-methyl-5-thioribose-1-phosphate isomerase activity
G0:0042998	3	positive regulation of Golgi to plasma membrane protein transport
G0:0071225	3	cellular response to muramyl dipeptide
G0:0023051	3	regulation of signaling
G0:0007431	3	salivary gland development
G0:0014809	3	regulation of skeletal muscle contraction by regulation of release of
sequestered calcium		ion
G0:0010498	3	proteasomal protein catabolic process
G0:0033561	3	regulation of water loss via skin
G0:0016668	3	oxidoreductase activity, acting on a sulfur group of donors, NAD(P) as
acceptor		
G0:0008384	3	IkappaB kinase activity
G0:0033693	3	neurofilament bundle assembly
G0:0016401	3	palmitoyl-CoA oxidase activity
G0:0097116	3	gephyrin clustering
G0:1902108	3	regulation of mitochondrial membrane permeability involved in apoptotic
process		
G0:0031692	3	alpha-1B adrenergic receptor binding
G0:0060244	3	negative regulation of cell proliferation involved in contact inhibition
G0:0060242	3	contact inhibition
G0:0009447	3	putrescine catabolic process
G0:0045058	3	T cell selection
G0:0031346	3	positive regulation of cell projection organization
G0:0023021	3	termination of signal transduction
G0:0023029	3	MHC class Ib protein binding
G0:0048014	3	Tie signaling pathway
G0:0030423	3	targeting of mRNA for destruction involved in RNA interference
G0:0004605	3	phosphatidate cytidyltransferase activity
G0:2000611	3	positive regulation of thyroid hormone generation
G0:2000347	3	positive regulation of hepatocyte proliferation
G0:0045425	3	positive regulation of granulocyte macrophage colony-stimulating factor

biosynthetic process

G0:0070044 3 synaptobrevin 2-SNAP-25-syntaxin-1a complex
 G0:0034651 3 cortisol biosynthetic process
 G0:0034653 3 retinoic acid catabolic process
 G0:0021570 3 rhombomere 4 development
 G0:0021562 3 vestibulocochlear nerve development
 G0:0030951 3 establishment or maintenance of microtubule cytoskeleton polarity
 G0:0051250 3 negative regulation of lymphocyte activation
 G0:0034502 3 protein localization to chromosome
 G0:0034508 3 centromere complex assembly
 G0:1901841 3 regulation of high voltage-gated calcium channel activity
 G0:0008173 3 RNA methyltransferase activity
 G0:1990126 3 retrograde transport, endosome to plasma membrane
 G0:0030422 3 production of siRNA involved in RNA interference
 G0:0035106 3 operant conditioning
 G0:0061384 3 heart trabecula morphogenesis
 G0:0031932 3 TORC2 complex
 G0:0030158 3 protein xylosyltransferase activity
 G0:0060523 3 prostate epithelial cord elongation
 G0:0035360 3 positive regulation of peroxisome proliferator activated receptor

signaling pathway

G0:0072385 3 minus-end-directed organelle transport along microtubule
 G0:0071800 3 podosome assembly
 G0:0042524 3 negative regulation of tyrosine phosphorylation of Stat5 protein
 G0:0003401 3 axis elongation
 G0:0043137 3 DNA replication, removal of RNA primer
 G0:0045254 3 pyruvate dehydrogenase complex
 G0:0045191 3 regulation of isotype switching
 G0:0004833 3 tryptophan 2,3-dioxygenase activity
 G0:0070863 3 positive regulation of protein exit from endoplasmic reticulum
 G0:0072034 3 renal vesicle induction
 G0:0007418 3 ventral midline development
 G0:0044249 3 cellular biosynthetic process
 G0:0044242 3 cellular lipid catabolic process
 G0:0019230 3 proprioception
 G0:0005119 3 smoothened binding
 G0:0010997 3 anaphase-promoting complex binding
 G0:0072553 3 terminal button organization
 G0:0071782 3 endoplasmic reticulum tubular network
 G0:0043734 3 DNA-N1-methyladenine dioxygenase activity
 G0:1901837 3 negative regulation of transcription of nuclear large rRNA transcript from

RNA polymerase I promoter

G0:0034198 2 cellular response to amino acid starvation
 G0:0034197 2 triglyceride transport
 G0:0030859 2 polarized epithelial cell differentiation
 G0:0034770 2 histone H4-K20 methylation
 G0:0034188 2 apolipoprotein A-I receptor activity
 G0:0097177 2 mitochondrial ribosome binding
 G0:0090343 2 positive regulation of cell aging
 G0:0006597 2 spermine biosynthetic process
 G0:0010909 2 positive regulation of heparan sulfate proteoglycan biosynthetic process
 G0:0005712 2 chiasma
 G0:0051875 2 pigment granule localization
 G0:0051873 2 killing by host of symbiont cells
 G0:0007620 2 copulation
 G0:0002296 2 T-helper 1 cell lineage commitment
 G0:2001171 2 positive regulation of ATP biosynthetic process
 G0:2001170 2 negative regulation of ATP biosynthetic process
 G0:0048382 2 mesendoderm development
 G0:0048385 2 regulation of retinoic acid receptor signaling pathway
 G0:0045076 2 regulation of interleukin-2 biosynthetic process
 G0:0004441 2 inositol-1,4-bisphosphate 1-phosphatase activity
 G0:0004447 2 iodide peroxidase activity
 G0:0004996 2 thyroid-stimulating hormone receptor activity
 G0:0004991 2 parathyroid hormone receptor activity
 G0:0055002 2 striated muscle cell development
 G0:0005427 2 proton-dependent oligopeptide secondary active transmembrane transporter activity
 G0:0006971 2 hypotonic response
 G0:0004666 2 prostaglandin-endoperoxide synthase activity
 G0:0004667 2 prostaglandin-D synthase activity
 G0:0004660 2 protein farnesyltransferase activity
 G0:0004661 2 protein geranylgeranyltransferase activity
 G0:2000623 2 negative regulation of nuclear-transcribed mRNA catabolic process, nonsense-mediated decay

G0:0021506	2	anterior neuropore closure
G0:0051270	2	regulation of cellular component movement
G0:0015501	2	glutamate:sodium symporter activity
G0:0010751	2	negative regulation of nitric oxide mediated signal transduction
G0:0033044	2	regulation of chromosome organization
G0:0002457	2	T cell antigen processing and presentation
G0:1901799	2	negative regulation of proteasomal protein catabolic process
G0:1901797	2	negative regulation of signal transduction by p53 class mediator
G0:0071338	2	positive regulation of hair follicle cell proliferation
G0:0046404	2	ATP-dependent polydeoxyribonucleotide 5'-hydroxyl-kinase activity
G0:0046403	2	polynucleotide 3'-phosphatase activity
G0:0042095	2	interferon-gamma biosynthetic process
G0:0016362	2	activin receptor activity, type II
G0:0008428	2	ribonuclease inhibitor activity
G0:0052314	2	phytoalexin metabolic process
G0:0034381	2	plasma lipoprotein particle clearance
G0:0006109	2	regulation of carbohydrate metabolic process
G0:0031711	2	bradykinin receptor binding
G0:0042406	2	extrinsic component of endoplasmic reticulum membrane
G0:0004850	2	uridine phosphorylase activity
G0:0060265	2	positive regulation of respiratory burst involved in inflammatory response
G0:0072014	2	proximal tubule development
G0:1902911	2	protein kinase complex
G0:0090288	2	negative regulation of cellular response to growth factor stimulus
G0:0050135	2	NAD(P)+ nucleosidase activity
G0:0090135	2	actin filament branching
G0:0015168	2	glycerol transmembrane transporter activity
G0:0005459	2	UDP-galactose transmembrane transporter activity
G0:0010902	2	positive regulation of very-low-density lipoprotein particle remodeling
G0:0060545	2	positive regulation of necroptotic process
G0:0051066	2	dihydrobiopterin metabolic process
G0:0003883	2	CTP synthase activity
G0:0003880	2	protein C-terminal carboxyl O-methyltransferase activity
G0:0052871	2	alpha-tocopherol omega-hydroxylase activity
G0:0001735	2	prenylcysteine oxidase activity
G0:0032431	2	activation of phospholipase A2 activity
G0:0032929	2	negative regulation of superoxide anion generation
G0:2000681	2	negative regulation of rubidium ion transport
G0:2000687	2	negative regulation of rubidium ion transmembrane transporter activity
G0:0019427	2	acetyl-CoA biosynthetic process from acetate
G0:0014846	2	esophagus smooth muscle contraction
G0:0045652	2	regulation of megakaryocyte differentiation
G0:0016198	2	axon choice point recognition
G0:0042392	2	sphingosine-1-phosphate phosphatase activity
G0:0003913	2	DNA photolyase activity
G0:0071104	2	response to interleukin-9
G0:0071109	2	superior temporal gyrus development
G0:0007622	2	rhythmic behavior
G0:0050816	2	phosphothreonine binding
G0:0097156	2	fasciculation of motor neuron axon
G0:0097157	2	pre-mRNA intronic binding
G0:0007198	2	adenylate cyclase-inhibiting serotonin receptor signaling pathway
G0:0007197	2	adenylate cyclase-inhibiting G-protein coupled acetylcholine receptor
signaling pathway		
G0:0010922	2	positive regulation of phosphatase activity
G0:0046671	2	negative regulation of retinal cell programmed cell death
G0:0030382	2	sperm mitochondrion organization
G0:0015038	2	glutathione disulfide oxidoreductase activity
G0:0002291	2	T cell activation via T cell receptor contact with antigen bound to MHC
molecule on antigen		presenting cell
G0:0035441	2	cell migration involved in vasculogenesis
G0:0030125	2	clathrin vesicle coat
G0:0031386	2	protein tag
G0:2001198	2	regulation of dendritic cell differentiation
G0:2000095	2	regulation of Wnt signaling pathway, planar cell polarity pathway
G0:0045010	2	actin nucleation
G0:0004468	2	lysine N-acetyltransferase activity
G0:0004649	2	poly(ADP-ribose) glycohydrolase activity
G0:0021523	2	somatic motor neuron differentiation
G0:0007206	2	phospholipase C-activating G-protein coupled glutamate receptor signaling
pathway		
G0:0010736	2	serum response element binding
G0:0050062	2	long-chain-fatty-acyl-CoA reductase activity
G0:0001694	2	histamine biosynthetic process
G0:0021784	2	postganglionic parasympathetic nervous system development

G0:0002920	2	regulation of humoral immune response
G0:0002924	2	negative regulation of humoral immune response mediated by circulating immunoglobulin
G0:0097187	2	dentinogenesis
G0:2000647	2	negative regulation of stem cell proliferation
G0:2000643	2	positive regulation of early endosome to late endosome transport
G0:0052741	2	(R)-limonene 6-monooxygenase activity
G0:0061034	2	olfactory bulb mitral cell layer development
G0:0033262	2	regulation of nuclear cell cycle DNA replication
G0:0006348	2	chromatin silencing at telomere
G0:0003195	2	tricuspid valve formation
G0:0003190	2	atrioventricular valve formation
G0:0003193	2	pulmonary valve formation
G0:0003192	2	mitral valve formation
G0:0004998	2	transferrin receptor activity
G0:0017038	2	protein import
G0:0086015	2	SA node cell action potential
G0:0010559	2	regulation of glycoprotein biosynthetic process
G0:0043179	2	rhythmic excitation
G0:0043178	2	alcohol binding
G0:0006123	2	mitochondrial electron transport, cytochrome c to oxygen
G0:0000182	2	rDNA binding
G0:0072079	2	nephron tubule formation
G0:0072073	2	kidney epithelium development
G0:0097459	2	iron ion import into cell
G0:0048537	2	mucosal-associated lymphoid tissue development
G0:0060123	2	regulation of growth hormone secretion
G0:0008732	2	L-allo-threonine aldolase activity
G0:0051046	2	regulation of secretion
G0:2001038	2	regulation of cellular response to drug
G0:0016404	2	15-hydroxyprostaglandin dehydrogenase (NAD+) activity
G0:0047238	2	glucuronosyl-N-acetylgalactosaminyl-proteoglycan 4-beta-N-acetylgalactosaminyltransferase activity
G0:0001754	2	eye photoreceptor cell differentiation
G0:2000124	2	regulation of endocannabinoid signaling pathway
G0:0032414	2	positive regulation of ion transmembrane transporter activity
G0:0032416	2	negative regulation of sodium:proton antiporter activity
G0:0035993	2	deltoid tuberosity development
G0:0035998	2	7,8-dihydroneopterin 3'-triphosphate biosynthetic process
G0:0016608	2	growth hormone-releasing hormone activity
G0:0070743	2	interleukin-23 complex
G0:0070740	2	tubulin-glutamic acid ligase activity
G0:0042823	2	pyridoxal phosphate biosynthetic process
G0:0042824	2	MHC class I peptide loading complex
G0:2000781	2	positive regulation of double-strand break repair
G0:0047017	2	prostaglandin-F synthase activity
G0:0072678	2	T cell migration
G0:0000406	2	double-strand/single-strand DNA junction binding
G0:0070560	2	protein secretion by platelet
G0:0070561	2	vitamin D receptor signaling pathway
G0:0034154	2	toll-like receptor 7 signaling pathway
G0:0034485	2	phosphatidylinositol-3,4,5-trisphosphate 5-phosphatase activity
G0:2000872	2	positive regulation of progesterone secretion
G0:0021644	2	vagus nerve morphogenesis
G0:0030815	2	negative regulation of cAMP metabolic process
G0:0033108	2	mitochondrial respiratory chain complex assembly
G0:0071812	2	positive regulation of fever generation by positive regulation of prostaglandin secretion
G0:0036413	2	histone H3-R26 citrullination
G0:2001205	2	negative regulation of osteoclast development
G0:0030103	2	vasopressin secretion
G0:0033306	2	phytol metabolic process
G0:0045031	2	ATP-activated nucleotide receptor activity
G0:2000111	2	positive regulation of macrophage apoptotic process
G0:0006664	2	glycolipid metabolic process
G0:0005315	2	inorganic phosphate transmembrane transporter activity
G0:0042610	2	CD8 receptor binding
G0:0090076	2	relaxation of skeletal muscle
G0:1902259	2	regulation of delayed rectifier potassium channel activity
G0:1902257	2	negative regulation of apoptotic process involved in outflow tract morphogenesis
G0:1902254	2	negative regulation of intrinsic apoptotic signaling pathway by p53 class mediator
G0:0000939	2	condensed chromosome inner kinetochore
G0:0044340	2	canonical Wnt signaling pathway involved in regulation of cell

proliferation

G0:0044346 2 fibroblast apoptotic process

G0:0060928 2 atrioventricular node cell development

G0:0090402 2 oncogene-induced cell senescence

G0:0032089 2 NACHT domain binding

G0:0070178 2 D-serine metabolic process

G0:0070171 2 negative regulation of tooth mineralization

G0:0070173 2 regulation of enamel mineralization

G0:0002945 2 cyclin K-CDK13 complex

G0:0002944 2 cyclin K-CDK12 complex

G0:0071376 2 cellular response to corticotropin-releasing hormone stimulus

G0:0071379 2 cellular response to prostaglandin stimulus

G0:2000663 2 negative regulation of interleukin-5 secretion

G0:2000664 2 positive regulation of interleukin-5 secretion

G0:2000666 2 negative regulation of interleukin-13 secretion

G0:2000667 2 positive regulation of interleukin-13 secretion

G0:0061326 2 renal tubule development

G0:0061324 2 canonical Wnt signaling pathway involved in positive regulation of cardiac outflow tract cell proliferation

G0:0061325 2 cell proliferation involved in outflow tract morphogenesis

G0:0060420 2 regulation of heart growth

G0:0004662 2 CAAX-protein geranylgeranyltransferase activity

G0:1900086 2 positive regulation of peptidyl-tyrosine autophosphorylation

G0:0017057 2 6-phosphogluconolactonase activity

G0:0017050 2 D-erythro-sphingosine kinase activity

G0:0045939 2 negative regulation of steroid metabolic process

G0:0042585 2 germinal vesicle

G0:0032831 2 positive regulation of CD4-positive, CD25-positive, alpha-beta regulatory T cell differentiation

G0:0035617 2 stress granule disassembly

G0:0072180 2 mesonephric duct morphogenesis

G0:0015802 2 basic amino acid transport

G0:0031755 2 Edg-2 lysophosphatidic acid receptor binding

G0:0031751 2 D4 dopamine receptor binding

G0:0048512 2 circadian behavior

G0:0005674 2 transcription factor TFIIF complex

G0:0009368 2 endopeptidase Clp complex

G0:0001300 2 chronological cell aging

G0:0001309 2 age-dependent telomere shortening

G0:0002377 2 immunoglobulin production

G0:0005415 2 nucleoside:sodium symporter activity

G0:0002204 2 somatic recombination of immunoglobulin genes involved in immune response

G0:0002378 2 immunoglobulin biosynthetic process

G0:2001015 2 negative regulation of skeletal muscle cell differentiation

G0:2001013 2 epithelial cell proliferation involved in renal tubule morphogenesis

G0:0001773 2 myeloid dendritic cell activation

G0:0002178 2 palmitoyltransferase complex

G0:0009994 2 oocyte differentiation

G0:0070765 2 gamma-secretase complex

G0:0071332 2 cellular response to fructose stimulus

G0:0072610 2 interleukin-12 secretion

G0:0016488 2 farnesol catabolic process

G0:0070541 2 response to platinum ion

G0:0032472 2 Golgi calcium ion transport

G0:0034137 2 positive regulation of toll-like receptor 2 signaling pathway

G0:2000854 2 positive regulation of corticosterone secretion

G0:2000504 2 positive regulation of blood vessel remodeling

G0:2000507 2 positive regulation of energy homeostasis

G0:0019285 2 glycine betaine biosynthetic process from choline

G0:0030832 2 regulation of actin filament length

G0:0030835 2 negative regulation of actin filament depolymerization

G0:0002572 2 pro-T cell differentiation

G0:0050859 2 negative regulation of B cell receptor signaling pathway

G0:0051725 2 protein de-ADP-ribosylation

G0:0071144 2 SMAD2-SMAD3 protein complex

G0:0046636 2 negative regulation of alpha-beta T cell activation

G0:0046631 2 alpha-beta T cell activation

G0:0030343 2 vitamin D3 25-hydroxylase activity

G0:0072545 2 tyrosine binding

G0:0097089 2 methyl-branched fatty acid metabolic process

G0:0035408 2 histone H3-T6 phosphorylation

G0:0042249 2 establishment of planar polarity of embryonic epithelium

G0:0042245 2 RNA repair

G0:0045098 2 type III intermediate filament

G0:0004421 2 hydroxymethylglutaryl-CoA synthase activity

G0:0004939	2	beta-adrenergic receptor activity
G0:0006682	2	galactosylceramide biosynthetic process
G0:0006681	2	galactosylceramide metabolic process
G0:0008934	2	inositol monophosphate 1-phosphatase activity
G0:0004687	2	myosin light chain kinase activity
G0:2000077	2	negative regulation of type B pancreatic cell development
G0:0098531	2	direct ligand regulated sequence-specific DNA binding transcription factor activity
G0:0098535	2	de novo centriole assembly
G0:0010085	2	polarity specification of proximal/distal axis
G0:0015375	2	glycine:sodium symporter activity
G0:0060947	2	cardiac vascular smooth muscle cell differentiation
G0:0036035	2	osteoclast development
G0:0032861	2	activation of Rap GTPase activity
G0:0044774	2	mitotic DNA integrity checkpoint
G0:0021874	2	Wnt signaling pathway involved in forebrain neuroblast division
G0:0021872	2	forebrain generation of neurons
G0:0021873	2	forebrain neuroblast division
G0:0038112	2	interleukin-8-mediated signaling pathway
G0:0038111	2	interleukin-7-mediated signaling pathway
G0:0061302	2	smooth muscle cell-matrix adhesion
G0:0043203	2	axon hillock
G0:0003156	2	regulation of organ formation
G0:0060350	2	endochondral bone morphogenesis
G0:0034678	2	integrin alpha8-beta1 complex
G0:0034677	2	integrin alpha7-beta1 complex
G0:0007181	2	transforming growth factor beta receptor complex assembly
G0:1990430	2	extracellular matrix protein binding
G0:0035672	2	oligopeptide transmembrane transport
G0:0031959	2	mineralocorticoid receptor signaling pathway
G0:0090261	2	positive regulation of inclusion body assembly
G0:0090265	2	positive regulation of immune complex clearance by monocytes and macrophages
G0:0010868	2	negative regulation of triglyceride biosynthetic process
G0:0010041	2	response to iron(III) ion
G0:0001094	2	TFIID-class transcription factor binding
G0:0044324	2	regulation of transcription involved in anterior/posterior axis specification
G0:0060168	2	positive regulation of adenosine receptor signaling pathway
G0:0060161	2	positive regulation of dopamine receptor signaling pathway
G0:1902608	2	positive regulation of large conductance calcium-activated potassium channel activity
G0:0007493	2	endodermal cell fate determination
G0:0007497	2	posterior midgut development
G0:1902603	2	carnitine transmembrane transport
G0:2001076	2	positive regulation of metanephric ureteric bud development
G0:2001070	2	starch binding
G0:0000059	2	protein import into nucleus, docking
G0:0000055	2	ribosomal large subunit export from nucleus
G0:0004741	2	[pyruvate dehydrogenase (lipoamide)] phosphatase activity
G0:0004743	2	pyruvate kinase activity
G0:0033861	2	negative regulation of NAD(P)H oxidase activity
G0:0003973	2	(S)-2-hydroxy-acid oxidase activity
G0:0051299	2	centrosome separation
G0:0019442	2	tryptophan catabolic process to acetyl-CoA
G0:0004021	2	L-alanine:2-oxoglutarate aminotransferase activity
G0:0045761	2	regulation of adenylate cyclase activity
G0:0019918	2	peptidyl-arginine methylation, to symmetrical-dimethyl arginine
G0:0006431	2	methionyl-tRNA aminoacylation
G0:0044092	2	negative regulation of molecular function
G0:0033142	2	progesterone receptor binding
G0:0051702	2	interaction with symbiont
G0:0070889	2	platelet alpha granule organization
G0:0035243	2	protein-arginine omega-N symmetric methyltransferase activity
G0:0030368	2	interleukin-17 receptor activity
G0:0031345	2	negative regulation of cell projection organization
G0:0005584	2	collagen type I trimer
G0:0035425	2	autocrine signaling
G0:0042990	2	regulation of transcription factor import into nucleus
G0:0042264	2	peptidyl-aspartic acid hydroxylation
G0:0031894	2	V1A vasopressin receptor binding
G0:0042262	2	DNA protection
G0:0006517	2	protein deglycosylation
G0:0047844	2	deoxycytidine deaminase activity
G0:0004915	2	interleukin-6 receptor activity

G0:0004917	2	interleukin-7 receptor activity
G0:0072393	2	microtubule anchoring at microtubule organizing center
G0:0090035	2	positive regulation of chaperone-mediated protein complex assembly
G0:0051147	2	regulation of muscle cell differentiation
G0:0018277	2	protein deamination
G0:0004008	2	copper-exporting ATPase activity
G0:0060965	2	negative regulation of gene silencing by miRNA
G0:0060964	2	regulation of gene silencing by miRNA
G0:0036018	2	cellular response to erythropoietin
G0:0001635	2	calcitonin gene-related polypeptide receptor activity
G0:1901981	2	phosphatidylinositol phosphate binding
G0:0032311	2	angiogenin-PR1 complex
G0:0060002	2	plus-end directed microfilament motor activity
G0:0071848	2	positive regulation of ERK1 and ERK2 cascade via TNFSF11-mediated signaling
G0:0071847	2	TNFSF11-mediated signaling pathway
G0:0043654	2	recognition of apoptotic cell
G0:0008665	2	2'-phosphotransferase activity
G0:0021855	2	hypothalamus cell migration
G0:0019050	2	suppression by virus of host apoptotic process
G0:0038179	2	neurotrophin signaling pathway
G0:0016052	2	carbohydrate catabolic process
G0:0045550	2	geranylgeranyl reductase activity
G0:0014740	2	negative regulation of muscle hyperplasia
G0:0042019	2	interleukin-23 binding
G0:0003179	2	heart valve morphogenesis
G0:0047023	2	androsterone dehydrogenase activity
G0:0003171	2	atrioventricular valve development
G0:1900041	2	negative regulation of interleukin-2 secretion
G0:1900625	2	positive regulation of monocyte aggregation
G0:0035651	2	AP-3 adaptor complex binding
G0:0060369	2	positive regulation of Fc receptor mediated stimulatory signaling pathway
G0:0015837	2	amine transport
G0:1902998	2	positive regulation of neurofibrillary tangle assembly
G0:0005989	2	lactose biosynthetic process
G0:0017098	2	sulfonylurea receptor binding
G0:0006720	2	isoprenoid metabolic process
G0:0030551	2	cyclic nucleotide binding
G0:0005185	2	neurohypophyseal hormone activity
G0:1903027	2	regulation of opsonization
G0:0009186	2	deoxyribonucleoside diphosphate metabolic process
G0:0009181	2	purine ribonucleoside diphosphate catabolic process
G0:0004766	2	spermidine synthase activity
G0:0072182	2	regulation of nephron tubule epithelial cell differentiation
G0:0072181	2	mesonephric duct formation
G0:0003914	2	DNA (6-4) photolyase activity
G0:0003884	2	D-amino-acid oxidase activity
G0:0047006	2	17-alpha,20-alpha-dihydroxypregn-4-en-3-one dehydrogenase activity
G0:2000721	2	positive regulation of transcription from RNA polymerase II promoter
involved in smooth	muscle cell differentiation	
G0:2000726	2	negative regulation of cardiac muscle cell differentiation
G0:2000098	2	negative regulation of smooth muscle cell-matrix adhesion
G0:0000461	2	endonucleolytic cleavage to generate mature 3'-end of SSU-rRNA from (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
G0:0032304	2	negative regulation of icosanoid secretion
G0:0032305	2	positive regulation of icosanoid secretion
G0:0032301	2	MutSalpha complex
G0:0032302	2	MutSbeta complex
G0:2000978	2	negative regulation of forebrain neuron differentiation
G0:0015248	2	sterol transporter activity
G0:0050347	2	trans-octaprenyltranstransferase activity
G0:0021623	2	oculomotor nerve formation
G0:0002532	2	production of molecular mediator involved in inflammatory response
G0:0048878	2	chemical homeostasis
G0:0002537	2	nitric oxide production involved in inflammatory response
G0:0046013	2	regulation of T cell homeostatic proliferation
G0:0038093	2	Fc receptor signaling pathway
G0:0071677	2	positive regulation of mononuclear cell migration
G0:0071676	2	negative regulation of mononuclear cell migration
G0:0071670	2	smooth muscle cell chemotaxis
G0:0071673	2	positive regulation of smooth muscle cell chemotaxis
G0:0071672	2	negative regulation of smooth muscle cell chemotaxis
G0:0030305	2	heparanase activity
G0:0047493	2	ceramide cholinephosphotransferase activity
G0:0061113	2	pancreas morphogenesis

G0:0072210	2	metanephric nephron development
G0:0042745	2	circadian sleep/wake cycle
G0:0006532	2	aspartate biosynthetic process
G0:0070375	2	ERK5 cascade
G0:0072134	2	nephrogenic mesenchyme morphogenesis
G0:2001269	2	positive regulation of cysteine-type endopeptidase activity involved in apoptotic signaling pathway
G0:2001268	2	negative regulation of cysteine-type endopeptidase activity involved in apoptotic signaling pathway
G0:0031213	2	RSF complex
G0:0031732	2	CCR7 chemokine receptor binding
G0:0048320	2	axial mesoderm formation
G0:0004392	2	heme oxygenase (decyclizing) activity
G0:0044322	2	endoplasmic reticulum quality control compartment
G0:0051295	2	establishment of meiotic spindle localization
G0:0051294	2	establishment of spindle orientation
G0:0004020	2	adenylylsulfate kinase activity
G0:0032798	2	Swi5-Sfr1 complex
G0:0032796	2	uropod organization
G0:0071864	2	positive regulation of cell proliferation in bone marrow
G0:2000393	2	negative regulation of lamellipodium morphogenesis
G0:0006880	2	intracellular sequestering of iron ion
G0:0038156	2	interleukin-3-mediated signaling pathway
G0:0038155	2	interleukin-23-mediated signaling pathway
G0:0070449	2	elongin complex
G0:0016524	2	latrotoxin receptor activity
G0:0070445	2	regulation of oligodendrocyte progenitor proliferation
G0:0034505	2	tooth mineralization
G0:0060341	2	regulation of cellular localization
G0:0034638	2	phosphatidylcholine catabolic process
G0:0097233	2	alveolar lamellar body membrane
G0:0015819	2	lysine transport
G0:0060435	2	bronchiole development
G0:0060437	2	lung growth
G0:0046755	2	viral budding
G0:0046208	2	spermine catabolic process
G0:0005965	2	protein farnesyltransferase complex
G0:0051935	2	L-glutamate uptake involved in synaptic transmission
G0:0045953	2	negative regulation of natural killer cell mediated cytotoxicity
G0:0045950	2	negative regulation of mitotic recombination
G0:1903225	2	negative regulation of endodermal cell differentiation
G0:1902174	2	positive regulation of keratinocyte apoptotic process
G0:0031914	2	negative regulation of synaptic plasticity
G0:1990034	2	calcium ion export from cell
G0:0004119	2	cGMP-inhibited cyclic-nucleotide phosphodiesterase activity
G0:0004565	2	beta-galactosidase activity
G0:0008074	2	guanylate cyclase complex, soluble
G0:0016890	2	site-specific endodeoxyribonuclease activity, specific for altered base
G0:0048179	2	activin receptor complex
G0:0000010	2	trans-hexaprenyltransferase activity
G0:0003938	2	IMP dehydrogenase activity
G0:0003934	2	GTP cyclohydrolase I activity
G0:0009798	2	axis specification
G0:1902177	2	positive regulation of oxidative stress-induced intrinsic apoptotic signaling pathway
G0:0010643	2	cell communication by chemical coupling
G0:0070970	2	interleukin-2 secretion
G0:0036324	2	vascular endothelial growth factor receptor-2 signaling pathway
G0:0000272	2	polysaccharide catabolic process
G0:0007549	2	dosage compensation
G0:0015265	2	urea channel activity
G0:0015266	2	protein channel activity
G0:0046985	2	positive regulation of hemoglobin biosynthetic process
G0:0046984	2	regulation of hemoglobin biosynthetic process
G0:0019958	2	C-X-C chemokine binding
G0:0019776	2	Atg8 ligase activity
G0:0019950	2	SMT3-dependent protein catabolic process
G0:0071472	2	cellular response to salt stress
G0:0010565	2	regulation of cellular ketone metabolic process
G0:0071475	2	cellular hyperosmotic salinity response
G0:0001866	2	NK T cell proliferation
G0:0001865	2	NK T cell differentiation
G0:0001869	2	negative regulation of complement activation, lectin pathway
G0:0051747	2	cytosine C-5 DNA demethylase activity
G0:0071315	2	cellular response to morphine

G0:0071657	2	positive regulation of granulocyte colony-stimulating factor production
G0:1901525	2	negative regulation of macromitophagy
G0:0030327	2	prenylated protein catabolic process
G0:0030328	2	prenylcysteine catabolic process
G0:0035759	2	mesangial cell-matrix adhesion
G0:0030981	2	cortical microtubule cytoskeleton
G0:0070845	2	polyubiquitinated misfolded protein transport
G0:0031056	2	regulation of histone modification
G0:0015616	2	DNA translocase activity
G0:0016539	2	intein-mediated protein splicing
G0:0043584	2	nose development
G0:0043585	2	nose morphogenesis
G0:0033188	2	sphingomyelin synthase activity
G0:0016532	2	superoxide dismutase copper chaperone activity
G0:0016534	2	cyclin-dependent protein kinase 5 activator activity
G0:0030187	2	melatonin biosynthetic process
G0:0014916	2	regulation of lung blood pressure
G0:0061138	2	morphogenesis of a branching epithelium
G0:0042226	2	interleukin-6 biosynthetic process
G0:0072236	2	metanephric loop of Henle development
G0:0000247	2	C-8 sterol isomerase activity
G0:0004951	2	cholecystokinin receptor activity
G0:0004956	2	prostaglandin D receptor activity
G0:0060086	2	circadian temperature homeostasis
G0:0031585	2	regulation of inositol 1,4,5-trisphosphate-sensitive calcium-release
channel activity		
G0:0060667	2	branch elongation involved in salivary gland morphogenesis
G0:0060661	2	submandibular salivary gland formation
G0:0031716	2	calcitonin receptor binding
G0:0002072	2	optic cup morphogenesis involved in camera-type eye development
G0:0048343	2	paraxial mesodermal cell fate commitment
G0:0034982	2	mitochondrial protein processing
G0:0010025	2	wax biosynthetic process
G0:0050510	2	N-acetylgalactosaminyl-proteoglycan 3-beta-glucuronosyltransferase
activity		
G0:0010792	2	DNA double-strand break processing involved in repair via single-strand
annealing		
G0:0032807	2	DNA ligase IV complex
G0:0032770	2	positive regulation of monooxygenase activity
G0:0032803	2	regulation of low-density lipoprotein particle receptor catabolic process
G0:0032513	2	negative regulation of protein phosphatase type 2B activity
G0:0038023	2	signaling receptor activity
G0:0008623	2	CHRA1
G0:0004560	2	alpha-L-fucosidase activity
G0:0032044	2	DSIF complex
G0:0019542	2	propionate biosynthetic process
G0:0070681	2	glutamyl-tRNA ^{Gln} biosynthesis via transamidation
G0:0032116	2	SMC loading complex
G0:0004450	2	isocitrate dehydrogenase (NADP+) activity
G0:0045519	2	interleukin-23 receptor binding
G0:0045518	2	interleukin-22 receptor binding
G0:0071226	2	cellular response to molecule of fungal origin
G0:0021988	2	olfactory lobe development
G0:0008078	2	mesodermal cell migration
G0:0021986	2	habenula development
G0:0007092	2	activation of mitotic anaphase-promoting complex activity
G0:0046226	2	coumarin catabolic process
G0:0046732	2	active induction of host immune response by virus
G0:0048753	2	pigment granule organization
G0:0010465	2	nerve growth factor receptor activity
G0:0044259	2	multicellular organismal macromolecule metabolic process
G0:1903206	2	negative regulation of hydrogen peroxide-induced cell death
G0:0006760	2	folic acid-containing compound metabolic process
G0:0018675	2	(S)-limonene 6-monooxygenase activity
G0:0060414	2	aorta smooth muscle tissue morphogenesis
G0:0000019	2	regulation of mitotic recombination
G0:0048486	2	parasympathetic nervous system development
G0:0048627	2	myoblast development
G0:0042732	2	D-xylose metabolic process
G0:1902336	2	positive regulation of retinal ganglion cell axon guidance
G0:0002865	2	negative regulation of acute inflammatory response to antigenic stimulus
G0:0051315	2	attachment of spindle microtubules to kinetochore involved in mitotic
sister chromatid segregation		
G0:0019201	2	nucleotide kinase activity
G0:0019207	2	kinase regulator activity

G0:2000766	2	negative regulation of cytoplasmic translation
G0:0005846	2	nuclear cap binding complex
G0:1901018	2	positive regulation of potassium ion transmembrane transporter activity
G0:1901019	2	regulation of calcium ion transmembrane transporter activity
G0:0023041	2	neuronal signal transduction
G0:0005607	2	laminin-2 complex
G0:0003223	2	ventricular compact myocardium morphogenesis
G0:0034421	2	post-translational protein acetylation
G0:0042412	2	taurine biosynthetic process
G0:0005592	2	collagen type XI trimer
G0:0003093	2	regulation of glomerular filtration
G0:0003097	2	renal water transport
G0:0017171	2	serine hydrolase activity
G0:0006570	2	tyrosine metabolic process
G0:0006577	2	amino-acid betaine metabolic process
G0:0006579	2	amino-acid betaine catabolic process
G0:0032810	2	sterol response element binding
G0:0060060	2	post-embryonic retina morphogenesis in camera-type eye
G0:0060061	2	Spemann organizer formation
G0:0060067	2	cervix development
G0:0072334	2	UDP-galactose transmembrane transport
G0:0072331	2	signal transduction by p53 class mediator
G0:0097006	2	regulation of plasma lipoprotein particle levels
G0:0090234	2	regulation of kinetochore assembly
G0:0035483	2	gastric emptying
G0:0009262	2	deoxyribonucleotide metabolic process
G0:0005006	2	epidermal growth factor-activated receptor activity
G0:0048368	2	lateral mesoderm development
G0:0051126	2	negative regulation of actin nucleation
G0:0051124	2	synaptic growth at neuromuscular junction
G0:0051120	2	hepoxilin A3 synthase activity
G0:0044338	2	canonical Wnt signaling pathway involved in mesenchymal stem cell differentiation
G0:0034694	2	response to prostaglandin
G0:0036315	2	cellular response to sterol
G0:0060443	2	mammary gland morphogenesis
G0:0032286	2	central nervous system myelin maintenance
G0:0003878	2	ATP citrate synthase activity
G0:1901224	2	positive regulation of NIK/NF-kappaB signaling
G0:0003870	2	5-aminolevulinate synthase activity
G0:0003875	2	ADP-ribosylarginine hydrolase activity
G0:0019550	2	glutamate catabolic process to aspartate
G0:0004069	2	L-aspartate:2-oxoglutarate aminotransferase activity
G0:0061547	2	glycogen synthase activity, transferring glucose-1-phosphate
G0:0004063	2	aryldialkylphosphatase activity
G0:0015433	2	peptide antigen-transporting ATPase activity
G0:0070404	2	NADH binding
G0:0032447	2	protein urmylation
G0:0004145	2	diamine N-acetyltransferase activity
G0:0016165	2	linoleate 13S-lipoxygenase activity
G0:0071752	2	secretory dimeric IgA immunoglobulin complex
G0:0071207	2	histone pre-mRNA stem-loop binding
G0:0015851	2	nucleobase transport
G0:0072554	2	blood vessel lumenization
G0:0097493	2	structural molecule activity conferring elasticity
G0:0030060	2	L-malate dehydrogenase activity
G0:0061074	2	regulation of neural retina development
G0:0046006	2	regulation of activated T cell proliferation
G0:0060478	2	acrosomal vesicle exocytosis
G0:0044058	2	regulation of digestive system process
G0:0000805	2	X chromosome
G0:0006452	2	translational frameshifting
G0:0009922	2	fatty acid elongase activity
G0:0072172	2	mesonephric tubule formation
G0:0006030	2	chitin metabolic process
G0:0006741	2	NADP biosynthetic process
G0:0006740	2	NADPH regeneration
G0:0014066	2	regulation of phosphatidylinositol 3-kinase signaling
G0:0014062	2	regulation of serotonin secretion
G0:0031523	2	Myb complex
G0:0010611	2	regulation of cardiac muscle hypertrophy
G0:0015226	2	carnitine transmembrane transporter activity
G0:0015229	2	L-ascorbic acid transporter activity
G0:0008292	2	acetylcholine biosynthetic process
G0:0071437	2	invadopodium

G0:0071436	2	sodium ion export
G0:0001820	2	serotonin secretion
G0:2000744	2	positive regulation of anterior head development
G0:2000035	2	regulation of stem cell division
G0:0070345	2	negative regulation of fat cell proliferation
G0:0052642	2	lysophosphatidic acid phosphatase activity
G0:0001650	2	fibrillar center
G0:0021681	2	cerebellar granular layer development
G0:0016577	2	histone demethylation
G0:0045875	2	negative regulation of sister chromatid cohesion
G0:0072272	2	proximal/distal pattern formation involved in metanephric nephron development
G0:0002384	2	hepatic immune response
G0:2000563	2	positive regulation of CD4-positive, alpha-beta T cell proliferation
G0:1900215	2	negative regulation of apoptotic process involved in metanephric collecting duct development
G0:1900218	2	negative regulation of apoptotic process involved in metanephric nephron tubule development
G0:0015677	2	copper ion import
G0:0060764	2	cell-cell signaling involved in mammary gland development
G0:0097021	2	lymphocyte migration into lymphoid organs
G0:0097539	2	ciliary transition fiber
G0:0060621	2	negative regulation of cholesterol import
G0:0009247	2	glycolipid biosynthetic process
G0:0021831	2	embryonic olfactory bulb interneuron precursor migration
G0:0021836	2	chemorepulsion involved in postnatal olfactory bulb interneuron migration
G0:0008194	2	UDP-glycosyltransferase activity
G0:0000172	2	ribonuclease MRP complex
G0:0004084	2	branched-chain-amino-acid transaminase activity
G0:0007208	2	phospholipase C-activating serotonin receptor signaling pathway
G0:2000481	2	positive regulation of cAMP-dependent protein kinase activity
G0:2000482	2	regulation of interleukin-8 secretion
G0:0016531	2	copper chaperone activity
G0:0040038	2	polar body extrusion after meiotic divisions
G0:0040030	2	regulation of molecular function, epigenetic
G0:0070427	2	nucleotide-binding oligomerization domain containing 1 signaling pathway
G0:0072487	2	MSL complex
G0:0033065	2	Rad51C-XRCC3 complex
G0:0072053	2	renal inner medulla development
G0:0045175	2	basal protein localization
G0:0033605	2	positive regulation of catecholamine secretion
G0:0004329	2	formate-tetrahydrofolate ligase activity
G0:0018126	2	protein hydroxylation
G0:0001030	2	RNA polymerase III type 1 promoter DNA binding
G0:0001031	2	RNA polymerase III type 2 promoter DNA binding
G0:0001032	2	RNA polymerase III type 3 promoter DNA binding
G0:0003413	2	chondrocyte differentiation involved in endochondral bone morphogenesis
G0:0030007	2	cellular potassium ion homeostasis
G0:0061056	2	sclerotome development
G0:0061052	2	negative regulation of cell growth involved in cardiac muscle cell development
G0:0003689	2	DNA clamp loader activity
G0:0004507	2	steroid 11-beta-monooxygenase activity
G0:1902110	2	positive regulation of mitochondrial membrane permeability involved in apoptotic process
G0:0006011	2	UDP-glucose metabolic process
G0:0048664	2	neuron fate determination
G0:0005275	2	amine transmembrane transporter activity
G0:0048669	2	collateral sprouting in absence of injury
G0:0014042	2	positive regulation of neuron maturation
G0:0072102	2	glomerulus morphogenesis
G0:0072104	2	glomerular capillary formation
G0:0071359	2	cellular response to dsRNA
G0:1902808	2	positive regulation of cell cycle G1/S phase transition
G0:0010512	2	negative regulation of phosphatidylinositol biosynthetic process
G0:0039529	2	RIG-I signaling pathway
G0:0039528	2	cytoplasmic pattern recognition receptor signaling pathway in response to virus
G0:0007521	2	muscle cell fate determination
G0:0007525	2	somatic muscle development
G0:0003998	2	acylphosphatase activity
G0:0003994	2	aconitate hydratase activity
G0:0003990	2	acetylcholinesterase activity
G0:0030050	2	vesicle transport along actin filament
G0:0032042	2	mitochondrial DNA metabolic process

G0:2000019	2	negative regulation of male gonad development
G0:2000010	2	positive regulation of protein localization to cell surface
G0:0072354	2	histone kinase activity (H3-T3 specific)
G0:0032071	2	regulation of endodeoxyribonuclease activity
G0:0008413	2	8-oxo-7,8-dihydroguanosine triphosphate pyrophosphatase activity
G0:2000860	2	positive regulation of aldosterone secretion
G0:0042171	2	lysophosphatidic acid acyltransferase activity
G0:0043564	2	Ku70:Ku80 complex
G0:0003057	2	regulation of the force of heart contraction by chemical signal
G0:0003050	2	regulation of systemic arterial blood pressure by atrial natriuretic peptide
G0:0070369	2	beta-catenin-TCF7L2 complex
G0:0042287	2	MHC protein binding
G0:0033292	2	T-tubule organization
G0:0019860	2	uracil metabolic process
G0:0019865	2	immunoglobulin binding
G0:0031034	2	myosin filament assembly
G0:0050902	2	leukocyte adhesive activation
G0:0050906	2	detection of stimulus involved in sensory perception
G0:0050904	2	diapedesis
G0:0097049	2	motor neuron apoptotic process
G0:0045818	2	negative regulation of glycogen catabolic process
G0:0045819	2	positive regulation of glycogen catabolic process
G0:0055090	2	acylglycerol homeostasis
G0:0090091	2	positive regulation of extracellular matrix disassembly
G0:0009220	2	pyrimidine ribonucleotide biosynthetic process
G0:0046108	2	uridine metabolic process
G0:0046101	2	hypoxanthine biosynthetic process
G0:0048858	2	cell projection morphogenesis
G0:0002019	2	regulation of renal output by angiotensin
G0:0002017	2	regulation of blood volume by renal aldosterone
G0:0005042	2	netrin receptor activity
G0:0031298	2	replication fork protection complex
G0:0008176	2	tRNA (guanine-N7-)-methyltransferase activity
G0:0008177	2	succinate dehydrogenase (ubiquinone) activity
G0:0008175	2	tRNA methyltransferase activity
G0:0000152	2	nuclear ubiquitin ligase complex
G0:0004314	2	[acyl-carrier-protein] S-malonyltransferase activity
G0:0004315	2	3-oxoacyl-[acyl-carrier-protein] synthase activity
G0:0008318	2	protein prenyltransferase activity
G0:0045244	2	succinate-CoA ligase complex (GDP-forming)
G0:0070991	2	medium-chain-acyl-CoA dehydrogenase activity
G0:0001672	2	regulation of chromatin assembly or disassembly
G0:0042903	2	tubulin deacetylase activity
G0:0034111	2	negative regulation of homotypic cell-cell adhesion
G0:0070193	2	synaptonemal complex organization
G0:0015386	2	potassium:proton antiporter activity
G0:0015382	2	sodium:sulfate symporter activity
G0:0033594	2	response to hydroxyisoflavone
G0:0033041	2	sweet taste receptor activity
G0:0010960	2	magnesium ion homeostasis
G0:0001785	2	prostaglandin J receptor activity
G0:0090526	2	regulation of gluconeogenesis involved in cellular glucose homeostasis
G0:0051424	2	corticotropin-releasing hormone binding
G0:0071712	2	ER-associated misfolded protein catabolic process
G0:0030249	2	guanylate cyclase regulator activity
G0:0008459	2	chondroitin 6-sulfotransferase activity
G0:0034988	2	Fc-gamma receptor I complex binding
G0:1901621	2	negative regulation of smoothened signaling pathway involved in dorsal/ventral neural tube patterning
G0:0033624	2	negative regulation of integrin activation
G0:1990254	2	keratin filament binding
G0:0035507	2	regulation of myosin-light-chain-phosphatase activity
G0:0061035	2	regulation of cartilage development
G0:0061032	2	visceral serous pericardium development
G0:0061033	2	secretion by lung epithelial cell involved in lung growth
G0:0031990	2	mRNA export from nucleus in response to heat stress
G0:0031999	2	negative regulation of fatty acid beta-oxidation
G0:0006784	2	heme a biosynthetic process
G0:0070232	2	regulation of T cell apoptotic process
G0:0002134	2	UTP binding
G0:0004781	2	sulfate adenylyltransferase (ATP) activity
G0:0031371	2	ubiquitin conjugating enzyme complex
G0:0031372	2	UBC13-MMS2 complex
G0:0072126	2	positive regulation of glomerular mesangial cell proliferation

G0:0032388	2	positive regulation of intracellular transport
G0:0005253	2	anion channel activity
G0:0009786	2	regulation of asymmetric cell division
G0:0009785	2	blue light signaling pathway
G0:0010652	2	positive regulation of cell communication by chemical coupling
G0:0001579	2	medium-chain fatty acid transport
G0:2000078	2	positive regulation of type B pancreatic cell development
G0:0008781	2	N-acylneuraminate cytidyltransferase activity
G0:2000074	2	regulation of type B pancreatic cell development
G0:0038037	2	G-protein coupled receptor dimeric complex
G0:0032055	2	negative regulation of translation in response to stress
G0:0035880	2	embryonic nail plate morphogenesis
G0:0035887	2	aortic smooth muscle cell differentiation
G0:0019264	2	glycine biosynthetic process from serine
G0:0019265	2	glycine biosynthetic process, by transamination of glyoxylate
G0:0033032	2	regulation of myeloid cell apoptotic process
G0:0090427	2	activation of meiosis
G0:0003032	2	detection of oxygen
G0:0043503	2	skeletal muscle fiber adaptation
G0:0072070	2	loop of Henle development
G0:0070384	2	Harderian gland development
G0:0047696	2	beta-adrenergic receptor kinase activity
G0:0071035	2	nuclear polyadenylation-dependent rRNA catabolic process
G0:0015891	2	siderophore transport
G0:0034593	2	phosphatidylinositol bisphosphate phosphatase activity
G0:0034597	2	phosphatidylinositol-4,5-bisphosphate 4-phosphatase activity
G0:0034594	2	phosphatidylinositol trisphosphate phosphatase activity
G0:0019842	2	vitamin binding
G0:0060003	2	copper ion export
G0:0060557	2	positive regulation of vitamin D biosynthetic process
G0:0050925	2	negative regulation of negative chemotaxis
G0:0034046	2	poly(G) binding
G0:0050922	2	negative regulation of chemotaxis
G0:0097061	2	dendritic spine organization
G0:0031800	2	type 3 metabotropic glutamate receptor binding
G0:0045837	2	negative regulation of membrane potential
G0:0048633	2	positive regulation of skeletal muscle tissue growth
G0:0048875	2	chemical homeostasis within a tissue
G0:0048871	2	multicellular organismal homeostasis
G0:0034686	2	integrin alphav-beta8 complex
G0:0065001	2	specification of axis polarity
G0:0034681	2	integrin alpha11-beta1 complex
G0:0048257	2	3'-flap endonuclease activity
G0:0048256	2	flap endonuclease activity
G0:0045161	2	neuronal ion channel clustering
G0:0070816	2	phosphorylation of RNA polymerase II C-terminal domain
G0:0004335	2	galactokinase activity
G0:0004337	2	geranyltranstransferase activity
G0:0008332	2	low voltage-gated calcium channel activity
G0:0070603	2	SWI/SNF superfamily-type complex
G0:0070977	2	bone maturation
G0:0061005	2	cell differentiation involved in kidney development
G0:0050942	2	positive regulation of pigment cell differentiation
G0:0021903	2	rostrocaudal neural tube patterning
G0:0004477	2	methenyltetrahydrofolate cyclohydrolase activity
G0:0018676	2	(S)-limonene 7-monooxygenase activity
G0:0019100	2	male germ-line sex determination
G0:0002315	2	marginal zone B cell differentiation
G0:0032998	2	Fc-epsilon receptor I complex
G0:0052869	2	arachidonic acid omega-hydroxylase activity
G0:0030221	2	basophil differentiation
G0:0030223	2	neutrophil differentiation
G0:0030222	2	eosinophil differentiation
G0:0061017	2	hepatoblast differentiation
G0:0042321	2	negative regulation of circadian sleep/wake cycle, sleep
G0:0042323	2	negative regulation of circadian sleep/wake cycle, non-REM sleep
G0:0042322	2	negative regulation of circadian sleep/wake cycle, REM sleep
G0:0006272	2	leading strand elongation
G0:0042328	2	heparan sulfate N-acetylglucosaminyltransferase activity
G0:0010882	2	regulation of cardiac muscle contraction by calcium ion signaling
G0:0000308	2	cytoplasmic cyclin-dependent protein kinase holoenzyme complex
G0:0010571	2	positive regulation of nuclear cell cycle DNA replication
G0:0006423	2	cysteinyl-tRNA aminoacylation
G0:0009949	2	polarity specification of anterior/posterior axis
G0:0006051	2	N-acetylmannosamine metabolic process

G0:2001037	2	positive regulation of tongue muscle cell differentiation
G0:0060769	2	positive regulation of epithelial cell proliferation involved in prostate gland development
G0:0060768	2	regulation of epithelial cell proliferation involved in prostate gland development
G0:0031314	2	extrinsic component of mitochondrial inner membrane
G0:0060760	2	positive regulation of response to cytokine stimulus
G0:0050713	2	negative regulation of interleukin-1 beta secretion
G0:0050711	2	negative regulation of interleukin-1 secretion
G0:0010260	2	organ senescence
G0:0050717	2	positive regulation of interleukin-1 alpha secretion
G0:0048403	2	brain-derived neurotrophic factor binding
G0:0050432	2	catecholamine secretion
G0:0005502	2	11-cis retinal binding
G0:0004103	2	choline kinase activity
G0:0004105	2	choline-phosphate cytidylyltransferase activity
G0:0004109	2	coproporphyrinogen oxidase activity
G0:0046922	2	peptide-O-fucosyltransferase activity
G0:0001550	2	ovarian cumulus expansion
G0:1902510	2	regulation of apoptotic DNA fragmentation
G0:0001555	2	oocyte growth
G0:0001554	2	luteolysis
G0:0001888	2	glucuronyl-galactosyl-proteoglycan 4-alpha-N-acetylglucosaminyltransferase activity
G0:0055099	2	response to high density lipoprotein particle
G0:0055096	2	low-density lipoprotein particle mediated signaling
G0:2000054	2	negative regulation of Wnt signaling pathway involved in dorsal/ventral axis specification
G0:2000051	2	negative regulation of non-canonical Wnt signaling pathway
G0:0032038	2	myosin II heavy chain binding
G0:1901094	2	negative regulation of protein homotetramerization
G0:0008453	2	alanine-glyoxylate transaminase activity
G0:0047322	2	[hydroxymethylglutaryl-CoA reductase (NADPH)] kinase activity
G0:0042132	2	fructose 1,6-bisphosphate 1-phosphatase activity
G0:1901894	2	regulation of calcium-transporting ATPase activity
G0:0003012	2	muscle system process
G0:0021592	2	fourth ventricle development
G0:2000594	2	positive regulation of metanephric DCT cell differentiation
G0:0034205	2	beta-amyloid formation
G0:1900273	2	positive regulation of long-term synaptic potentiation
G0:1900271	2	regulation of long-term synaptic potentiation
G0:0019828	2	aspartic-type endopeptidase inhibitor activity
G0:0060577	2	pulmonary vein morphogenesis
G0:0090325	2	regulation of locomotion involved in locomotory behavior
G0:0015911	2	plasma membrane long-chain fatty acid transport
G0:0046499	2	S-adenosylmethioninamine metabolic process
G0:0002762	2	negative regulation of myeloid leukocyte differentiation
G0:0034344	2	regulation of type III interferon production
G0:0006427	2	histidyl-tRNA aminoacylation
G0:0006424	2	glutamyl-tRNA aminoacylation
G0:0006420	2	arginyl-tRNA aminoacylation
G0:0009882	2	blue light photoreceptor activity
G0:0006428	2	isoleucyl-tRNA aminoacylation
G0:0006429	2	leucyl-tRNA aminoacylation
G0:0035339	2	SPOTS complex
G0:0086089	2	voltage-gated potassium channel activity involved in atrial cardiac muscle cell action potential repolarization
G0:0060685	2	regulation of prostatic bud formation
G0:0052815	2	medium-chain acyl-CoA hydrolase activity
G0:0019086	2	late viral transcription
G0:0000117	2	regulation of transcription involved in G2/M transition of mitotic cell cycle
G0:0042498	2	diacyl lipopeptide binding
G0:0004356	2	glutamate-ammonia ligase activity
G0:0042495	2	detection of triacyl bacterial lipopeptide
G0:0004352	2	glutamate dehydrogenase (NAD+) activity
G0:0009081	2	branched-chain amino acid metabolic process
G0:0009082	2	branched-chain amino acid biosynthetic process
G0:0045204	2	MAPK export from nucleus
G0:0031436	2	BRCA1-BARD1 complex
G0:0090140	2	regulation of mitochondrial fission
G0:0035994	2	response to muscle stretch
G0:0003207	2	cardiac chamber formation
G0:0070488	2	neutrophil aggregation
G0:0070483	2	detection of hypoxia

G0:0007468	2	regulation of rhodopsin gene expression
G0:0044236	2	multicellular organismal metabolic process
G0:0010701	2	positive regulation of norepinephrine secretion
G0:0003209	2	cardiac atrium morphogenesis
G0:0035566	2	regulation of metanephros size
G0:0090537	2	CERF complex
G0:0051562	2	negative regulation of mitochondrial calcium ion concentration
G0:0015129	2	lactate transmembrane transporter activity
G0:0010447	2	response to acidity
G0:0007070	2	negative regulation of transcription from RNA polymerase II promoter
during mitosis		
G0:0071281	2	cellular response to iron ion
G0:0071286	2	cellular response to magnesium ion
G0:0071287	2	cellular response to manganese ion
G0:0004359	2	glutaminase activity
G0:0033004	2	negative regulation of mast cell activation
G0:0033005	2	positive regulation of mast cell activation
G0:0004357	2	glutamate-cysteine ligase activity
G0:0030200	2	heparan sulfate proteoglycan catabolic process
G0:0004353	2	glutamate dehydrogenase [NAD(P)+] activity
G0:0032510	2	endosome to lysosome transport via multivesicular body sorting pathway
G0:1901661	2	quinone metabolic process
G0:0061564	2	axon development
G0:0005945	2	6-phosphofructokinase complex
G0:0002667	2	regulation of T cell anergy
G0:0042309	2	homiothermy
G0:0047150	2	betaine-homocysteine S-methyltransferase activity
G0:0015193	2	L-proline transmembrane transporter activity
G0:0043316	2	cytotoxic T cell degranulation
G0:0043314	2	negative regulation of neutrophil degranulation
G0:0043313	2	regulation of neutrophil degranulation
G0:0006212	2	uracil catabolic process
G0:0004854	2	xanthine dehydrogenase activity
G0:0004174	2	electron-transferring-flavoprotein dehydrogenase activity
G0:0050882	2	voluntary musculoskeletal movement
G0:1903202	2	negative regulation of oxidative stress-induced cell death
G0:0031339	2	negative regulation of vesicle fusion
G0:0060215	2	primitive hemopoiesis
G0:0060748	2	tertiary branching involved in mammary gland duct morphogenesis
G0:0008252	2	nucleotidase activity
G0:0050779	2	RNA destabilization
G0:0097324	2	melanocyte migration
G0:0022839	2	ion gated channel activity
G0:0030641	2	regulation of cellular pH
G0:2001295	2	malonyl-CoA biosynthetic process
G0:0036304	2	umbilical cord morphogenesis
G0:1990380	2	Lys48-specific deubiquitinase activity
G0:0070564	2	positive regulation of vitamin D receptor signaling pathway
G0:0002246	2	wound healing involved in inflammatory response
G0:0001970	2	positive regulation of activation of membrane attack complex
G0:0004161	2	dimethylallyltranstransferase activity
G0:0016402	2	pristanoyl-CoA oxidase activity
G0:2000650	2	negative regulation of sodium ion transmembrane transporter activity
G0:0031060	2	regulation of histone methylation
G0:1901299	2	negative regulation of hydrogen peroxide-mediated programmed cell death
G0:0031061	2	negative regulation of histone methylation
G0:0035565	2	regulation of pronephros size
G0:0070034	2	telomeric RNA binding
G0:0070033	2	synaptobrevin 2-SNAP-25-syntaxin-1a-complexin II complex
G0:1901877	2	negative regulation of calcium ion binding
G0:1901874	2	negative regulation of post-translational protein modification
G0:0090498	2	extrinsic component of Golgi membrane
G0:0032541	2	cortical endoplasmic reticulum
G0:0016314	2	phosphatidylinositol-3,4,5-trisphosphate 3-phosphatase activity
G0:0016316	2	phosphatidylinositol-3,4-bisphosphate 4-phosphatase activity
G0:0034551	2	mitochondrial respiratory chain complex III assembly
G0:0009628	2	response to abiotic stimulus
G0:1900220	2	semaphorin-plexin signaling pathway involved in bone trabecula
morphogenesis		
G0:0035686	2	sperm fibrous sheath
G0:0032204	2	regulation of telomere maintenance
G0:0035354	2	Toll-like receptor 1-Toll-like receptor 2 protein complex
G0:0035355	2	Toll-like receptor 2-Toll-like receptor 6 protein complex
G0:0032202	2	telomere assembly
G0:0035358	2	regulation of peroxisome proliferator activated receptor signaling pathway

G0:0035359	2	negative regulation of peroxisome proliferator activated receptor signaling pathway
G0:0006408	2	snRNA export from nucleus
G0:0052832	2	inositol monophosphate 3-phosphatase activity
G0:0034736	2	cholesterol O-acyltransferase activity
G0:0006407	2	rRNA export from nucleus
G0:0005171	2	hepatocyte growth factor receptor binding
G0:0008119	2	thiopurine S-methyltransferase activity
G0:0048743	2	positive regulation of skeletal muscle fiber development
G0:0005174	2	CD40 receptor binding
G0:0004373	2	glycogen (starch) synthase activity
G0:0004379	2	glycylpeptide N-tetradecanoyltransferase activity
G0:1902963	2	negative regulation of metalloendopeptidase activity involved in amyloid precursor protein catabolic process
G0:1902966	2	positive regulation of protein localization to early endosome
G0:0090169	2	regulation of spindle assembly
G0:0090166	2	Golgi disassembly
G0:0090160	2	Golgi to lysosome transport
G0:0032227	2	negative regulation of synaptic transmission, dopaminergic
G0:0044216	2	other organism cell
G0:0009609	2	response to symbiotic bacterium
G0:0019322	2	pentose biosynthetic process
G0:0014819	2	regulation of skeletal muscle contraction
G0:0014816	2	skeletal muscle satellite cell differentiation
G0:0051583	2	dopamine uptake involved in synaptic transmission
G0:0051563	2	smooth endoplasmic reticulum calcium ion homeostasis
G0:2000401	2	regulation of lymphocyte migration
G0:0019144	2	ADP-sugar diphosphatase activity
G0:0032483	2	regulation of Rab protein signal transduction
G0:0032487	2	regulation of Rap protein signal transduction
G0:0016670	2	oxidoreductase activity, acting on a sulfur group of donors, oxygen as acceptor
G0:0016679	2	oxidoreductase activity, acting on diphenols and related substances as donors
G0:0033578	2	protein glycosylation in Golgi
G0:0021941	2	negative regulation of cerebellar granule cell precursor proliferation
G0:0030884	2	exogenous lipid antigen binding
G0:0030888	2	regulation of B cell proliferation
G0:0017042	2	glycosylceramidase activity
G0:0045629	2	negative regulation of T-helper 2 cell differentiation
G0:0000492	2	box C/D snoRNP assembly
G0:0004727	2	prenylated protein tyrosine phosphatase activity
G0:0031645	2	negative regulation of neurological system process
G0:0031134	2	sister chromatid biorientation
G0:0006097	2	glyoxylate cycle
G0:0046619	2	optic placode formation involved in camera-type eye formation
G0:0031685	2	adenosine receptor binding
G0:0031687	2	A2A adenosine receptor binding
G0:0090312	2	positive regulation of protein deacetylation
G0:0060729	2	intestinal epithelial structure maintenance
G0:0043185	2	vascular endothelial growth factor receptor 3 binding
G0:0043532	2	angiostatin binding
G0:0009450	2	gamma-aminobutyric acid catabolic process
G0:0002268	2	follicular dendritic cell differentiation
G0:0005549	2	odorant binding
G0:0004830	2	tryptophan-tRNA ligase activity
G0:0046960	2	sensitization
G0:0048007	2	antigen processing and presentation, exogenous lipid antigen via MHC class Ib
G0:0018153	2	isopeptide cross-linking via N6-(L-isoglutamyl)-L-lysine
G0:0035922	2	foramen ovale closure
G0:0030109	2	HLA-B specific inhibitory MHC class I receptor activity
G0:1901857	2	positive regulation of cellular respiration
G0:0021551	2	central nervous system morphogenesis
G0:0021882	2	regulation of transcription from RNA polymerase II promoter involved in forebrain neuron fate commitment
G0:0021553	2	olfactory nerve development
G0:0021557	2	oculomotor nerve development
G0:0021558	2	trochlear nerve development
G0:0035461	2	vitamin transmembrane transport
G0:0033743	2	peptide-methionine (R)-S-oxide reductase activity
G0:0021773	2	striatal medium spiny neuron differentiation
G0:0021778	2	oligodendrocyte cell fate specification
G0:0015680	2	intracellular copper ion transport
G0:0071895	2	odontoblast differentiation

G0:0071896	2	protein localization to adherens junction
G0:0002725	2	negative regulation of T cell cytokine production
G0:0002724	2	regulation of T cell cytokine production
G0:0002720	2	positive regulation of cytokine production involved in immune response
G0:0038188	2	cholecystokinin signaling pathway
G0:0038181	2	bile acid receptor activity
G0:0002093	2	auditory receptor cell morphogenesis
G0:0002431	2	Fc receptor mediated stimulatory signaling pathway
G0:0030976	2	thiamine pyrophosphate binding
G0:0048588	2	developmental cell growth
G0:0035370	2	UBC13-UEV1A complex
G0:0045980	2	negative regulation of nucleotide metabolic process
G0:0052852	2	very-long-chain-(S)-2-hydroxy-acid oxidase activity
G0:0003415	2	chondrocyte hypertrophy
G0:0043120	2	tumor necrosis factor binding
G0:0005153	2	interleukin-8 receptor binding
G0:0005151	2	interleukin-1, Type II receptor binding
G0:0005150	2	interleukin-1, Type I receptor binding
G0:0045180	2	basal cortex
G0:0070876	2	S0SS complex
G0:0004825	2	methionine-tRNA ligase activity
G0:0004821	2	histidine-tRNA ligase activity
G0:0004822	2	isoleucine-tRNA ligase activity
G0:0004823	2	leucine-tRNA ligase activity
G0:0004829	2	threonine-tRNA ligase activity
G0:0060392	2	negative regulation of SMAD protein import into nucleus
G0:0032349	2	positive regulation of aldosterone biosynthetic process
G0:0015204	2	urea transmembrane transporter activity
G0:0015205	2	nucleobase transmembrane transporter activity
G0:0042986	2	positive regulation of amyloid precursor protein biosynthetic process
G0:0034098	2	Cdc48p-Npl4p-Ufdlp AAA ATPase complex
G0:0010157	2	response to chlorate
G0:0036294	2	cellular response to decreased oxygen levels
G0:0008396	2	oxysterol 7-alpha-hydroxylase activity
G0:0014873	2	response to muscle activity involved in regulation of muscle adaptation
G0:0010485	2	H4 histone acetyltransferase activity
G0:0010484	2	H3 histone acetyltransferase activity
G0:0001705	2	ectoderm formation
G0:0032971	2	regulation of muscle filament sliding
G0:0071799	2	cellular response to prostaglandin D stimulus
G0:0071791	2	chemokine (C-C motif) ligand 5 binding
G0:0035963	2	cellular response to interleukin-13
G0:0019303	2	D-ribose catabolic process
G0:0019307	2	mannose biosynthetic process
G0:0032602	2	chemokine production
G0:0045605	2	negative regulation of epidermal cell differentiation
G0:0045608	2	negative regulation of auditory receptor cell differentiation
G0:0034189	2	very-low-density lipoprotein particle binding
G0:0072537	2	fibroblast activation
G0:0072536	2	interleukin-23 receptor complex
G0:0034184	2	positive regulation of maintenance of mitotic sister chromatid cohesion
G0:0031111	2	negative regulation of microtubule polymerization or depolymerization
G0:0031119	2	tRNA pseudouridine synthesis
G0:0006437	2	tyrosyl-tRNA aminoacylation
G0:0034769	2	basement membrane disassembly
G0:0097107	2	postsynaptic density assembly
G0:0035585	2	calcium-mediated signaling using extracellular calcium source
G0:0051797	2	regulation of hair follicle development
G0:0051791	2	medium-chain fatty acid metabolic process
G0:0097363	2	protein O-GlcNAc transferase activity
G0:2001162	2	positive regulation of histone H3-K79 methylation
G0:1902202	2	regulation of hepatocyte growth factor receptor signaling pathway
G0:0004910	2	interleukin-1, Type II, blocking receptor activity
G0:0003310	2	pancreatic A cell differentiation
G0:0023052	2	signaling
G0:0048020	2	CCR chemokine receptor binding
G0:0048023	2	positive regulation of melanin biosynthetic process
G0:0004613	2	phosphoenolpyruvate carboxykinase (GTP) activity
G0:0004611	2	phosphoenolpyruvate carboxykinase activity
G0:0004616	2	phosphogluconate dehydrogenase (decarboxylating) activity
G0:0004615	2	phosphomannomutase activity
G0:0004618	2	phosphoglycerate kinase activity
G0:0070075	2	tear secretion
G0:0034970	2	histone H3-R2 methylation
G0:2000342	2	negative regulation of chemokine (C-X-C motif) ligand 2 production

G0:2000346	2	negative regulation of hepatocyte proliferation
G0:2000587	2	negative regulation of platelet-derived growth factor receptor-beta signaling pathway
G0:0021759	2	globus pallidus development
G0:0021750	2	vestibular nucleus development
G0:1901838	2	positive regulation of transcription of nuclear large rRNA transcript from RNA polymerase I promoter
G0:2000394	2	positive regulation of lamellipodium morphogenesis
G0:0035403	2	histone kinase activity (H3-T6 specific)
G0:0090336	2	positive regulation of brown fat cell differentiation
G0:0033093	2	Weibel-Palade body
G0:0060219	2	camera-type eye photoreceptor cell differentiation
G0:0051659	2	maintenance of mitochondrion location
G0:0051654	2	establishment of mitochondrion localization
G0:0004814	2	arginine-tRNA ligase activity
G0:0033092	2	positive regulation of immature T cell proliferation in thymus
G0:1901165	2	positive regulation of trophoblast cell migration
G0:0048561	2	establishment of organ orientation
G0:0048563	2	post-embryonic organ morphogenesis
G0:0017002	2	activin-activated receptor activity
G0:0017004	2	cytochrome complex assembly
G0:0052870	2	tocopherol omega-hydroxylase activity
G0:0086029	2	Purkinje myocyte to ventricular cardiac muscle cell signaling
G0:0006114	2	glycerol biosynthetic process
G0:0043148	2	mitotic spindle stabilization
G0:0005137	2	interleukin-5 receptor binding
G0:0005133	2	interferon-gamma receptor binding
G0:0070890	2	sodium-dependent L-ascorbate transmembrane transporter activity
G0:0044062	2	regulation of excretion
G0:0090291	2	negative regulation of osteoclast proliferation
G0:0003943	2	N-acetylgalactosamine-4-sulfatase activity
G0:0008124	2	4-alpha-hydroxytetrahydrobiopterin dehydratase activity
G0:0007402	2	ganglion mother cell fate determination
G0:0015189	2	L-lysine transmembrane transporter activity
G0:2000116	2	regulation of cysteine-type endopeptidase activity
G0:0001729	2	ceramide kinase activity
G0:0032918	2	spermidine acetylation
G0:0032915	2	positive regulation of transforming growth factor beta2 production
G0:0032911	2	negative regulation of transforming growth factor beta1 production
G0:0032912	2	negative regulation of transforming growth factor beta2 production
G0:0008510	2	sodium:bicarbonate symporter activity
G0:0008511	2	sodium:potassium:chloride symporter activity
G0:0003272	2	endocardial cushion formation
G0:0014854	2	response to inactivity
G0:0032623	2	interleukin-2 production
G0:0047751	2	cholestenone 5-alpha-reductase activity
G0:0047750	2	cholestenol delta-isomerase activity
G0:0060433	2	bronchus development
G0:0005953	2	CAAX-protein geranylgeranyltransferase complex
G0:0071482	2	cellular response to light stimulus
G0:0070538	2	oleic acid binding
G0:0045661	2	regulation of myoblast differentiation
G0:0002495	2	antigen processing and presentation of peptide antigen via MHC class II
G0:0019981	2	interleukin-6 binding
G0:0030849	2	autosome
G0:0016499	2	orexin receptor activity
G0:0050820	2	positive regulation of coagulation
G0:0034701	2	tripeptidase activity
G0:1900194	2	negative regulation of oocyte maturation
G0:0061097	2	regulation of protein tyrosine kinase activity
G0:0006583	2	melanin biosynthetic process from tyrosine
G0:0050794	2	regulation of cellular process
G0:0046666	2	retinal cell programmed cell death
G0:0010918	2	positive regulation of mitochondrial membrane potential
G0:0022890	2	inorganic cation transmembrane transporter activity
G0:0002115	2	store-operated calcium entry
G0:0022898	2	regulation of transmembrane transporter activity
G0:0001941	2	postsynaptic membrane organization
G0:0006636	2	unsaturated fatty acid biosynthetic process
G0:0005583	2	fibrillar collagen trimer
G0:2001183	2	negative regulation of interleukin-12 secretion
G0:1902263	2	apoptotic process involved in embryonic digit morphogenesis
G0:2001189	2	negative regulation of T cell activation via T cell receptor contact with antigen bound to MHC molecule on antigen presenting cell
G0:1902269	2	positive regulation of polyamine transmembrane transport

GO:0004452 2 isopentenyl-diphosphate delta-isomerase activity
 GO:0055014 2 atrial cardiac muscle cell development
 GO:0006965 2 positive regulation of biosynthetic process of antibacterial peptides
 active against Gram-positive bacteria
 GO:0034124 2 regulation of MyD88-dependent toll-like receptor signaling pathway
 GO:0021514 2 ventral spinal cord interneuron differentiation
 GO:0060914 2 heart formation
 GO:0046879 2 hormone secretion
 GO:0010720 2 positive regulation of cell development
 GO:0046877 2 regulation of saliva secretion
 GO:0002930 2 trabecular meshwork development
 GO:2000637 2 positive regulation of gene silencing by miRNA
 GO:0003331 2 positive regulation of extracellular matrix constituent secretion
 GO:0072534 2 perineuronal net
 GO:0033257 2 Bcl3/NF-kappaB2 complex
 GO:0031251 2 PAN complex
 GO:0044209 2 AMP salvage
 GO:0015333 2 peptide:proton symporter activity
 GO:0086003 2 cardiac muscle cell contraction
 GO:0033872 2 [heparan sulfate]-glucosamine 3-sulfotransferase 3 activity
 GO:0033135 2 regulation of peptidyl-serine phosphorylation
 GO:0050867 2 positive regulation of cell activation
 GO:0042418 2 epinephrine biosynthetic process
 GO:0015888 2 thiamine transport
 GO:0015882 2 L-ascorbic acid transport
 GO:0048549 2 positive regulation of pinocytosis
 GO:0060139 2 positive regulation of apoptotic process by virus
 GO:0060133 2 somatotropin secreting cell development
 GO:0002322 2 B cell proliferation involved in immune response
 GO:0018342 2 protein prenylation
 GO:0008476 2 protein-tyrosine sulfotransferase activity
 GO:0032937 2 SREBP-SCAP-Insig complex
 GO:0032422 2 purine-rich negative regulatory element binding
 GO:0032429 2 regulation of phospholipase A2 activity
 GO:0003218 2 cardiac left ventricle formation
 GO:0019346 2 transsulfuration
 GO:0017055 2 negative regulation of RNA polymerase II transcriptional preinitiation
 complex assembly
 GO:0031652 2 positive regulation of heat generation
 GO:0034140 2 negative regulation of toll-like receptor 3 signaling pathway
 GO:0034499 2 late endosome to Golgi transport
 GO:0030862 2 positive regulation of polarized epithelial cell differentiation
 GO:0034727 2 piecemeal microautophagy of nucleus
 GO:0006481 2 C-terminal protein methylation
 GO:0046602 2 regulation of mitotic centrosome separation
 GO:0030395 2 lactose binding
 GO:0002133 2 polycystin complex
 GO:2001212 2 regulation of vasculogenesis
 GO:0032493 2 response to bacterial lipoprotein
 GO:0036396 2 MIS complex
 GO:0097296 2 activation of cysteine-type endopeptidase activity involved in apoptotic
 signaling pathway
 GO:0004478 2 methionine adenosyltransferase activity
 GO:0004473 2 malate dehydrogenase (decarboxylating) (NADP+) activity
 GO:0046884 2 follicle-stimulating hormone secretion
 GO:0046885 2 regulation of hormone biosynthetic process
 GO:0008969 2 phosphohistidine phosphatase activity
 GO:0018283 2 iron incorporation into metallo-sulfur cluster
 GO:0044210 2 'de novo' CTP biosynthetic process
 GO:0004651 2 polynucleotide 5'-phosphatase activity
 GO:0098506 2 polynucleotide 3' dephosphorylation
 GO:0098507 2 polynucleotide 5' dephosphorylation
 GO:0090241 2 negative regulation of histone H4 acetylation
 GO:0016684 2 oxidoreductase activity, acting on peroxide as acceptor
 GO:0090240 2 positive regulation of histone H4 acetylation
 GO:0021937 2 cerebellar Purkinje cell-granule cell precursor cell signaling involved in
 regulation of granule cell precursor cell proliferation
 GO:0044354 2 macropinosome
 GO:0072054 2 renal outer medulla development
 GO:0019087 2 transformation of host cell by virus
 GO:0032090 2 Pyrin domain binding
 GO:0046851 2 negative regulation of bone remodeling
 GO:0070168 2 negative regulation of biomineral tissue development
 GO:0070165 2 positive regulation of adiponectin secretion
 GO:0002481 2 antigen processing and presentation of exogenous protein antigen via MHC

class Ib, TAP-dependent

G0:0007352 2 zygotic specification of dorsal/ventral axis

G0:0007356 2 thorax and anterior abdomen determination

G0:0007354 2 zygotic determination of anterior/posterior axis, embryo

G0:0071344 2 diphosphate metabolic process

G0:0001976 2 neurological system process involved in regulation of systemic arterial blood pressure

G0:2000309 2 positive regulation of tumor necrosis factor (ligand) superfamily member 11 production

G0:2000653 2 regulation of genetic imprinting

G0:2000300 2 regulation of synaptic vesicle exocytosis

G0:0033274 2 response to vitamin B2

G0:0035607 2 fibroblast growth factor receptor signaling pathway involved in orbitofrontal cortex development

G0:0061462 2 protein localization to lysosome

G0:0014733 2 regulation of skeletal muscle adaptation

G0:0046475 2 glycerophospholipid catabolic process

G0:0045923 2 positive regulation of fatty acid metabolic process

G0:0045920 2 negative regulation of exocytosis

G0:0043183 2 vascular endothelial growth factor receptor 1 binding

G0:0009822 2 alkaloid catabolic process

G0:0009820 2 alkaloid metabolic process

G0:0008355 2 olfactory learning

G0:0097286 2 iron ion import

G0:0031729 2 CCR4 chemokine receptor binding

G0:0031720 2 haptoglobin binding

G0:0060488 2 orthogonal dichotomous subdivision of terminal units involved in lung branching morphogenesis

G0:0060489 2 planar dichotomous subdivision of terminal units involved in lung branching morphogenesis

G0:0090259 2 regulation of retinal ganglion cell axon guidance

G0:0050610 2 methylarsonate reductase activity

G0:0046294 2 formaldehyde catabolic process

G0:0005688 2 U6 snRNP

G0:0005684 2 U2-type spliceosomal complex

G0:0060152 2 microtubule-based peroxisome localization

G0:0005462 2 UDP-N-acetylglucosamine transmembrane transporter activity

G0:0048298 2 positive regulation of isotype switching to IgA isotypes

G0:0051055 2 negative regulation of lipid biosynthetic process

G0:0051053 2 negative regulation of DNA metabolic process

G0:0051051 2 negative regulation of transport

G0:0010133 2 proline catabolic process to glutamate

G0:0050262 2 ribosylnicotinamide kinase activity

G0:2001023 2 regulation of response to drug

G0:2001027 2 negative regulation of endothelial cell chemotaxis

G0:0042942 2 D-serine transport

G0:0005135 2 interleukin-3 receptor binding

G0:0070080 2 titin Z domain binding

G0:0003231 2 cardiac ventricle development

G0:0035985 2 senescence-associated heterochromatin focus

G0:0019413 2 acetate biosynthetic process

G0:0019417 2 sulfur oxidation

G0:0016492 2 G-protein coupled neurotensin receptor activity

G0:0032401 2 establishment of melanosome localization

G0:0001838 2 embryonic epithelial tube formation

G0:0071930 2 negative regulation of transcription involved in G1/S transition of mitotic cell cycle

G0:0071931 2 positive regulation of transcription involved in G1/S transition of mitotic cell cycle

G0:0021678 2 third ventricle development

G0:0015111 2 iodide transmembrane transporter activity

G0:0002540 2 leukotriene production involved in inflammatory response

G0:0002543 2 activation of blood coagulation via clotting cascade

G0:0002542 2 Factor XII activation

G0:0046592 2 polyamine oxidase activity

G0:0071621 2 granulocyte chemotaxis

G0:0071624 2 positive regulation of granulocyte chemotaxis

G0:0046629 2 gamma-delta T cell activation

G0:0001162 2 RNA polymerase II intronic transcription regulatory region sequence-specific DNA binding

G0:0046625 2 sphingolipid binding

G0:0070409 2 carbamoyl phosphate biosynthetic process

G0:0038039 2 G-protein coupled receptor heterodimeric complex

G0:0030112 2 glycocalyx

G0:0035470 2 positive regulation of vascular wound healing

G0:0061144	2	alveolar secondary septum development
G0:0004776	2	succinate-CoA ligase (GDP-forming) activity
G0:0005093	2	Rab GDP-dissociation inhibitor activity
G0:0045029	2	UDP-activated nucleotide receptor activity
G0:0045026	2	plasma membrane fusion
G0:0045023	2	G0 to G1 transition
G0:0004360	2	glutamine-fructose-6-phosphate transaminase (isomerizing) activity
G0:0004416	2	hydroxyacylglutathione hydrolase activity
G0:0006678	2	glucosylceramide metabolic process
G0:0008940	2	nitrate reductase activity
G0:0005324	2	long-chain fatty acid transporter activity
G0:0042628	2	mating plug formation
G0:0097136	2	Bcl-2 family protein complex
G0:0005724	2	nuclear telomeric heterochromatin
G0:0072676	2	lymphocyte migration
G0:0019062	2	virion attachment to host cell
G0:0070535	2	histone H2A K63-linked ubiquitination
G0:0046836	2	glycolipid transport
G0:0046831	2	regulation of RNA export from nucleus
G0:0046833	2	positive regulation of RNA export from nucleus
G0:0046832	2	negative regulation of RNA export from nucleus
G0:0046839	2	phospholipid dephosphorylation
G0:2000676	2	positive regulation of type B pancreatic cell apoptotic process
G0:2000672	2	negative regulation of motor neuron apoptotic process
G0:2000670	2	positive regulation of dendritic cell apoptotic process
G0:0006788	2	heme oxidation
G0:0033883	2	pyridoxal phosphatase activity
G0:1901898	2	negative regulation of relaxation of cardiac muscle
G0:0038109	2	Kit signaling pathway
G0:0072178	2	nephric duct morphogenesis
G0:0061448	2	connective tissue development
G0:0042020	2	interleukin-23 receptor activity
G0:0006313	2	transposition, DNA-mediated
G0:0043217	2	myelin maintenance
G0:0046459	2	short-chain fatty acid metabolic process
G0:0045905	2	positive regulation of translational termination
G0:0052834	2	inositol monophosphate phosphatase activity
G0:1903016	2	negative regulation of exo-alpha-sialidase activity
G0:0031749	2	D2 dopamine receptor binding
G0:0052833	2	inositol monophosphate 4-phosphatase activity
G0:0010872	2	regulation of cholesterol esterification
G0:0010874	2	regulation of cholesterol efflux
G0:0006403	2	RNA localization
G0:0060342	2	photoreceptor inner segment membrane
G0:0060178	2	regulation of exocyst localization
G0:0009378	2	four-way junction helicase activity
G0:0060171	2	stereocilium membrane
G0:0043146	2	spindle stabilization
G0:0002369	2	T cell cytokine production
G0:0071751	2	secretory IgA immunoglobulin complex
G0:0071756	2	pentameric IgM immunoglobulin complex
G0:0071757	2	hexameric IgM immunoglobulin complex
G0:0004756	2	selenide, water dikinase activity
G0:0004370	2	glycerol kinase activity
G0:0004372	2	glycine hydroxymethyltransferase activity
G0:0014718	2	positive regulation of satellite cell activation involved in skeletal muscle regeneration
G0:0033278	2	cell proliferation in midbrain
G0:0046717	2	acid secretion
G0:0072606	2	interleukin-8 secretion
G0:0000430	2	regulation of transcription from RNA polymerase II promoter by glucose
G0:0045684	2	positive regulation of epidermis development
G0:0070557	2	PCNA-p21 complex
G0:2000538	2	positive regulation of B cell chemotaxis
G0:0034455	2	t-UTP complex
G0:0021610	2	facial nerve morphogenesis
G0:0030825	2	positive regulation of cGMP metabolic process
G0:0030822	2	positive regulation of cAMP catabolic process
G0:0030821	2	negative regulation of cAMP catabolic process
G0:0010519	2	negative regulation of phospholipase activity
G0:0033157	2	regulation of intracellular protein transport
G0:0046022	2	positive regulation of transcription from RNA polymerase II promoter during mitosis
G0:0051718	2	DNA (cytosine-5-)-methyltransferase activity, acting on CpG substrates
G0:0075732	2	viral penetration into host nucleus

G0:0071600	2	otic vesicle morphogenesis
G0:0060738	2	epithelial-mesenchymal signaling involved in prostate gland development
G0:0035279	2	mRNA cleavage involved in gene silencing by miRNA
G0:1902560	2	GMP reductase complex
G0:0001507	2	acetylcholine catabolic process in synaptic cleft
G0:0035419	2	activation of MAPK activity involved in innate immune response
G0:0048312	2	intracellular distribution of mitochondria
G0:0048319	2	axial mesoderm morphogenesis
G0:0004923	2	leukemia inhibitory factor receptor activity
G0:0031085	2	BL0C-3 complex
G0:0004430	2	1-phosphatidylinositol 4-kinase activity
G0:0072384	2	organelle transport along microtubule
G0:0031223	2	auditory behavior
G0:0090042	2	tubulin deacetylation
G0:0021508	2	floor plate formation
G0:0010070	2	zygote asymmetric cell division
G0:0060595	2	fibroblast growth factor receptor signaling pathway involved in mammary gland specification
G0:0008545	2	JUN kinase kinase activity
G0:0019046	2	release from viral latency
G0:0019043	2	establishment of viral latency
G0:0019049	2	evasion or tolerance of host defenses by virus
G0:0060976	2	coronary vasculature development
G0:0060977	2	coronary vasculature morphogenesis
G0:0032856	2	activation of Ras GTPase activity
G0:1901253	2	negative regulation of intracellular transport of viral material
G0:0021869	2	forebrain ventricular zone progenitor cell division
G0:0032143	2	single thymine insertion binding
G0:0038162	2	erythropoietin-mediated signaling pathway
G0:0047522	2	15-oxoprostaglandin 13-oxidase activity
G0:0080019	2	fatty-acyl-CoA reductase (alcohol-forming) activity
G0:0043686	2	co-translational protein modification
G0:1990077	2	primosome complex
G0:0003160	2	endocardium morphogenesis
G0:0003169	2	coronary vein morphogenesis
G0:0034669	2	integrin alpha4-beta7 complex
G0:0019858	2	cytosine metabolic process
G0:0006196	2	AMP catabolic process
G0:0034665	2	integrin alpha1-beta1 complex
G0:0034667	2	integrin alpha3-beta1 complex
G0:0060490	2	lateral sprouting involved in lung morphogenesis
G0:0061312	2	BMP signaling pathway involved in heart development
G0:0061317	2	canonical Wnt signaling pathway involved in cardiac muscle cell fate commitment
G0:0031943	2	regulation of glucocorticoid metabolic process
G0:0031766	2	type 3 galanin receptor binding
G0:0060370	2	susceptibility to T cell mediated cytotoxicity
G0:0015820	2	leucine transport
G0:0004152	2	dihydroorotate dehydrogenase activity
G0:0097421	2	liver regeneration
G0:0097427	2	microtubule bundle
G0:0045964	2	positive regulation of dopamine metabolic process
G0:0045963	2	negative regulation of dopamine metabolic process
G0:0006738	2	nicotinamide riboside catabolic process
G0:0005035	2	death receptor activity
G0:0030540	2	female genitalia development
G0:0060368	2	regulation of Fc receptor mediated stimulatory signaling pathway
G0:0015207	2	adenine transmembrane transporter activity
G0:0008043	2	intracellular ferritin complex
G0:0000064	2	L-ornithine transmembrane transporter activity
G0:0042780	2	tRNA 3'-end processing
G0:0004771	2	sterol esterase activity
G0:0004772	2	sterol O-acyltransferase activity
G0:0052548	2	regulation of endopeptidase activity
G0:0008594	2	photoreceptor cell morphogenesis
G0:0003904	2	deoxyribodipyrimidine photo-lyase activity
G0:0008260	2	3-oxoacid CoA-transferase activity
G0:0071633	2	dihydroceramidase activity
G0:0005026	2	transforming growth factor beta receptor activity, type II
G0:0033314	2	mitotic DNA replication checkpoint
G0:2000552	2	negative regulation of T-helper 2 cell cytokine production
G0:2000553	2	positive regulation of T-helper 2 cell cytokine production
G0:0031627	2	telomeric loop formation
G0:0021633	2	optic nerve structural organization
G0:0021636	2	trigeminal nerve morphogenesis

G0:0002507	2	tolerance induction
G0:0035261	2	external genitalia morphogenesis
G0:0015014	2	heparan sulfate proteoglycan biosynthetic process, polysaccharide chain biosynthetic process
G0:0001855	2	complement component C4b binding
G0:0003140	2	determination of left/right asymmetry in lateral mesoderm
G0:0060297	2	regulation of sarcomere organization
G0:0007100	2	mitotic centrosome separation
G0:0006556	2	S-adenosylmethionine biosynthetic process
G0:0050968	2	detection of chemical stimulus involved in sensory perception of pain
G0:0035250	2	UDP-galactosyltransferase activity
G0:0035256	2	G-protein coupled glutamate receptor binding
G0:0006421	2	asparaginyl-tRNA aminoacylation
G0:0033173	2	calcineurin-NFAT signaling cascade
G0:0030156	2	benzodiazepine receptor binding
G0:0061104	2	adrenal chromaffin cell differentiation
G0:0042271	2	susceptibility to natural killer cell mediated cytotoxicity
G0:0048332	2	mesoderm morphogenesis
G0:0004909	2	interleukin-1, Type I, activating receptor activity
G0:0004906	2	interferon-gamma receptor activity
G0:0004905	2	type I interferon receptor activity
G0:0072368	2	regulation of lipid transport by negative regulation of transcription from RNA polymerase II promoter
G0:0072369	2	regulation of lipid transport by positive regulation of transcription from RNA polymerase II promoter
G0:2001274	2	negative regulation of glucose import in response to insulin stimulus
G0:0001640	2	adenylate cyclase inhibiting G-protein coupled glutamate receptor activity
G0:0031208	2	POZ domain binding
G0:0090024	2	negative regulation of neutrophil chemotaxis
G0:0008607	2	phosphorylase kinase regulator activity
G0:0046898	2	response to cycloheximide
G0:0044339	2	canonical Wnt signaling pathway involved in osteoblast differentiation
G0:0009059	2	macromolecule biosynthetic process
G0:0051170	2	nuclear import
G0:0044334	2	canonical Wnt signaling pathway involved in positive regulation of epithelial to mesenchymal transition
G0:0044335	2	canonical Wnt signaling pathway involved in neural crest cell differentiation
G0:0044337	2	canonical Wnt signaling pathway involved in positive regulation of apoptotic process
G0:0050567	2	glutamyl-tRNA synthase (glutamine-hydrolyzing) activity
G0:0035407	2	histone H3-T11 phosphorylation
G0:0035402	2	histone kinase activity (H3-T11 specific)
G0:0004019	2	adenylosuccinate synthase activity
G0:0060312	2	regulation of blood vessel remodeling
G0:0051284	2	positive regulation of sequestering of calcium ion
G0:0007290	2	spermatid nucleus elongation
G0:0007296	2	vitellogenesis
G0:0060319	2	primitive erythrocyte differentiation
G0:0032783	2	ELL-EAF complex
G0:0032785	2	negative regulation of DNA-templated transcription, elongation
G0:0032787	2	monocarboxylic acid metabolic process
G0:0001991	2	regulation of systemic arterial blood pressure by circulatory renin-angiotensin
G0:0043649	2	dicarboxylic acid catabolic process
G0:0021849	2	neuroblast division in subventricular zone
G0:0038145	2	macrophage colony-stimulating factor signaling pathway
G0:0055105	2	ubiquitin-protein transferase inhibitor activity
G0:0070101	2	positive regulation of chemokine-mediated signaling pathway
G0:0070104	2	negative regulation of interleukin-6-mediated signaling pathway
G0:0070106	2	interleukin-27-mediated signaling pathway
G0:0030956	2	glutamyl-tRNA(Gln) amidotransferase complex
G0:1901984	2	negative regulation of protein acetylation
G0:0033686	2	positive regulation of luteinizing hormone secretion
G0:0035989	2	tendon development
G0:0034315	2	regulation of Arp2/3 complex-mediated actin nucleation
G0:0034316	2	negative regulation of Arp2/3 complex-mediated actin nucleation
G0:0034648	2	histone demethylase activity (H3-dimethyl-K4 specific)
G0:0003863	2	3-methyl-2-oxobutanoate dehydrogenase (2-methylpropanoyl-transferring) activity
G0:0097228	2	sperm principal piece
G0:0060352	2	cell adhesion molecule production
G0:0015222	2	serotonin transmembrane transporter activity
G0:0005999	2	xylulose biosynthetic process
G0:0005997	2	xylulose metabolic process

G0:0051904	2	pigment granule transport
G0:0009331	2	glycerol-3-phosphate dehydrogenase complex
G0:0007509	2	mesoderm migration involved in gastrulation
G0:0036273	2	response to statin
G0:0042976	2	activation of Janus kinase activity
G0:0004427	2	inorganic diphosphatase activity
G0:0004572	2	mannosyl-oligosaccharide 1,3-1,6-alpha-mannosidase activity
G0:0052901	2	spermine:oxygen oxidoreductase (spermidine-forming) activity
G0:0008065	2	establishment of blood-nerve barrier
G0:0048101	2	calcium- and calmodulin-regulated 3',5'-cyclic-GMP phosphodiesterase activity
G0:0048105	2	establishment of body hair planar orientation
G0:0043813	2	phosphatidylinositol-3,5-bisphosphate 5-phosphatase activity
G0:0014034	2	neural crest cell fate commitment
G0:0072190	2	ureter urothelium development
G0:0035986	2	senescence-associated heterochromatin focus assembly
G0:0003920	2	GMP reductase activity
G0:0003290	2	atrial septum secundum morphogenesis
G0:0004791	2	thioredoxin-disulfide reductase activity
G0:0070873	2	regulation of glycogen metabolic process
G0:0000472	2	endonucleolytic cleavage to generate mature 5'-end of SSU-rRNA from (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
G0:0070593	2	dendrite self-avoidance
G0:0051349	2	positive regulation of lyase activity
G0:0051348	2	negative regulation of transferase activity
G0:0015252	2	hydrogen ion channel activity
G0:0071920	2	cleavage body
G0:0002522	2	leukocyte migration involved in immune response
G0:0002520	2	immune system development
G0:0015788	2	UDP-N-acetylglucosamine transport
G0:0071460	2	cellular response to cell-matrix adhesion
G0:0001872	2	(1->3)-beta-D-glucan binding
G0:0070435	2	Shc-EGFR complex
G0:0034418	2	urate biosynthetic process
G0:2000570	2	positive regulation of T-helper 2 cell activation
G0:0045155	2	electron transporter, transferring electrons from CoQH2-cytochrome c reductase complex and cytochrome c oxidase complex activity
G0:0061290	2	canonical Wnt signaling pathway involved in metanephric kidney development
G0:0032093	2	SAM domain binding
G0:0002082	2	regulation of oxidative phosphorylation
G0:0017129	2	triglyceride binding
G0:0002086	2	diaphragm contraction
G0:0017123	2	Ral GTPase activator activity
G0:0072208	2	metanephric smooth muscle tissue development
G0:0072203	2	cell proliferation involved in metanephros development
G0:0043067	2	regulation of programmed cell death
G0:0045082	2	positive regulation of interleukin-10 biosynthetic process
G0:0004968	2	gonadotropin-releasing hormone receptor activity
G0:0004962	2	endothelin receptor activity
G0:0050992	2	dimethylallyl diphosphate biosynthetic process
G0:0050994	2	regulation of lipid catabolic process
G0:0005329	2	dopamine transmembrane transporter activity
G0:0031595	2	nuclear proteasome complex
G0:0009295	2	nucleoid
G0:0002060	2	purine nucleobase binding
G0:0050509	2	N-acetylglucosaminyl-proteoglycan 4-beta-glucuronosyltransferase activity
G0:0010032	2	meiotic chromosome condensation
G0:0018205	2	peptidyl-lysine modification
G0:0004031	2	aldehyde oxidase activity
G0:0001607	2	neuromedin U receptor activity
G0:0032764	2	negative regulation of mast cell cytokine production
G0:0032765	2	positive regulation of mast cell cytokine production
G0:0071873	2	response to norepinephrine
G0:0071871	2	response to epinephrine
G0:0071879	2	positive regulation of adrenergic receptor signaling pathway
G0:0070698	2	type I activin receptor binding
G0:0019002	2	GMP binding
G0:0019008	2	molybdopterin synthase complex
G0:0050756	2	fractalkine metabolic process
G0:0045509	2	interleukin-27 receptor activity
G0:0016062	2	adaptation of rhodopsin mediated signaling
G0:0000806	2	Y chromosome
G0:0000802	2	transverse filament
G0:0070473	2	negative regulation of uterine smooth muscle contraction
G0:0003127	2	detection of nodal flow

G0:0034378	2	chylomicron assembly
G0:0090086	2	negative regulation of protein deubiquitination
G0:0034625	2	fatty acid elongation, monounsaturated fatty acid
G0:0034626	2	fatty acid elongation, polyunsaturated fatty acid
G0:0005760	2	gamma DNA polymerase complex
G0:0015866	2	ADP transport
G0:0050694	2	galactose 3-O-sulfotransferase activity
G0:0010817	2	regulation of hormone levels
G0:0005602	2	complement component C1 complex
G0:0005608	2	laminin-3 complex
G0:0035578	2	azurophil granule lumen
G0:0002381	2	immunoglobulin production involved in immunoglobulin mediated immune response
G0:0046527	2	glucosyltransferase activity
G0:0071748	2	monomeric IgA immunoglobulin complex
G0:0045728	2	respiratory burst after phagocytosis
G0:1902306	2	negative regulation of sodium ion transmembrane transport
G0:0004557	2	alpha-galactosidase activity
G0:0000022	2	mitotic spindle elongation
G0:0004738	2	pyruvate dehydrogenase activity
G0:0014015	2	positive regulation of gliogenesis
G0:0014010	2	Schwann cell proliferation
G0:0004658	2	propionyl-CoA carboxylase activity
G0:0004365	2	glyceraldehyde-3-phosphate dehydrogenase (NAD+) (phosphorylating) activity
G0:0045337	2	farnesyl diphosphate biosynthetic process
G0:0070840	2	dynein complex binding
G0:0004817	2	cysteine-tRNA ligase activity
G0:0004816	2	asparagine-tRNA ligase activity
G0:0004368	2	glycerol-3-phosphate dehydrogenase activity
G0:0014908	2	myotube differentiation involved in skeletal muscle regeneration
G0:0019948	2	SUMO activating enzyme activity
G0:0019767	2	IgE receptor activity
G0:0015056	2	corticotrophin-releasing factor receptor activity
G0:0071400	2	cellular response to oleic acid
G0:0001812	2	positive regulation of type I hypersensitivity
G0:2000779	2	regulation of double-strand break repair
G0:2000777	2	positive regulation of proteasomal ubiquitin-dependent protein catabolic process involved in cellular response to hypoxia
G0:0015747	2	urate transport
G0:0032596	2	protein transport into membrane raft
G0:0034437	2	glycoprotein transporter activity
G0:0035747	2	natural killer cell chemotaxis
G0:0046967	2	cytosol to ER transport
G0:0042180	2	cellular ketone metabolic process
G0:0016509	2	long-chain-3-hydroxyacyl-CoA dehydrogenase activity
G0:0016507	2	mitochondrial fatty acid beta-oxidation multienzyme complex
G0:0046511	2	sphinganine biosynthetic process
G0:2001140	2	positive regulation of phospholipid transport
G0:0017109	2	glutamate-cysteine ligase complex
G0:0014904	2	myotube cell development
G0:0006540	2	glutamate decarboxylation to succinate
G0:0006542	2	glutamine biosynthetic process
G0:0001519	2	peptide amidation
G0:0031010	2	ISWI-type complex
G0:0004947	2	bradykinin receptor activity
G0:0004944	2	C5a anaphylatoxin receptor activity
G0:0004942	2	anaphylatoxin receptor activity
G0:0060091	2	kinocilium
G0:0039003	2	pronephric field specification
G0:0030197	2	extracellular matrix constituent, lubricant activity
G0:0031247	2	actin rod assembly
G0:2000981	2	negative regulation of inner ear receptor cell differentiation
G0:0060049	2	regulation of protein glycosylation
G0:0005011	2	macrophage colony-stimulating factor receptor activity
G0:0048378	2	regulation of lateral mesodermal cell fate specification
G0:0005019	2	platelet-derived growth factor beta-receptor activity
G0:0044805	2	late nucleophagy
G0:0072233	2	metanephric thick ascending limb development
G0:0004053	2	arginase activity
G0:1902445	2	regulation of mitochondrial membrane permeability involved in programmed necrotic cell death
G0:0001665	2	alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase activity
G0:0097025	2	MPP7-DLG1-LIN7 complex
G0:0043368	2	positive T cell selection
G0:0032290	2	peripheral nervous system myelin formation

G0:0032298	2	positive regulation of DNA-dependent DNA replication initiation
G0:0070671	2	response to interleukin-12
G0:0019682	2	glyceraldehyde-3-phosphate metabolic process
G0:0070417	2	cellular response to cold
G0:0071233	2	cellular response to leucine
G0:1900016	2	negative regulation of cytokine production involved in inflammatory response
G0:0060849	2	regulation of transcription involved in lymphatic endothelial cell fate commitment
G0:0015842	2	synaptic vesicle amine transport
G0:0015847	2	putrescine transport
G0:0046724	2	oxalic acid secretion
G0:0010810	2	regulation of cell-substrate adhesion
G0:0004146	2	dihydrofolate reductase activity
G0:0042030	2	ATPase inhibitor activity
G0:1990226	2	histone methyltransferase binding
G0:0030070	2	insulin processing
G0:0035552	2	oxidative single-stranded DNA demethylation
G0:0035553	2	oxidative single-stranded RNA demethylation
G0:0004060	2	arylamine N-acetyltransferase activity
G0:0060466	2	activation of meiosis involved in egg activation
G0:0060465	2	pharynx development
G0:0060460	2	left lung morphogenesis
G0:0044240	2	multicellular organismal lipid catabolic process
G0:0043205	2	fibril
G0:0048499	2	synaptic vesicle membrane organization
G0:0004531	2	deoxyribonuclease II activity
G0:0006020	2	inositol metabolic process
G0:0006021	2	inositol biosynthetic process
G0:0048635	2	negative regulation of muscle organ development
G0:0060282	2	positive regulation of oocyte development
G0:0008280	2	cohesin core heterodimer
G0:0008281	2	sulfonylurea receptor activity
G0:0042891	2	antibiotic transport
G0:0042895	2	antibiotic transporter activity
G0:0047196	2	long-chain-alcohol O-fatty-acyltransferase activity
G0:0002876	2	positive regulation of chronic inflammatory response to antigenic stimulus
G0:0002879	2	positive regulation of acute inflammatory response to non-antigenic stimulus
G0:0051303	2	establishment of chromosome localization
G0:0032350	2	regulation of hormone metabolic process
G0:0070085	2	glycosylation
G0:0070084	2	protein initiator methionine removal
G0:0001834	2	trophectodermal cell proliferation
G0:0060915	2	mesenchymal cell differentiation involved in lung development
G0:0034679	2	integrin alpha9-beta1 complex
G0:2000757	2	negative regulation of peptidyl-lysine acetylation
G0:0038043	2	interleukin-5-mediated signaling pathway
G0:0052654	2	L-leucine transaminase activity
G0:0052655	2	L-valine transaminase activity
G0:0052656	2	L-isoleucine transaminase activity
G0:0052650	2	NADP-retinol dehydrogenase activity
G0:0016743	2	carboxyl- or carbamoyltransferase activity
G0:0021692	2	cerebellar Purkinje cell layer morphogenesis
G0:0016295	2	myristoyl-[acyl-carrier-protein] hydrolase activity
G0:0016296	2	palmitoyl-[acyl-carrier-protein] hydrolase activity
G0:0016297	2	acyl-[acyl-carrier-protein] hydrolase activity
G0:0021885	2	forebrain cell migration
G0:0086100	2	endothelin receptor signaling pathway
G0:0006560	2	proline metabolic process
G0:0072249	2	metanephric glomerular visceral epithelial cell development
G0:0060073	2	micturition
G0:0046395	2	carboxylic acid catabolic process
G0:0097546	2	ciliary base
G0:0035494	2	SNARE complex disassembly
G0:0060615	2	mammary gland bud formation
G0:0009258	2	10-formyltetrahydrofolate catabolic process
G0:0009259	2	ribonucleotide metabolic process
G0:0097091	2	synaptic vesicle clustering
G0:0048820	2	hair follicle maturation
G0:0002023	2	reduction of food intake in response to dietary excess
G0:0035947	2	regulation of gluconeogenesis by regulation of transcription from RNA polymerase II promoter
G0:0035411	2	catenin import into nucleus
G0:0000171	2	ribonuclease MRP activity

G0:0001641	2	group II metabotropic glutamate receptor activity
G0:0046890	2	regulation of lipid biosynthetic process
G0:0046899	2	nucleoside triphosphate adenylate kinase activity
G0:0034241	2	positive regulation of macrophage fusion
G0:0032613	2	interleukin-10 production
G0:0017143	2	insecticide metabolic process
G0:0003868	2	4-hydroxyphenylpyruvate dioxygenase activity
G0:0008615	2	pyridoxine biosynthetic process
G0:0003865	2	3-oxo-5-alpha-steroid 4-dehydrogenase activity
G0:0045277	2	respiratory chain complex IV
G0:0004074	2	biliverdin reductase activity
G0:0070436	2	Grb2-EGFR complex
G0:0097411	2	hypoxia-inducible factor-1alpha signaling pathway
G0:2000253	2	positive regulation of feeding behavior
G0:0017077	2	oxidative phosphorylation uncoupler activity
G0:0070831	2	basement membrane assembly
G0:0010430	2	fatty acid omega-oxidation
G0:0002689	2	negative regulation of leukocyte chemotaxis
G0:0005850	2	eukaryotic translation initiation factor 2 complex
G0:0009304	2	tRNA transcription
G0:0046931	2	pore complex assembly
G0:0046709	2	IDP catabolic process
G0:0048681	2	negative regulation of axon regeneration
G0:0072160	2	nephron tubule epithelial cell differentiation
G0:0035026	2	leading edge cell differentiation
G0:0030011	2	maintenance of cell polarity
G0:0035539	2	8-oxo-7,8-dihydrodeoxyguanosine triphosphate pyrophosphatase activity
G0:0060449	2	bud elongation involved in lung branching
G0:0043366	2	beta selection
G0:0004920	2	interleukin-10 receptor activity
G0:0000354	2	cis assembly of pre-catalytic spliceosome
G0:0004510	2	tryptophan 5-monooxygenase activity
G0:0004514	2	nicotinate-nucleotide diphosphorylase (carboxylating) activity
G0:0006001	2	fructose catabolic process
G0:0014053	2	negative regulation of gamma-aminobutyric acid secretion
G0:0014056	2	regulation of acetylcholine secretion, neurotransmission
G0:0014057	2	positive regulation of acetylcholine secretion, neurotransmission
G0:0042701	2	progesterone secretion
G0:0030576	2	Cajal body organization
G0:0031630	2	regulation of synaptic vesicle fusion to presynaptic membrane
G0:2000483	2	negative regulation of interleukin-8 secretion
G0:0072166	2	posterior mesonephric tubule development
G0:0039530	2	MDA-5 signaling pathway
G0:0039536	2	negative regulation of RIG-I signaling pathway
G0:0039534	2	negative regulation of MDA-5 signaling pathway
G0:0039535	2	regulation of RIG-I signaling pathway
G0:0001588	2	dopamine neurotransmitter receptor activity, coupled via Gs
G0:0001582	2	detection of chemical stimulus involved in sensory perception of sweet taste
G0:0007518	2	myoblast fate determination
G0:0003989	2	acetyl-CoA carboxylase activity
G0:0003986	2	acetyl-CoA hydrolase activity
G0:0003987	2	acetate-CoA ligase activity
G0:0003980	2	UDP-glucose:glycoprotein glucosyltransferase activity
G0:0002588	2	positive regulation of antigen processing and presentation of peptide antigen via MHC class II
G0:0002587	2	negative regulation of antigen processing and presentation of peptide antigen via MHC class II
G0:0038063	2	collagen-activated tyrosine kinase receptor signaling pathway
G0:0038062	2	protein tyrosine kinase collagen receptor activity
G0:0038065	2	collagen-activated signaling pathway
G0:0038064	2	collagen receptor activity
G0:0003329	2	pancreatic PP cell fate commitment
G0:0035854	2	eosinophil fate commitment
G0:0042148	2	strand invasion
G0:0043555	2	regulation of translation in response to stress
G0:0003064	2	regulation of heart rate by hormone
G0:0043558	2	regulation of translational initiation in response to stress
G0:1901028	2	regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway
G0:0033842	2	N-acetyl-beta-glucosaminyl-glycoprotein 4-beta-N-acetylgalactosaminyltransferase activity
G0:1900224	2	positive regulation of nodal signaling pathway involved in determination of lateral mesoderm left/right asymmetry
G0:1900221	2	regulation of beta-amyloid clearance

G0:1900229	2	negative regulation of single-species biofilm formation in or on host organism
G0:0031022	2	nuclear migration along microfilament
G0:0060053	2	neurofilament cytoskeleton
G0:0060050	2	positive regulation of protein glycosylation
G0:0070358	2	actin polymerization-dependent cell motility
G0:0019551	2	glutamate catabolic process to 2-oxoglutarate
G0:0097035	2	regulation of membrane lipid distribution
G0:0061188	2	negative regulation of chromatin silencing at rDNA
G0:0046386	2	deoxyribose phosphate catabolic process
G0:0031282	2	regulation of guanylate cyclase activity
G0:0060633	2	negative regulation of transcription initiation from RNA polymerase II promoter
G0:0003858	2	3-hydroxybutyrate dehydrogenase activity
G0:0005055	2	laminin receptor activity
G0:0005052	2	peroxisome matrix targeting signal-1 binding
G0:0048840	2	otolith development
G0:0010727	2	negative regulation of hydrogen peroxide metabolic process
G0:0060718	2	chorionic trophoblast cell differentiation
G0:0071409	2	cellular response to cycloheximide
G0:0003326	2	pancreatic A cell fate commitment
G0:0072305	2	negative regulation of mesenchymal cell apoptotic process involved in metanephric nephron morphogenesis
G0:0002302	2	CD8-positive, alpha-beta T cell differentiation involved in immune response
G0:0031691	2	alpha-1A adrenergic receptor binding
G0:0090362	2	positive regulation of platelet-derived growth factor production
G0:0060715	2	syncytiotrophoblast cell differentiation involved in labyrinthine layer development
G0:0006837	2	serotonin transport
G0:0019531	2	oxalate transmembrane transporter activity
G0:0019532	2	oxalate transport
G0:0045252	2	oxoglutarate dehydrogenase complex
G0:0072308	2	negative regulation of metanephric nephron tubule epithelial cell differentiation
G0:2000491	2	positive regulation of hepatic stellate cell activation
G0:0016149	2	translation release factor activity, codon specific
G0:0070188	2	Stn1-Ten1 complex
G0:0032707	2	negative regulation of interleukin-23 production
G0:2000272	2	negative regulation of receptor activity
G0:2000276	2	negative regulation of oxidative phosphorylation uncoupler activity
G0:0090260	2	negative regulation of retinal ganglion cell axon guidance
G0:0051538	2	3 iron, 4 sulfur cluster binding
G0:0052854	2	medium-chain-(S)-2-hydroxy-acid oxidase activity
G0:0016155	2	formyltetrahydrofolate dehydrogenase activity
G0:0052853	2	long-chain-(S)-2-hydroxy-long-chain-acid oxidase activity
G0:0071763	2	nuclear membrane organization
G0:0003419	2	growth plate cartilage chondrocyte proliferation
G0:0044609	2	DBIRD complex
G0:1901631	2	positive regulation of presynaptic membrane organization
G0:0005152	2	interleukin-1 receptor antagonist activity
G0:0035515	2	oxidative RNA demethylation activity
G0:0061047	2	positive regulation of branching involved in lung morphogenesis
G0:0042351	2	'de novo' GDP-L-fucose biosynthetic process
G0:0048769	2	sarcomerogenesis
G0:0009446	2	putrescine biosynthetic process
G0:0000084	2	mitotic S phase
G0:0000080	2	mitotic G1 phase
G0:0046811	2	histone deacetylase inhibitor activity
G0:0004797	2	thymidine kinase activity
G0:0004794	2	L-threonine ammonia-lyase activity
G0:0031344	2	regulation of cell projection organization
G0:0072111	2	cell proliferation involved in kidney development
G0:0045188	2	regulation of circadian sleep/wake cycle, non-REM sleep
G0:0010256	2	endomembrane system organization
G0:0021526	2	medial motor column neuron differentiation
G0:0008525	2	phosphatidylcholine transporter activity
G0:0004827	2	proline-tRNA ligase activity
G0:0010983	2	positive regulation of high-density lipoprotein particle clearance
G0:0004137	2	deoxycytidine kinase activity
G0:0010623	2	developmental programmed cell death
G0:0001562	2	response to protozoan
G0:0072262	2	metanephric glomerular mesangial cell proliferation involved in metanephros development
G0:0071973	2	bacterial-type flagellum-dependent cell motility

G0:0030029	2	actin filament-based process
G0:0003420	2	regulation of growth plate cartilage chondrocyte proliferation
G0:0038001	2	paracrine signaling
G0:0035879	2	plasma membrane lactate transport
G0:0008422	2	beta-glucosidase activity
G0:0035870	2	dITP diphosphatase activity
G0:0000961	2	negative regulation of mitochondrial RNA catabolic process
G0:0019255	2	glucose 1-phosphate metabolic process
G0:0071396	2	cellular response to lipid
G0:0043163	2	cell envelope organization
G0:1900248	2	negative regulation of cytoplasmic translational elongation
G0:1900244	2	positive regulation of synaptic vesicle endocytosis
G0:0035726	2	common myeloid progenitor cell proliferation
G0:0060032	2	notochord regression
G0:0034059	2	response to anoxia
G0:0097059	2	CNTR-CLCF1 complex
G0:0097055	2	agmatine biosynthetic process
G0:0002793	2	positive regulation of peptide secretion
G0:0097050	2	type B pancreatic cell apoptotic process
G0:0097053	2	L-kynurenine catabolic process
G0:0097052	2	L-kynurenine metabolic process
G0:0045053	2	protein retention in Golgi apparatus
G0:0006478	2	peptidyl-tyrosine sulfation
G0:0090083	2	regulation of inclusion body assembly
G0:0035523	2	protein K29-linked deubiquitination
G0:0005072	2	transforming growth factor beta receptor, cytoplasmic mediator activity
G0:2000525	2	positive regulation of T cell costimulation
G0:0048866	2	stem cell fate specification
G0:0061051	2	positive regulation of cell growth involved in cardiac muscle cell development
G0:0042700	2	luteinizing hormone signaling pathway
G0:2001303	2	lipoxin A4 biosynthetic process
G0:0038163	2	thrombopoietin-mediated signaling pathway
G0:0021602	2	cranial nerve morphogenesis
G0:0008160	2	protein tyrosine phosphatase activator activity
G0:0043045	2	DNA methylation involved in embryo development
G0:0004307	2	ethanolaminephosphotransferase activity
G0:0002046	2	opsin binding
G0:0003826	2	alpha-ketoacid dehydrogenase activity
G0:0045236	2	CXCR chemokine receptor binding
G0:2000473	2	positive regulation of hematopoietic stem cell migration
G0:2000474	2	regulation of opioid receptor signaling pathway
G0:0045585	2	positive regulation of cytotoxic T cell differentiation
G0:0051081	2	nuclear envelope disassembly
G0:0032181	2	dinucleotide repeat insertion binding
G0:0001798	2	positive regulation of type IIa hypersensitivity
G0:0015114	2	phosphate ion transmembrane transporter activity
G0:0071568	2	UFM1 conjugating enzyme activity
G0:0051438	2	regulation of ubiquitin-protein transferase activity
G0:0046039	2	GTP metabolic process
G0:0035794	2	positive regulation of mitochondrial membrane permeability
G0:1901387	2	positive regulation of voltage-gated calcium channel activity
G0:0071709	2	membrane assembly
G0:1901383	2	negative regulation of chorionic trophoblast cell proliferation
G0:0045174	2	glutathione dehydrogenase (ascorbate) activity
G0:0042335	2	cuticle development
G0:0031981	2	nuclear lumen
G0:0043323	2	positive regulation of natural killer cell degranulation
G0:0010899	2	regulation of phosphatidylcholine catabolic process
G0:0006041	2	glucosamine metabolic process
G0:0006045	2	N-acetylglucosamine biosynthetic process
G0:0045428	2	regulation of nitric oxide biosynthetic process
G0:0072139	2	glomerular parietal epithelial cell differentiation
G0:0046778	2	modification by virus of host mRNA processing
G0:0048476	2	Holliday junction resolvase complex
G0:0005110	2	frizzled-2 binding
G0:0048659	2	smooth muscle cell proliferation
G0:0002215	2	defense response to nematode
G0:1902902	2	negative regulation of autophagic vacuole assembly
G0:0014040	2	positive regulation of Schwann cell differentiation
G0:0010641	2	positive regulation of platelet-derived growth factor receptor signaling pathway
G0:0001546	2	preantral ovarian follicle growth
G0:0001543	2	ovarian follicle rupture
G0:0071954	2	chemokine (C-C motif) ligand 11 production

G0:0055081	2	anion homeostasis
G0:0038025	2	reelin receptor activity
G0:0032515	2	negative regulation of phosphoprotein phosphatase activity
G0:0009826	2	unidimensional cell growth
G0:0003366	2	cell-matrix adhesion involved in ameboidal cell migration
G0:0035898	2	parathyroid hormone secretion
G0:0019276	2	UDP-N-acetylgalactosamine metabolic process
G0:0042109	2	lymphotoxin A biosynthetic process
G0:0043514	2	interleukin-12 complex
G0:0043516	2	regulation of DNA damage response, signal transduction by p53 class mediator
G0:0043512	2	inhibin A complex
G0:0030997	2	regulation of centriole-centriole cohesion
G0:0021589	2	cerebellum structural organization
G0:0021722	2	superior olivary nucleus maturation
G0:0019853	2	L-ascorbic acid biosynthetic process
G0:0097241	2	hematopoietic stem cell migration to bone marrow
G0:0060014	2	granulosa cell differentiation
G0:0060547	2	negative regulation of necrotic cell death
G0:0015966	2	diadenosine tetraphosphate biosynthetic process
G0:0060019	2	radial glial cell differentiation
G0:0009893	2	positive regulation of metabolic process
G0:0009890	2	negative regulation of biosynthetic process
G0:0030149	2	sphingolipid catabolic process
G0:0031765	2	type 2 galanin receptor binding
G0:0031762	2	follicle-stimulating hormone receptor binding
G0:0021965	2	spinal cord ventral commissure morphogenesis
G0:0072125	2	negative regulation of glomerular mesangial cell proliferation
G0:0006551	2	leucine metabolic process
G0:0035305	2	negative regulation of dephosphorylation
G0:0008147	2	structural constituent of bone
G0:0048227	2	plasma membrane to endosome transport
G0:0042488	2	positive regulation of odontogenesis of dentin-containing tooth
G0:0000124	2	SAGA complex
G0:0000120	2	RNA polymerase I transcription factor complex
G0:0004320	2	oleoyl-[acyl-carrier-protein] hydrolase activity
G0:0045213	2	neurotransmitter receptor metabolic process
G0:0070940	2	dephosphorylation of RNA polymerase II C-terminal domain
G0:0005642	2	annulate lamellae
G0:0032214	2	negative regulation of telomere maintenance via semi-conservative replication
G0:0021913	2	regulation of transcription from RNA polymerase II promoter involved in ventral spinal cord interneuron specification
G0:0051572	2	negative regulation of histone H3-K4 methylation
G0:0016433	2	rRNA (adenine) methyltransferase activity
G0:0003845	2	11-beta-hydroxysteroid dehydrogenase [NAD(P)] activity
G0:0051410	2	detoxification of nitrogen compound
G0:0007007	2	inner mitochondrial membrane organization
G0:0071727	2	cellular response to triacyl bacterial lipopeptide
G0:0071726	2	cellular response to diacyl bacterial lipopeptide
G0:0035939	2	microsatellite binding
G0:0033031	2	positive regulation of neutrophil apoptotic process
G0:0072224	2	metanephric glomerulus development
G0:0034683	2	integrin alphav-beta3 complex
G0:0034680	2	integrin alpha10-beta1 complex
G0:0016445	2	somatic diversification of immunoglobulins
G0:0043308	2	eosinophil degranulation
G0:0072563	2	endothelial microparticle
G0:0004914	2	interleukin-5 receptor activity
G0:0004913	2	interleukin-4 receptor activity
G0:0050893	2	sensory processing
G0:0004918	2	interleukin-8 receptor activity
G0:0090324	2	negative regulation of oxidative phosphorylation
G0:0072156	2	distal tubule morphogenesis
G0:2000820	2	negative regulation of transcription from RNA polymerase II promoter involved in smooth muscle cell differentiation
G0:0009405	2	pathogenesis
G0:0004912	2	interleukin-3 receptor activity
G0:0038194	2	thyroid-stimulating hormone signaling pathway
G0:0002232	2	leukocyte chemotaxis involved in inflammatory response
G0:0002238	2	response to molecule of fungal origin
G0:0036309	2	protein localization to M-band
G0:0006990	2	positive regulation of transcription from RNA polymerase II promoter involved in unfolded protein response
G0:0006991	2	response to sterol depletion

G0:0008466	2	glycogenin glucosyltransferase activity
G0:0031543	2	peptidyl-proline dioxygenase activity
G0:0070009	2	serine-type aminopeptidase activity
G0:0042126	2	nitrate metabolic process
G0:0072711	2	cellular response to hydroxyurea
G0:0045794	2	negative regulation of cell volume
G0:0045796	2	negative regulation of intestinal cholesterol absorption
G0:0060988	2	lipid tube assembly
G0:0032534	2	regulation of microvillus assembly
G0:0034274	2	Atg12-Atg5-Atg16 complex
G0:0010324	2	membrane invagination
G0:0002439	2	chronic inflammatory response to antigenic stimulus
G0:0019836	2	hemolysis by symbiont of host erythrocytes
G0:0030977	2	taurine binding
G0:0016309	2	1-phosphatidylinositol-5-phosphate 4-kinase activity
G0:0016035	2	zeta DNA polymerase complex
G0:0035802	2	adrenal cortex formation
G0:0071065	2	alpha9-beta1 integrin-vascular cell adhesion molecule-1 complex
G0:0006435	2	threonyl-tRNA aminoacylation
G0:0006434	2	seryl-tRNA aminoacylation
G0:0006436	2	tryptophanyl-tRNA aminoacylation
G0:0006433	2	prolyl-tRNA aminoacylation
G0:1900825	2	regulation of membrane depolarization during cardiac muscle cell action potential
G0:1990168	2	protein K33-linked deubiquitination
G0:0031952	2	regulation of protein autophosphorylation
G0:0060560	2	developmental growth involved in morphogenesis
G0:0006086	2	acetyl-CoA biosynthetic process from pyruvate
G0:0051799	2	negative regulation of hair follicle development
G0:0051792	2	medium-chain fatty acid biosynthetic process
G0:0008410	2	CoA-transferase activity
G0:0048203	2	vesicle targeting, trans-Golgi to endosome
G0:0045159	2	myosin II binding
G0:0031802	2	type 5 metabotropic glutamate receptor binding
G0:0004345	2	glucose-6-phosphate dehydrogenase activity
G0:0006850	2	mitochondrial pyruvate transport
G0:0019249	2	lactate biosynthetic process
G0:0071586	2	CAAX-box protein processing
G0:0060700	2	regulation of ribonuclease activity
G0:0019244	2	lactate biosynthetic process from pyruvate
G0:0031444	2	slow-twitch skeletal muscle fiber contraction
G0:0003221	2	right ventricular cardiac muscle tissue morphogenesis
G0:0033384	2	geranyl diphosphate biosynthetic process
G0:0007128	2	meiotic prophase I
G0:0033615	2	mitochondrial proton-transporting ATP synthase complex assembly
G0:0019483	2	beta-alanine biosynthetic process
G0:0051594	2	detection of glucose
G0:0090541	2	MIT domain binding
G0:0005879	2	axonemal microtubule
G0:0015489	2	putrescine transmembrane transporter activity
G0:0032943	2	mononuclear cell proliferation
G0:0021933	2	radial glia guided migration of cerebellar granule cell
G0:0030892	2	mitotic cohesin complex
G0:0030899	2	calcium-dependent ATPase activity
G0:0047787	2	delta4-3-oxosteroid 5beta-reductase activity
G0:0043138	2	3'-5' DNA helicase activity
G0:0043490	2	malate-aspartate shuttle
G0:0000480	2	endonucleolytic cleavage in 5'-ETS of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
G0:0045634	2	regulation of melanocyte differentiation
G0:0008263	2	pyrimidine-specific mismatch base pair DNA N-glycosylase activity
G0:0045199	2	maintenance of epithelial cell apical/basal polarity
G0:0061578	2	Lys63-specific deubiquitinase activity
G0:0008240	2	tripeptidyl-peptidase activity
G0:0060968	2	regulation of gene silencing
G0:0070363	2	mitochondrial light strand promoter sense binding
G0:1900121	2	negative regulation of receptor binding
G0:0050748	2	negative regulation of lipoprotein metabolic process
G0:0010949	2	negative regulation of intestinal phytosterol absorption
G0:0060221	2	retinal rod cell differentiation
G0:0072170	2	metanephric tubule development
G0:0022843	2	voltage-gated cation channel activity
G0:0022841	2	potassium ion leak channel activity
G0:0097359	2	UDP-glucosylation
G0:0004485	2	methylcrotonoyl-CoA carboxylase activity

G0:0004488	2	methylenetetrahydrofolate dehydrogenase (NADP+) activity
G0:2001288	2	positive regulation of caveolin-mediated endocytosis
G0:0050405	2	[acetyl-CoA carboxylase] kinase activity
G0:0048697	2	positive regulation of collateral sprouting in absence of injury
G0:0002635	2	negative regulation of germinal center formation
G0:0019777	2	Atg12 ligase activity
G0:0030250	2	guanylate cyclase activator activity
G0:0051683	2	establishment of Golgi localization
G0:0000715	2	nucleotide-excision repair, DNA damage recognition
G0:0004157	2	dihydropyrimidinase activity
G0:0034227	2	tRNA thio-modification
G0:0008481	2	sphinganine kinase activity
G0:0045401	2	positive regulation of interleukin-3 biosynthetic process
G0:0047223	2	beta-1,3-galactosyl-0-glycosyl-glycoprotein beta-1,3-N-acetylglucosaminyltransferase activity
G0:2000373	2	positive regulation of DNA topoisomerase (ATP-hydrolyzing) activity
G0:0021546	2	rhombomere development
G0:0021893	2	cerebral cortex GABAergic interneuron fate commitment
G0:0033206	2	meiotic cytokinesis
G0:0033754	2	indoleamine 2,3-dioxygenase activity
G0:0021761	2	limbic system development
G0:0097199	2	cysteine-type endopeptidase activity involved in apoptotic signaling pathway
G0:0030953	2	astral microtubule organization
G0:0002415	2	immunoglobulin transcytosis in epithelial cells mediated by polymeric immunoglobulin receptor
G0:0030950	2	establishment or maintenance of actin cytoskeleton polarity
G0:0097386	2	glial cell projection
G0:0071888	2	macrophage apoptotic process
G0:0097195	2	pilomotor reflex
G0:0071886	2	1-(4-iodo-2,5-dimethoxyphenyl)propan-2-amine binding
G0:0050975	2	sensory perception of touch
G0:0015920	2	lipopolysaccharide transport
G0:0016320	2	endoplasmic reticulum membrane fusion
G0:0035517	2	PR-DUB complex
G0:0034021	2	response to silicon dioxide
G0:0048597	2	post-embryonic camera-type eye morphogenesis
G0:0090285	2	negative regulation of protein glycosylation in Golgi
G0:0042508	2	tyrosine phosphorylation of Stat1 protein
G0:0008106	2	alcohol dehydrogenase (NADP+) activity
G0:0005146	2	leukemia inhibitory factor receptor binding
G0:0004366	2	glycerol-3-phosphate 0-acyltransferase activity
G0:0004815	2	aspartate-tRNA ligase activity
G0:0004818	2	glutamate-tRNA ligase activity
G0:1902958	2	positive regulation of mitochondrial electron transport, NADH to ubiquinone
G0:0070904	2	transepithelial L-ascorbic acid transport
G0:0090177	2	establishment of planar polarity involved in neural tube closure
G0:0039692	2	single stranded viral RNA replication via double stranded DNA intermediate
G0:0014806	2	smooth muscle hyperplasia
G0:0009223	2	pyrimidine deoxyribonucleotide catabolic process
G0:0071506	2	cellular response to mycophenolic acid
G0:0071502	2	cellular response to temperature stimulus
G0:0010385	2	double-stranded methylated DNA binding
G0:0036117	2	hyaluronan cable
G0:0051466	2	positive regulation of corticotropin-releasing hormone secretion
G0:2000418	2	positive regulation of eosinophil migration
G0:0070278	2	extracellular matrix constituent secretion
G0:0042306	2	regulation of protein import into nucleus
G0:0052593	2	tryptamine:oxygen oxidoreductase (deaminating) activity
G0:0052596	2	phenethylamine:oxygen oxidoreductase (deaminating) activity
G0:0052595	2	aliphatic-amine oxidase activity
G0:0052594	2	aminoacetone:oxygen oxidoreductase(deaminating) activity
G0:0046104	2	thymidine metabolic process
G0:0016667	2	oxidoreductase activity, acting on a sulfur group of donors
G0:0071267	2	L-methionine salvage
G0:0005049	2	nuclear export signal receptor activity
G0:0033692	2	cellular polysaccharide biosynthetic process
G0:0016403	2	dimethylargininase activity
G0:0005046	2	KDEL sequence binding
G0:0070782	2	phosphatidylserine exposure on apoptotic cell surface
G0:0033007	2	negative regulation of mast cell activation involved in immune response
G0:1903019	2	negative regulation of glycoprotein metabolic process
G0:0034750	2	Scrib-APC-beta-catenin complex
G0:0097118	2	neuroligin clustering

G0:0031697	2	beta-1 adrenergic receptor binding
G0:0031696	2	alpha-2C adrenergic receptor binding
G0:0031699	2	beta-3 adrenergic receptor binding
G0:0010966	2	regulation of phosphate transport
G0:0009449	2	gamma-aminobutyric acid biosynthetic process
G0:0036132	2	13-prostaglandin reductase activity
G0:0006601	2	creatine biosynthetic process
G0:0009440	2	cyanate catabolic process
G0:0030619	2	U1 snRNA binding
G0:0002277	2	myeloid dendritic cell activation involved in immune response
G0:0030617	2	transforming growth factor beta receptor, inhibitory cytoplasmic mediator activity
G0:0009330	2	DNA topoisomerase complex (ATP-hydrolyzing)
G0:2001150	2	positive regulation of dipeptide transmembrane transport
G0:0003365	2	establishment of cell polarity involved in ameboidal cell migration
G0:0055026	2	negative regulation of cardiac muscle tissue development
G0:0004609	2	phosphatidylserine decarboxylase activity
G0:0033364	2	mast cell secretory granule organization
G0:0019784	2	NEDD8-specific protease activity
G0:0019781	2	NEDD8 activating enzyme activity
G0:0072757	2	cellular response to camptothecin
G0:0021568	2	rhombomere 2 development
G0:0032571	2	response to vitamin K
G0:0097252	2	oligodendrocyte apoptotic process
G0:0033549	2	MAP kinase phosphatase activity
G0:0033227	2	dsRNA transport
G0:0021740	2	principal sensory nucleus of trigeminal nerve development
G0:0005943	2	1-phosphatidylinositol-4-phosphate 3-kinase, class IA complex
G0:0021747	2	cochlear nucleus development
G0:0071314	2	cellular response to cocaine
G0:0001922	2	B-1 B cell homeostasis
G0:0016340	2	calcium-dependent cell-matrix adhesion
G0:0002711	2	positive regulation of T cell mediated immunity
G0:0051648	2	vesicle localization
G0:0002717	2	positive regulation of natural killer cell mediated immunity
G0:0051646	2	mitochondrion localization
G0:0051647	2	nucleus localization
G0:0042496	2	detection of diacyl bacterial lipopeptide
G0:0038191	2	neuropilin binding
G0:0038190	2	VEGF-activated neuropilin signaling pathway
G0:0008523	2	sodium-dependent multivitamin transmembrane transporter activity
G0:0090204	2	protein localization to nuclear pore
G0:0060529	2	squamous basal epithelial stem cell differentiation involved in prostate gland acinus development
G0:0035368	2	selenocysteine insertion sequence binding
G0:0035363	2	histone locus body
G0:0003402	2	planar cell polarity pathway involved in axis elongation
G0:0071801	2	regulation of podosome assembly
G0:0006168	2	adenine salvage
G0:1902995	2	positive regulation of phospholipid efflux
G0:0010845	2	positive regulation of reciprocal meiotic recombination
G0:0048710	2	regulation of astrocyte differentiation
G0:0061101	2	neuroendocrine cell differentiation
G0:0005128	2	erythropoietin receptor binding
G0:0004828	2	serine-tRNA ligase activity
G0:0004831	2	tyrosine-tRNA ligase activity
G0:0045103	2	intermediate filament-based process
G0:0072033	2	renal vesicle formation
G0:0008269	2	JAK pathway signal transduction adaptor activity
G0:0042270	2	protection from natural killer cell mediated cytotoxicity
G0:0009384	2	N-acylmannosamine kinase activity
G0:0090118	2	receptor-mediated endocytosis of low-density lipoprotein particle involved in cholesterol transport
G0:0005981	2	regulation of glycogen catabolic process
G0:0031780	2	corticotropin hormone receptor binding
G0:0051917	2	regulation of fibrinolysis
G0:0010999	2	regulation of eIF2 alpha phosphorylation by heme
G0:0008381	2	mechanically-gated ion channel activity
G0:0043006	2	activation of phospholipase A2 activity by calcium-mediated signaling
G0:0070781	2	response to biotin
G0:0015198	2	oligopeptide transporter activity
G0:0010994	2	free ubiquitin chain polymerization
G0:0015197	2	peptide transporter activity
G0:0001710	2	mesodermal cell fate commitment
G0:0035268	2	protein mannosylation

G0:0008311	2	double-stranded DNA 3'-5' exodeoxyribonuclease activity
G0:0032902	2	nerve growth factor production
G0:0031783	2	type 5 melanocortin receptor binding
G0:0008520	2	L-ascorbate:sodium symporter activity
G0:2000297	2	negative regulation of synapse maturation
G0:0046912	2	transferase activity, transferring acyl groups, acyl groups converted into alkyl on transfer
G0:0015732	2	prostaglandin transport
G0:0032633	2	interleukin-4 production
G0:0070256	2	negative regulation of mucus secretion
G0:0070253	2	somatostatin secretion
G0:0070994	1	detection of oxidative stress
G0:0047127	1	thiomorpholine-carboxylate dehydrogenase activity
G0:0030852	1	regulation of granulocyte differentiation
G0:0031104	1	dendrite regeneration
G0:0031109	1	microtubule polymerization or depolymerization
G0:0034773	1	histone H4-K20 trimethylation
G0:1900168	1	positive regulation of glial cell line-derived neurotrophic factor secretion
G0:1900163	1	positive regulation of phospholipid scramblase activity
G0:0051786	1	all-trans-retinol 13,14-reductase activity
G0:0090340	1	positive regulation of secretion of lysosomal enzymes
G0:0090341	1	negative regulation of secretion of lysosomal enzymes
G0:0006592	1	ornithine biosynthetic process
G0:0006593	1	ornithine catabolic process
G0:0010905	1	negative regulation of UDP-glucose catabolic process
G0:0050780	1	dopamine receptor binding
G0:0010900	1	negative regulation of phosphatidylcholine catabolic process
G0:0050783	1	cocaine metabolic process
G0:2000836	1	positive regulation of androgen secretion
G0:0007624	1	ultradian rhythm
G0:0036458	1	hepatocyte growth factor binding
G0:0030677	1	ribonuclease P complex
G0:1902212	1	negative regulation of prolactin signaling pathway
G0:1902215	1	negative regulation of interleukin-4-mediated signaling pathway
G0:0048389	1	intermediate mesoderm development
G0:0045075	1	regulation of interleukin-12 biosynthetic process
G0:0004446	1	inositol-hexakisphosphate phosphatase activity
G0:0004990	1	oxytocin receptor activity
G0:0008798	1	beta-aspartyl-peptidase activity
G0:0048034	1	heme O biosynthetic process
G0:0018106	1	peptidyl-histidine phosphorylation
G0:2000062	1	negative regulation of ureter smooth muscle cell differentiation
G0:0031204	1	posttranslational protein targeting to membrane, translocation
G0:0008794	1	arsenate reductase (glutaredoxin) activity
G0:0070069	1	cytochrome complex
G0:2000334	1	positive regulation of blood microparticle formation
G0:2000627	1	positive regulation of miRNA catabolic process
G0:2000620	1	positive regulation of histone H4-K16 acetylation
G0:0021502	1	neural fold elevation formation
G0:0021503	1	neural fold bending
G0:0021501	1	prechordal plate formation
G0:0052817	1	very long chain acyl-CoA hydrolase activity
G0:0010752	1	regulation of cGMP-mediated signaling
G0:0010754	1	negative regulation of cGMP-mediated signaling
G0:0010758	1	regulation of macrophage chemotaxis
G0:0002904	1	positive regulation of B cell apoptotic process
G0:0071335	1	hair follicle cell proliferation
G0:0071336	1	regulation of hair follicle cell proliferation
G0:0001909	1	leukocyte mediated cytotoxicity
G0:1901796	1	regulation of signal transduction by p53 class mediator
G0:0051660	1	establishment of centrosome localization
G0:0051661	1	maintenance of centrosome location
G0:0051665	1	membrane raft localization
G0:0004801	1	sedoheptulose-7-phosphate:D-glyceraldehyde-3-phosphate glycerone transferase activity
G0:1900169	1	regulation of glucocorticoid mediated signaling pathway
G0:1990108	1	protein linear deubiquitination
G0:0017018	1	myosin phosphatase activity
G0:0052866	1	phosphatidylinositol phosphate phosphatase activity
G0:0033867	1	Fas-activated serine/threonine kinase activity
G0:0006106	1	fumarate metabolic process
G0:0060262	1	negative regulation of N-terminal protein palmitoylation
G0:0044330	1	canonical Wnt signaling pathway involved in positive regulation of wound healing

G0:0031710	1	neuromedin B receptor binding
G0:0004855	1	xanthine oxidase activity
G0:0004856	1	xylulokinase activity
G0:0004853	1	uroporphyrinogen decarboxylase activity
G0:0090287	1	regulation of cellular response to growth factor stimulus
G0:1902910	1	positive regulation of melanosome transport
G0:0031812	1	P2Y1 nucleotide receptor binding
G0:0050647	1	5-hydroxy-6E,8Z,11Z,14Z-icosatetraenoic acid binding
G0:0050646	1	5-oxo-6E,8Z,11Z,14Z-icosatetraenoic acid binding
G0:0008118	1	N-acetyllactosaminide alpha-2,3-sialyltransferase activity
G0:0000965	1	mitochondrial RNA 3'-end processing
G0:0052918	1	dol-P-Man:Man(8)GlcNAc(2)-PP-Dol alpha-1,2-mannosyltransferase activity
G0:0098703	1	calcium ion import across plasma membrane
G0:0090138	1	regulation of actin cytoskeleton organization by cell-cell adhesion
G0:0060101	1	negative regulation of phagocytosis, engulfment
G0:0090134	1	cell migration involved in mesendoderm migration
G0:0090131	1	mesenchyme migration
G0:0005456	1	CMP-N-acetylneuraminase transmembrane transporter activity
G0:0002335	1	mature B cell differentiation
G0:0004709	1	alkenylglycerophosphoethanolamine hydrolase activity
G0:0009041	1	uridylyltransferase activity
G0:0010106	1	cellular response to iron ion starvation
G0:0009107	1	lipoate biosynthetic process
G0:0018377	1	protein myristoylation
G0:0052726	1	inositol-1,3,4-trisphosphate 5-kinase activity
G0:0004760	1	serine-pyruvate transaminase activity
G0:0003882	1	CDP-diacylglycerol-serine O-phosphatidyltransferase activity
G0:0003881	1	CDP-diacylglycerol-inositol 3-phosphatidyltransferase activity
G0:0004768	1	stearoyl-CoA 9-desaturase activity
G0:2000108	1	positive regulation of leukocyte apoptotic process
G0:0005367	1	myo-inositol:sodium symporter activity
G0:0032920	1	putrescine acetylation
G0:0032928	1	regulation of superoxide anion generation
G0:0032383	1	regulation of intracellular cholesterol transport
G0:0008507	1	sodium:iodide symporter activity
G0:0016999	1	antibiotic metabolic process
G0:0016997	1	alpha-sialidase activity
G0:0045381	1	regulation of interleukin-18 biosynthetic process
G0:0060165	1	regulation of timing of subpallium neuron differentiation
G0:0032655	1	regulation of interleukin-12 production
G0:0047726	1	iron-cytochrome-c reductase activity
G0:0043795	1	glyceraldehyde oxidoreductase activity
G0:0043438	1	acetoacetic acid metabolic process
G0:0016917	1	GABA receptor activity
G0:0045655	1	regulation of monocyte differentiation
G0:0070506	1	high-density lipoprotein particle receptor activity
G0:0071103	1	DNA conformation change
G0:0071105	1	response to interleukin-11
G0:0043380	1	regulation of memory T cell differentiation
G0:2000812	1	regulation of barbed-end actin filament capping
G0:0043383	1	negative T cell selection
G0:0033387	1	putrescine biosynthetic process from ornithine
G0:0033386	1	geranylgeranyl diphosphate biosynthetic process
G0:0033388	1	putrescine biosynthetic process from arginine
G0:1900365	1	positive regulation of mRNA polyadenylation
G0:0050812	1	regulation of acyl-CoA biosynthetic process
G0:1900180	1	regulation of protein localization to nucleus
G0:0097152	1	mesenchymal cell apoptotic process
G0:0097158	1	pre-mRNA intronic pyrimidine-rich binding
G0:0001626	1	nociceptin receptor activity
G0:0061085	1	regulation of histone H3-K27 methylation
G0:0061081	1	positive regulation of myeloid leukocyte cytokine production involved in
immune response		
G0:0020005	1	symbiont-containing vacuole membrane
G0:0020003	1	symbiont-containing vacuole
G0:0010920	1	negative regulation of inositol phosphate biosynthetic process
G0:0010921	1	regulation of phosphatase activity
G0:0010925	1	positive regulation of inositol-polyphosphate 5-phosphatase activity
G0:0018192	1	enzyme active site formation via L-cysteine persulfide
G0:0030387	1	fructosamine-3-kinase activity
G0:0030380	1	interleukin-17E receptor binding
G0:0002077	1	acrosome matrix dispersal
G0:0030389	1	fructosamine metabolic process
G0:0006643	1	membrane lipid metabolic process
G0:0006649	1	phospholipid transfer to membrane

G0:0030128	1	clathrin coat of endocytic vesicle
G0:0002292	1	T cell differentiation involved in immune response
G0:0005591	1	collagen type VIII trimer
G0:0005595	1	collagen type XII trimer
G0:0072283	1	metanephric renal vesicle morphogenesis
G0:1903181	1	positive regulation of dopamine biosynthetic process
G0:0031835	1	substance P receptor binding
G0:2001190	1	positive regulation of T cell activation via T cell receptor contact with antigen bound to MHC molecule on antigen presenting cell
G0:2001193	1	positive regulation of gamma-delta T cell activation involved in immune response
G0:0050651	1	dermatan sulfate proteoglycan biosynthetic process
G0:2000724	1	positive regulation of cardiac vascular smooth muscle cell differentiation
G0:0045014	1	negative regulation of transcription by glucose
G0:0047451	1	3-hydroxyoctanoyl-[acyl-carrier-protein] dehydratase activity
G0:0004462	1	lactoylglutathione lyase activity
G0:0004463	1	leukotriene-A4 hydrolase activity
G0:0018293	1	protein-FAD linkage
G0:0048050	1	post-embryonic eye morphogenesis
G0:0000773	1	phosphatidyl-N-methylethanolamine N-methyltransferase activity
G0:0048058	1	compound eye corneal lens development
G0:0004648	1	O-phospho-L-serine:2-oxoglutarate aminotransferase activity
G0:0004641	1	phosphoribosylformylglycinamide cyclo-ligase activity
G0:0004642	1	phosphoribosylformylglycinamide synthase activity
G0:0004643	1	phosphoribosylaminoimidazolecarboxamide formyltransferase activity
G0:0004644	1	phosphoribosylglycinamide formyltransferase activity
G0:1990046	1	stress-induced mitochondrial fusion
G0:0003245	1	cardiac muscle tissue growth involved in heart morphogenesis
G0:0080164	1	regulation of nitric oxide metabolic process
G0:0021830	1	interneuron migration from the subpallium to the cortex
G0:0021528	1	commissural neuron differentiation in spinal cord
G0:0060901	1	regulation of hair cycle by canonical Wnt signaling pathway
G0:0060900	1	embryonic camera-type eye formation
G0:0060904	1	regulation of protein folding in endoplasmic reticulum
G0:0010734	1	negative regulation of protein glutathionylation
G0:0001692	1	histamine metabolic process
G0:0021785	1	branchiomotor neuron axon guidance
G0:0051350	1	negative regulation of lyase activity
G0:2000066	1	positive regulation of cortisol biosynthetic process
G0:0007344	1	pronuclear fusion
G0:0007343	1	egg activation
G0:0071357	1	cellular response to type I interferon
G0:0071351	1	cellular response to interleukin-18
G0:2000312	1	regulation of kainate selective glutamate receptor activity
G0:2000645	1	negative regulation of receptor catabolic process
G0:2000642	1	negative regulation of early endosome to late endosome transport
G0:0052740	1	1-acyl-2-lysophosphatidylserine acylhydrolase activity
G0:0052746	1	inositol phosphorylation
G0:0052745	1	inositol phosphate phosphatase activity
G0:0000285	1	1-phosphatidylinositol-3-phosphate 5-kinase activity
G0:0035639	1	purine ribonucleoside triphosphate binding
G0:2000659	1	regulation of interleukin-1-mediated signaling pathway
G0:0014722	1	regulation of skeletal muscle contraction by calcium ion signaling
G0:0006343	1	establishment of chromatin silencing
G0:0046466	1	membrane lipid catabolic process
G0:0046464	1	acylglycerol catabolic process
G0:0045340	1	mercury ion binding
G0:2000549	1	positive regulation of dendritic cell dendrite assembly
G0:0086019	1	cell-cell signaling involved in cardiac conduction
G0:0004997	1	thyrotropin-releasing hormone receptor activity
G0:0043177	1	organic acid binding
G0:0043176	1	amine binding
G0:0043175	1	RNA polymerase core enzyme binding
G0:0002790	1	peptide secretion
G0:0002792	1	negative regulation of peptide secretion
G0:1903044	1	protein localization to membrane raft
G0:0004877	1	complement component C3b receptor activity
G0:0004875	1	complement receptor activity
G0:0004874	1	aryl hydrocarbon receptor activity
G0:0072077	1	renal vesicle morphogenesis
G0:0004878	1	complement component C5a receptor activity
G0:0050666	1	regulation of homocysteine metabolic process
G0:0050664	1	oxidoreductase activity, acting on NAD(P)H, oxygen as acceptor
G0:0050668	1	positive regulation of homocysteine metabolic process
G0:0097454	1	Schwann cell microvillus

G0:0060127	1	prolactin secreting cell differentiation
G0:0060125	1	negative regulation of growth hormone secretion
G0:0043924	1	suramin binding
G0:0042265	1	peptidyl-asparagine hydroxylation
G0:0002314	1	germinal center B cell differentiation
G0:0002316	1	follicular B cell differentiation
G0:0005477	1	pyruvate secondary active transmembrane transporter activity
G0:0005471	1	ATP:ADP antiporter activity
G0:0002312	1	B cell activation involved in immune response
G0:0002313	1	mature B cell differentiation involved in immune response
G0:0051042	1	negative regulation of calcium-independent cell-cell adhesion
G0:0010124	1	phenylacetate catabolic process
G0:0050277	1	sedoheptulokinase activity
G0:2001032	1	regulation of double-strand break repair via nonhomologous end joining
G0:2001033	1	negative regulation of double-strand break repair via nonhomologous end joining
G0:2001031	1	positive regulation of cellular glucuronidation
G0:0010171	1	body morphogenesis
G0:0090082	1	positive regulation of heart induction by negative regulation of canonical Wnt signaling pathway
G0:0018352	1	protein-pyridoxal-5-phosphate linkage
G0:0018350	1	protein esterification
G0:0044252	1	negative regulation of multicellular organismal metabolic process
G0:0015065	1	uridine nucleotide receptor activity
G0:0071987	1	WD40-repeat domain binding
G0:0015791	1	polyol transport
G0:0036179	1	osteoclast maturation
G0:0001840	1	neural plate development
G0:2000120	1	positive regulation of sodium-dependent phosphate transport
G0:0015798	1	myo-inositol transport
G0:0015068	1	glycine amidinotransferase activity
G0:0032415	1	regulation of sodium:proton antiporter activity
G0:0032412	1	regulation of ion transmembrane transporter activity
G0:0046015	1	regulation of transcription by glucose
G0:2000233	1	negative regulation of rRNA processing
G0:0016260	1	selenocysteine biosynthetic process
G0:0016603	1	glutaminy-peptide cyclotransferase activity
G0:0019402	1	galactitol metabolic process
G0:0042827	1	platelet dense granule
G0:0047545	1	2-hydroxyglutarate dehydrogenase activity
G0:0047704	1	bile-salt sulfotransferase activity
G0:0047708	1	biotinidase activity
G0:0072675	1	osteoclast fusion
G0:0043413	1	macromolecule glycosylation
G0:0043418	1	homocysteine catabolic process
G0:0070563	1	negative regulation of vitamin D receptor signaling pathway
G0:0071164	1	RNA trimethylguanosine synthase activity
G0:0071167	1	ribonucleoprotein complex import into nucleus
G0:0034158	1	toll-like receptor 8 signaling pathway
G0:0072588	1	box H/ACA RNP complex
G0:0034150	1	toll-like receptor 6 signaling pathway
G0:2000870	1	regulation of progesterone secretion
G0:0021642	1	trochlear nerve formation
G0:0032674	1	regulation of interleukin-5 production
G0:0046070	1	dGTP metabolic process
G0:0021768	1	nucleus accumbens development
G0:0046079	1	dUMP catabolic process
G0:0046078	1	dUMP metabolic process
G0:0015067	1	amidinotransferase activity
G0:0002128	1	tRNA nucleoside ribose methylation
G0:0003138	1	primary heart field specification
G0:0035280	1	miRNA loading onto RISC involved in gene silencing by miRNA
G0:0046618	1	drug export
G0:2001200	1	positive regulation of dendritic cell differentiation
G0:2001204	1	regulation of osteoclast development
G0:2001206	1	positive regulation of osteoclast development
G0:0030108	1	HLA-A specific activating MHC class I receptor activity
G0:0030107	1	HLA-A specific inhibitory MHC class I receptor activity
G0:1901509	1	regulation of endothelial tube morphogenesis
G0:2000118	1	regulation of sodium-dependent phosphate transport
G0:2000119	1	negative regulation of sodium-dependent phosphate transport
G0:0004788	1	thiamine diphosphokinase activity
G0:0045030	1	UTP-activated nucleotide receptor activity
G0:0045032	1	ADP-activated nucleotide receptor activity
G0:0004408	1	holocytochrome-c synthase activity

G0:0030309	1	poly-N-acetyllactosamine metabolic process
G0:0006668	1	sphinganine-1-phosphate metabolic process
G0:0006669	1	sphinganine-1-phosphate biosynthetic process
G0:1902078	1	positive regulation of lateral motor column neuron migration
G0:1902073	1	positive regulation of hypoxia-inducible factor-1alpha signaling pathway
G0:0006666	1	3-keto-sphinganine metabolic process
G0:1902074	1	response to salt
G0:0048074	1	negative regulation of eye pigmentation
G0:0005314	1	high-affinity glutamate transmembrane transporter activity
G0:0000797	1	condensin core heterodimer
G0:0000799	1	nuclear condensin complex
G0:0031507	1	heterochromatin assembly
G0:0031508	1	centromeric heterochromatin assembly
G0:0090075	1	relaxation of muscle
G0:1902396	1	protein localization to tight junction
G0:1902255	1	positive regulation of intrinsic apoptotic signaling pathway by p53 class mediator
G0:1902251	1	negative regulation of erythrocyte apoptotic process
G0:0010640	1	regulation of platelet-derived growth factor receptor signaling pathway
G0:0060427	1	lung connective tissue development
G0:0051186	1	cofactor metabolic process
G0:0051181	1	cofactor transport
G0:0051183	1	vitamin transporter activity
G0:0044345	1	stromal-epithelial cell signaling involved in prostate gland development
G0:0090544	1	BAF-type complex
G0:0021814	1	cell motility involved in cerebral cortex radial glia guided migration
G0:0021816	1	extension of a leading process involved in cell motility in cerebral cortex radial glia guided migration
G0:0021812	1	neuronal-glial interaction involved in cerebral cortex radial glia guided migration
G0:0021813	1	cell-cell adhesion involved in neuronal-glial interactions involved in cerebral cortex radial glia guided migration
G0:2000628	1	regulation of miRNA metabolic process
G0:0060929	1	atrioventricular node cell fate commitment
G0:0051238	1	sequestering of metal ion
G0:0010712	1	regulation of collagen metabolic process
G0:0046824	1	positive regulation of nucleocytoplasmic transport
G0:0019677	1	NAD catabolic process
G0:0002947	1	tumor necrosis factor receptor superfamily complex
G0:0071373	1	cellular response to luteinizing hormone stimulus
G0:2000660	1	negative regulation of interleukin-1-mediated signaling pathway
G0:0038133	1	ERBB2-ERBB3 signaling pathway
G0:0016011	1	dystroglycan complex
G0:0090230	1	regulation of centromere complex assembly
G0:0061452	1	retrotrapezoid nucleus neuron differentiation
G0:0003270	1	Notch signaling pathway involved in regulation of secondary heart field cardioblast proliferation
G0:0014705	1	C zone
G0:0060354	1	negative regulation of cell adhesion molecule production
G0:0047066	1	phospholipid-hydroperoxide glutathione peroxidase activity
G0:0090239	1	regulation of histone H4 acetylation
G0:0045938	1	positive regulation of circadian sleep/wake cycle, sleep
G0:0042583	1	chromaffin granule
G0:1990379	1	lipid transport across blood brain barrier
G0:0042586	1	peptide deformylase activity
G0:0086077	1	gap junction channel activity involved in AV node cell-bundle of His cell electrical coupling
G0:0043199	1	sulfate binding
G0:0035616	1	histone H2B conserved C-terminal lysine deubiquitination
G0:0097291	1	renal phosphate ion absorption
G0:0060327	1	cytoplasmic actin-based contraction involved in cell motility
G0:0090249	1	regulation of cell motility involved in somitogenic axis elongation
G0:0047982	1	homocysteine desulfhydrase activity
G0:0009360	1	DNA polymerase III complex
G0:0015727	1	lactate transport
G0:0060143	1	positive regulation of syncytium formation by plasma membrane fusion
G0:0002372	1	myeloid dendritic cell cytokine production
G0:0002371	1	dendritic cell cytokine production
G0:0006867	1	asparagine transport
G0:0005991	1	trehalose metabolic process
G0:2001012	1	mesenchymal cell differentiation involved in renal system development
G0:0006535	1	cysteine biosynthetic process from serine
G0:0008894	1	guanosine-5'-triphosphate,3'-diphosphate diphosphatase activity
G0:0008897	1	holo-[acyl-carrier-protein] synthase activity
G0:0008891	1	glycolate oxidase activity

G0:0008893	1	guanosine-3',5'-bis(diphosphate) 3'-diphosphatase activity
G0:0008892	1	guanine deaminase activity
G0:0005464	1	UDP-xylose transmembrane transporter activity
G0:0001770	1	establishment of natural killer cell polarity
G0:0016830	1	carbon-carbon lyase activity
G0:0003957	1	NAD(P)+ transhydrogenase (B-specific) activity
G0:0003220	1	left ventricular cardiac muscle tissue morphogenesis
G0:0045342	1	MHC class II biosynthetic process
G0:0014889	1	muscle atrophy
G0:1902531	1	regulation of intracellular signal transduction
G0:0014883	1	transition between fast and slow fiber
G0:0003829	1	beta-1,3-galactosyl-0-glycosyl-glycoprotein beta-1,6-N-acetylglucosaminyltransferase activity
G0:0019464	1	glycine decarboxylation via glycine cleavage system
G0:0042801	1	polo kinase kinase activity
G0:0036353	1	histone H2A-K119 monoubiquitination
G0:0047277	1	globoside alpha-N-acetylgalactosaminyltransferase activity
G0:0047273	1	galactosylgalactosylglucosylceramide beta-D-acetylgalactosaminyltransferase activity
G0:0045092	1	interleukin-18 receptor complex
G0:1901798	1	positive regulation of signal transduction by p53 class mediator
G0:0070543	1	response to linoleic acid
G0:0042930	1	enterobactin transport
G0:0032474	1	otolith morphogenesis
G0:0032470	1	positive regulation of endoplasmic reticulum calcium ion concentration
G0:2000506	1	negative regulation of energy homeostasis
G0:0021660	1	rhombomere 3 formation
G0:0021666	1	rhombomere 5 formation
G0:0019284	1	L-methionine biosynthetic process from S-adenosylmethionine
G0:0030834	1	regulation of actin filament depolymerization
G0:0002575	1	basophil chemotaxis
G0:0033124	1	regulation of GTP catabolic process
G0:0046587	1	positive regulation of calcium-dependent cell-cell adhesion
G0:0046588	1	negative regulation of calcium-dependent cell-cell adhesion
G0:0051722	1	protein C-terminal methylesterase activity
G0:0051724	1	NAD transporter activity
G0:0051729	1	germline cell cycle switching, mitotic to meiotic cell cycle
G0:1902103	1	negative regulation of metaphase/anaphase transition of meiotic cell cycle
G0:0071146	1	SMAD3-SMAD4 protein complex
G0:0071635	1	negative regulation of transforming growth factor beta production
G0:0046633	1	alpha-beta T cell proliferation
G0:0001172	1	transcription, RNA-templated
G0:0030342	1	1-alpha,25-dihydroxyvitamin D3 24-hydroxylase activity
G0:0030167	1	proteoglycan catabolic process
G0:0035401	1	histone kinase activity (H3-Y41 specific)
G0:0061151	1	BMP signaling pathway involved in renal system segmentation
G0:0061155	1	pulmonary artery endothelial tube morphogenesis
G0:0035409	1	histone H3-Y41 phosphorylation
G0:0060795	1	cell fate commitment involved in formation of primary germ layer
G0:0043033	1	isoamylase complex
G0:0043035	1	chromatin insulator sequence binding
G0:0048894	1	efferent axon development in a lateral line nerve
G0:0000221	1	vacuolar proton-transporting V-type ATPase, V1 domain
G0:0000224	1	peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase activity
G0:0000225	1	N-acetylglucosaminylphosphatidylinositol deacetylase activity
G0:0004375	1	glycine dehydrogenase (decarboxylating) activity
G0:0004420	1	hydroxymethylglutaryl-CoA reductase (NADPH) activity
G0:0047865	1	dimethylglycine dehydrogenase activity
G0:0006683	1	galactosylceramide catabolic process
G0:0006680	1	glucosylceramide catabolic process
G0:0005333	1	norepinephrine transmembrane transporter activity
G0:0005330	1	dopamine:sodium symporter activity
G0:0005335	1	serotonin:sodium symporter activity
G0:0042637	1	catagen
G0:0042636	1	negative regulation of hair cycle
G0:0004686	1	elongation factor-2 kinase activity
G0:0017082	1	mineralocorticoid receptor activity
G0:0060649	1	mammary gland bud elongation
G0:0043990	1	histone H2A-S1 phosphorylation
G0:0098532	1	histone H3-K27 trimethylation
G0:1902109	1	negative regulation of mitochondrial membrane permeability involved in apoptotic process
G0:0080125	1	multicellular structure septum development
G0:0080121	1	AMP transport
G0:0080122	1	AMP transmembrane transporter activity

G0:0036030	1	protein C inhibitor-plasma kallikrein complex
G0:0036031	1	recruitment of mRNA capping enzyme to RNA polymerase II holoenzyme complex
G0:0070159	1	mitochondrial threonyl-tRNA aminoacylation
G0:2000560	1	positive regulation of CD24 biosynthetic process
G0:0071820	1	N-box binding
G0:0052909	1	18S rRNA (adenine(1779)-N(6)/adenine(1780)-N(6))-dimethyltransferase activity
G0:1901731	1	positive regulation of platelet aggregation
G0:0021870	1	Cajal-Retzius cell differentiation
G0:0032509	1	endosome transport via multivesicular body sorting pathway
G0:0002002	1	regulation of angiotensin levels in blood
G0:0038113	1	interleukin-9-mediated signaling pathway
G0:0038117	1	C-C motif chemokine 19 receptor activity
G0:0038116	1	chemokine (C-C motif) ligand 21 signaling pathway
G0:0038115	1	chemokine (C-C motif) ligand 19 signaling pathway
G0:0038114	1	interleukin-21-mediated signaling pathway
G0:0052902	1	spermidine:oxygen oxidoreductase (3-aminopropanal-forming) activity
G0:0052903	1	N1-acetylspermine:oxygen oxidoreductase (3-acetamidopropanal-forming) activity
G0:0045575	1	basophil activation
G0:0061301	1	cerebellum vasculature morphogenesis
G0:0061308	1	cardiac neural crest cell development involved in heart development
G0:0047042	1	androsterone dehydrogenase (B-specific) activity
G0:0042033	1	chemokine biosynthetic process
G0:0072428	1	signal transduction involved in intra-S DNA damage checkpoint
G0:1900063	1	regulation of peroxisome organization
G0:0035883	1	enteroendocrine cell differentiation
G0:0086053	1	AV node cell to bundle of His cell communication by electrical coupling
G0:0086052	1	membrane repolarization during SA node cell action potential
G0:0051164	1	L-xylitol metabolic process
G0:0034676	1	integrin alpha6-beta4 complex
G0:0086059	1	voltage-gated calcium channel activity involved SA node cell action potential
G0:0008434	1	calcitriol receptor activity
G0:0097272	1	ammonia homeostasis
G0:0097275	1	cellular ammonia homeostasis
G0:0097277	1	cellular urea homeostasis
G0:0097276	1	cellular creatinine homeostasis
G0:0035674	1	tricarboxylic acid transmembrane transport
G0:0031770	1	growth hormone-releasing hormone receptor binding
G0:0031771	1	type 1 hypocretin receptor binding
G0:0031772	1	type 2 hypocretin receptor binding
G0:1903006	1	positive regulation of protein K63-linked deubiquitination
G0:1903001	1	negative regulation of lipid transport across blood brain barrier
G0:1903002	1	positive regulation of lipid transport across blood brain barrier
G0:0031779	1	melanocortin receptor binding
G0:0010869	1	regulation of receptor biosynthetic process
G0:0044326	1	dendritic spine neck
G0:0010861	1	thyroid hormone receptor activator activity
G0:0001093	1	TFIIB-class transcription factor binding
G0:0010477	1	response to sulfur dioxide
G0:0050577	1	GDP-L-fucose synthase activity
G0:0010046	1	response to mycotoxin
G0:0002684	1	positive regulation of immune system process
G0:0002683	1	negative regulation of immune system process
G0:0051977	1	lysophospholipid transport
G0:0045917	1	positive regulation of complement activation
G0:0051972	1	regulation of telomerase activity
G0:0090198	1	negative regulation of chemokine secretion
G0:0090195	1	chemokine secretion
G0:0090194	1	negative regulation of glomerulus development
G0:0060163	1	subpallium neuron fate commitment
G0:0014036	1	neural crest cell fate specification
G0:0001792	1	polymeric immunoglobulin receptor activity
G0:0035090	1	maintenance of apical/basal cell polarity
G0:0002353	1	plasma kallikrein-kinin cascade
G0:0007495	1	visceral mesoderm-endoderm interaction involved in midgut development
G0:0007499	1	ectoderm and mesoderm interaction
G0:0071384	1	cellular response to corticosteroid stimulus
G0:0016854	1	racemase and epimerase activity
G0:0000053	1	argininosuccinate metabolic process
G0:0000054	1	ribosomal subunit export from nucleus
G0:0033862	1	UMP kinase activity
G0:0042799	1	histone methyltransferase activity (H4-K20 specific)
G0:0009817	1	defense response to fungus, incompatible interaction

G0:0004744	1	retinal isomerase activity
G0:0004747	1	ribokinase activity
G0:0052572	1	response to host immune response
G0:2000691	1	negative regulation of cardiac muscle cell myoblast differentiation
G0:0008215	1	spermine metabolic process
G0:0016933	1	extracellular-glycine-gated ion channel activity
G0:0045368	1	positive regulation of interleukin-13 biosynthetic process
G0:0070703	1	outer mucus layer
G0:0070701	1	mucus layer
G0:2000696	1	regulation of epithelial cell differentiation involved in kidney development
G0:0003294	1	atrial ventricular junction remodeling
G0:0051296	1	establishment of meiotic spindle orientation
G0:0043152	1	induction of bacterial agglutination
G0:0032458	1	slow endocytic recycling
G0:0032459	1	regulation of protein oligomerization
G0:0032328	1	alanine transport
G0:0034441	1	plasma lipoprotein particle oxidation
G0:2000522	1	positive regulation of immunological synapse formation
G0:0033490	1	cholesterol biosynthetic process via lathosterol
G0:2000529	1	positive regulation of myeloid dendritic cell chemotaxis
G0:0019912	1	cyclin-dependent protein kinase activating kinase activity
G0:0002517	1	T cell tolerance induction
G0:0002518	1	lymphocyte chemotaxis across high endothelial venule
G0:0044091	1	membrane biogenesis
G0:0010522	1	regulation of calcium ion transport into cytosol
G0:0033145	1	positive regulation of intracellular steroid hormone receptor signaling pathway
G0:0016206	1	catechol O-methyltransferase activity
G0:0033143	1	regulation of intracellular steroid hormone receptor signaling pathway
G0:0046031	1	ADP metabolic process
G0:0046032	1	ADP catabolic process
G0:0030690	1	Noc1p-Noc2p complex
G0:0051709	1	regulation of killing of cells of other organism
G0:0031343	1	positive regulation of cell killing
G0:0044549	1	GTP cyclohydrolase binding
G0:0044547	1	DNA topoisomerase binding
G0:0044540	1	L-cystine L-cysteine-lyase (deaminating)
G0:0071617	1	lysophospholipid acyltransferase activity
G0:0071615	1	oxidative deethylation
G0:0071614	1	linoleic acid epoxidase activity
G0:1901076	1	positive regulation of engulfment of apoptotic cell
G0:1901074	1	regulation of engulfment of apoptotic cell
G0:0070884	1	regulation of calcineurin-NFAT signaling cascade
G0:0001156	1	TFIIIC-class transcription factor binding
G0:0031714	1	C5a anaphylatoxin chemotactic receptor binding
G0:0047693	1	ATP diphosphatase activity
G0:0030692	1	Noc4p-Nop14p complex
G0:0035790	1	platelet-derived growth factor receptor-alpha signaling pathway
G0:1990144	1	intrinsic apoptotic signaling pathway in response to hypoxia
G0:0004852	1	uroporphyrinogen-III synthase activity
G0:0035428	1	hexose transmembrane transport
G0:0090284	1	positive regulation of protein glycosylation in Golgi
G0:0030144	1	alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase activity
G0:0003170	1	heart valve development
G0:0042694	1	muscle cell fate specification
G0:0043017	1	positive regulation of lymphotoxin A biosynthetic process
G0:0033906	1	hyaluronoglucuronidase activity
G0:0072395	1	signal transduction involved in cell cycle checkpoint
G0:0004919	1	interleukin-9 receptor activity
G0:1902033	1	regulation of hematopoietic stem cell proliferation
G0:2001247	1	positive regulation of phosphatidylcholine biosynthetic process
G0:2001246	1	negative regulation of phosphatidylcholine biosynthetic process
G0:0005350	1	pyrimidine nucleobase transmembrane transporter activity
G0:0005353	1	fructose transmembrane transporter activity
G0:0009756	1	carbohydrate mediated signaling
G0:0042659	1	regulation of cell fate specification
G0:0042658	1	MHC class II protein binding, via antigen binding groove
G0:0031231	1	intrinsic component of peroxisomal membrane
G0:0090030	1	regulation of steroid hormone biosynthetic process
G0:0090038	1	negative regulation of protein kinase C signaling
G0:0051148	1	negative regulation of muscle cell differentiation
G0:0044301	1	climbing fiber
G0:0080101	1	phosphatidyl-N-dimethylethanolamine N-methyltransferase activity

G0:0044302	1	dentate gyrus mossy fiber
G0:0018271	1	biotin-protein ligase activity
G0:0018272	1	protein-pyridoxal-5-phosphate linkage via peptidyl-N6-pyridoxal phosphate-L-lysine
G0:0004001	1	adenosine kinase activity
G0:0001632	1	leukotriene B4 receptor activity
G0:0001631	1	cysteinyl leukotriene receptor activity
G0:0032848	1	negative regulation of cellular pH reduction
G0:0070131	1	positive regulation of mitochondrial translation
G0:0070130	1	negative regulation of mitochondrial translation
G0:0032841	1	calcitonin binding
G0:0001984	1	vasodilation of artery involved in baroreceptor response to increased systemic arterial blood pressure
G0:0001985	1	negative regulation of heart rate involved in baroreceptor response to increased systemic arterial blood pressure
G0:0001986	1	negative regulation of the force of heart contraction involved in baroreceptor response to increased systemic arterial blood pressure
G0:0001987	1	vasoconstriction of artery involved in baroreceptor response to lowering of systemic arterial blood pressure
G0:0001980	1	regulation of systemic arterial blood pressure by ischemic conditions
G0:1901247	1	negative regulation of lung ciliated cell differentiation
G0:0001988	1	positive regulation of heart rate involved in baroreceptor response to decreased systemic arterial blood pressure
G0:0021859	1	pyramidal neuron differentiation
G0:0019056	1	modulation by virus of host transcription
G0:0000293	1	ferric-chelate reductase activity
G0:0038178	1	complement component C5a signaling pathway
G0:0050354	1	triokinase activity
G0:0038172	1	interleukin-33-mediated signaling pathway
G0:0055113	1	epiboly involved in gastrulation with mouth forming second
G0:0052725	1	inositol-1,3,4-trisphosphate 6-kinase activity
G0:0033791	1	3alpha,7alpha,12alpha-trihydroxy-5beta-cholestanoyl-CoA 24-hydroxylase activity
G0:0045556	1	positive regulation of TRAIL biosynthetic process
G0:0019637	1	organophosphate metabolic process
G0:0014741	1	negative regulation of muscle hypertrophy
G0:0042018	1	interleukin-22 receptor activity
G0:0043697	1	cell dedifferentiation
G0:0047536	1	2-aminoadipate transaminase activity
G0:0042015	1	interleukin-20 binding
G0:0047021	1	15-hydroxyprostaglandin dehydrogenase (NADP+) activity
G0:0047020	1	15-hydroxyprostaglandin-D dehydrogenase (NADP+) activity
G0:0003176	1	aortic valve development
G0:0003175	1	tricuspid valve development
G0:0003174	1	mitral valve development
G0:1902991	1	regulation of amyloid precursor protein catabolic process
G0:0050929	1	induction of negative chemotaxis
G0:1900044	1	regulation of protein K63-linked ubiquitination
G0:1900045	1	negative regulation of protein K63-linked ubiquitination
G0:0006188	1	IMP biosynthetic process
G0:0006185	1	dGDP biosynthetic process
G0:0035655	1	interleukin-18-mediated signaling pathway
G0:0061360	1	optic chiasma development
G0:0031936	1	negative regulation of chromatin silencing
G0:0031935	1	regulation of chromatin silencing
G0:0031933	1	telomeric heterochromatin
G0:0090205	1	positive regulation of cholesterol metabolic process
G0:0090207	1	regulation of triglyceride metabolic process
G0:0060366	1	lambdoid suture morphogenesis
G0:1902992	1	negative regulation of amyloid precursor protein catabolic process
G0:0010847	1	regulation of chromatin assembly
G0:0072544	1	L-DOPA binding
G0:0010844	1	recombination hotspot binding
G0:1902999	1	negative regulation of phospholipid efflux
G0:0010849	1	regulation of proton-transporting ATPase activity, rotational mechanism
G0:0005130	1	granulocyte colony-stimulating factor receptor binding
G0:0005984	1	disaccharide metabolic process
G0:0005985	1	sucrose metabolic process
G0:0017090	1	mephrin A complex
G0:0017096	1	acetylserotonin O-methyltransferase activity
G0:0017099	1	very-long-chain-acyl-CoA dehydrogenase activity
G0:0045977	1	positive regulation of mitotic cell cycle, embryonic
G0:0008721	1	D-serine ammonia-lyase activity
G0:0060187	1	cell pole
G0:0008725	1	DNA-3-methyladenine glycosylase activity

G0:0005183	1	gonadotropin hormone-releasing hormone activity
G0:0006638	1	neutral lipid metabolic process
G0:0031592	1	centrosomal corona
G0:2001051	1	positive regulation of tendon cell differentiation
G0:0036220	1	ITP diphosphatase activity
G0:2001057	1	reactive nitrogen species metabolic process
G0:0071466	1	cellular response to xenobiotic stimulus
G0:0004588	1	orotate phosphoribosyltransferase activity
G0:0004587	1	ornithine-oxo-acid transaminase activity
G0:0004586	1	ornithine decarboxylase activity
G0:0004585	1	ornithine carbamoyltransferase activity
G0:0004581	1	dolichyl-phosphate beta-glucosyltransferase activity
G0:0001879	1	detection of yeast
G0:0008050	1	female courtship behavior
G0:0008052	1	sensory organ boundary specification
G0:0008057	1	eye pigment granule organization
G0:0072183	1	negative regulation of nephron tubule epithelial cell differentiation
G0:0072184	1	renal vesicle progenitor cell differentiation
G0:0050121	1	N-acylglucosamine 2-epimerase activity
G0:0008275	1	gamma-tubulin small complex
G0:0070722	1	Tle3-Aes complex
G0:2000723	1	negative regulation of cardiac vascular smooth muscle cell differentiation
G0:2000097	1	regulation of smooth muscle cell-matrix adhesion
G0:0033860	1	regulation of NAD(P)H oxidase activity
G0:0071242	1	cellular response to ammonium ion
G0:0070586	1	cell-cell adhesion involved in gastrulation
G0:0051355	1	proprioception involved in equilibrioception
G0:0032307	1	negative regulation of prostaglandin secretion
G0:2000979	1	positive regulation of forebrain neuron differentiation
G0:2000545	1	negative regulation of endothelial cell chemotaxis to fibroblast growth factor
G0:2000547	1	regulation of dendritic cell dendrite assembly
G0:2000541	1	positive regulation of protein geranylgeranylation
G0:2000548	1	negative regulation of dendritic cell dendrite assembly
G0:0019935	1	cyclic-nucleotide-mediated signaling
G0:1900452	1	regulation of long term synaptic depression
G0:0002534	1	cytokine production involved in inflammatory response
G0:2000976	1	regulation of transcription from RNA polymerase II promoter involved in detection of glucose
G0:0015797	1	mannitol transport
G0:0015790	1	UDP-xylose transport
G0:0001844	1	protein insertion into mitochondrial membrane involved in apoptotic signaling pathway
G0:0001847	1	opsonin receptor activity
G0:0016263	1	glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase activity
G0:0015692	1	lead ion transport
G0:0038098	1	sequestering of BMP from receptor via BMP binding
G0:0034463	1	90S preribosome assembly
G0:0071678	1	olfactory bulb axon guidance
G0:0035229	1	positive regulation of glutamate-cysteine ligase activity
G0:0030302	1	deoxynucleotide transport
G0:0075606	1	transport of viral material towards nucleus
G0:0033165	1	interphotoreceptor matrix
G0:0033164	1	glycolipid 6-alpha-mannosyltransferase activity
G0:0017130	1	poly(C) RNA binding
G0:0061115	1	lung proximal/distal axis specification
G0:0072219	1	metanephric cortical collecting duct development
G0:0072213	1	metanephric capsule development
G0:0072214	1	metanephric cortex development
G0:0003721	1	telomeric template RNA reverse transcriptase activity
G0:0000262	1	mitochondrial chromosome
G0:0045091	1	regulation of single stranded viral RNA replication via double stranded DNA intermediate
G0:0004978	1	corticotropin receptor activity
G0:0004979	1	beta-endorphin receptor activity
G0:0072377	1	blood coagulation, common pathway
G0:0072376	1	protein activation cascade
G0:0050983	1	deoxyhypusine biosynthetic process from spermidine
G0:2001264	1	negative regulation of C-C chemokine binding
G0:0005334	1	norepinephrine:sodium symporter activity
G0:0060648	1	mammary gland bud morphogenesis
G0:0090010	1	transforming growth factor beta receptor signaling pathway involved in primitive streak formation
G0:0010309	1	acireductone dioxygenase [iron(II)-requiring] activity
G0:0048327	1	axial mesodermal cell fate specification

G0:0004398	1	histidine decarboxylase activity
G0:0051160	1	L-xylitol catabolic process
G0:0004397	1	histidine ammonia-lyase activity
G0:0004395	1	hexaprenyldihydroxybenzoate methyltransferase activity
G0:0044329	1	canonical Wnt signaling pathway involved in positive regulation of cell-cell adhesion
G0:0044328	1	canonical Wnt signaling pathway involved in positive regulation of endothelial cell migration
G0:0010045	1	response to nickel cation
G0:0032385	1	positive regulation of intracellular cholesterol transport
G0:0032386	1	regulation of intracellular transport
G0:0032439	1	endosome localization
G0:0004027	1	alcohol sulfotransferase activity
G0:0007285	1	primary spermatocyte growth
G0:0001616	1	growth hormone secretagogue receptor activity
G0:0036071	1	N-glycan fucosylation
G0:0043378	1	positive regulation of CD8-positive, alpha-beta T cell differentiation
G0:0032799	1	low-density lipoprotein receptor particle metabolic process
G0:0032791	1	lead ion binding
G0:0071866	1	negative regulation of apoptotic process in bone marrow
G0:0071869	1	response to catecholamine
G0:0015636	1	short-chain fatty acid uptake transporter activity
G0:2000391	1	positive regulation of neutrophil extravasation
G0:2000392	1	regulation of lamellipodium morphogenesis
G0:0019035	1	viral integration complex
G0:0038154	1	interleukin-11-mediated signaling pathway
G0:0050692	1	DBD domain binding
G0:1901194	1	negative regulation of formation of translation preinitiation complex
G0:0055130	1	D-alanine catabolic process
G0:0055131	1	C3HC4-type RING finger domain binding
G0:0016072	1	rRNA metabolic process
G0:0016073	1	snRNA metabolic process
G0:0016074	1	snoRNA metabolic process
G0:0016077	1	snoRNA catabolic process
G0:0016078	1	tRNA catabolic process
G0:0070119	1	ciliary neurotrophic factor binding
G0:0070442	1	integrin alphaIIb-beta3 complex
G0:0070447	1	positive regulation of oligodendrocyte progenitor proliferation
G0:0070446	1	negative regulation of oligodendrocyte progenitor proliferation
G0:0060431	1	primary lung bud formation
G0:0071247	1	cellular response to chromate
G0:0071241	1	cellular response to inorganic substance
G0:1901994	1	negative regulation of meiotic cell cycle phase transition
G0:0043244	1	regulation of protein complex disassembly
G0:0003117	1	regulation of vasoconstriction by circulating norepinephrine
G0:0043241	1	protein complex disassembly
G0:2000971	1	negative regulation of detection of glucose
G0:2000973	1	regulation of pro-B cell differentiation
G0:1900020	1	positive regulation of protein kinase C activity
G0:0034635	1	glutathione transport
G0:0034632	1	retinol transporter activity
G0:0034633	1	retinol transport
G0:0097237	1	cellular response to toxic substance
G0:0043370	1	regulation of CD4-positive, alpha-beta T cell differentiation
G0:0061347	1	planar cell polarity pathway involved in outflow tract morphogenesis
G0:0061348	1	planar cell polarity pathway involved in ventricular septum morphogenesis
G0:0061349	1	planar cell polarity pathway involved in cardiac right atrium morphogenesis
G0:0090222	1	centrosome-templated microtubule nucleation
G0:0060436	1	bronchiole morphogenesis
G0:0015817	1	histidine transport
G0:0010825	1	positive regulation of centrosome duplication
G0:0046203	1	spermidine catabolic process
G0:0010823	1	negative regulation of mitochondrion organization
G0:0010822	1	positive regulation of mitochondrion organization
G0:0051939	1	gamma-aminobutyric acid import
G0:0005960	1	glycine cleavage complex
G0:0005969	1	serine-pyruvate aminotransferase complex
G0:0045957	1	negative regulation of complement activation, alternative pathway
G0:1902170	1	cellular response to reactive nitrogen species
G0:1902178	1	fibroblast growth factor receptor apoptotic signaling pathway
G0:0005618	1	cell wall
G0:0072202	1	cell differentiation involved in metanephros development
G0:0036245	1	cellular response to menadione
G0:1990035	1	calcium ion import into cell

G0:1990037	1	Lewy body core
G0:1990032	1	parallel fiber
G0:0004561	1	alpha-N-acetylglucosaminidase activity
G0:0004567	1	beta-mannosidase activity
G0:0008843	1	endochitinase activity
G0:0052917	1	dol-P-Man:Man(7)GlcNAc(2)-PP-Dol alpha-1,6-mannosyltransferase activity
G0:0098909	1	regulation of cardiac muscle cell action potential involved in regulation of contraction
G0:0008079	1	translation termination factor activity
G0:0008336	1	gamma-butyrobetaine dioxygenase activity
G0:0070179	1	D-serine biosynthetic process
G0:0000016	1	lactase activity
G0:0031662	1	positive regulation of cyclin-dependent protein serine/threonine kinase activity involved in G2/M transition of mitotic cell cycle
G0:1903223	1	positive regulation of oxidative stress-induced neuron death
G0:0003937	1	IMP cyclohydrolase activity
G0:0003284	1	septum primum development
G0:0045324	1	late endosome to vacuole transport
G0:0070110	1	ciliary neurotrophic factor receptor complex
G0:0045081	1	negative regulation of interleukin-10 biosynthetic process
G0:0070975	1	FHA domain binding
G0:0002882	1	positive regulation of chronic inflammatory response to non-antigenic stimulus
G0:0002885	1	positive regulation of hypersensitivity
G0:0036323	1	vascular endothelial growth factor receptor-1 signaling pathway
G0:0032366	1	intracellular sterol transport
G0:0032361	1	pyridoxal phosphate catabolic process
G0:0046980	1	tapasin binding
G0:0046986	1	negative regulation of hemoglobin biosynthetic process
G0:0019778	1	Atg12 activating enzyme activity
G0:0019779	1	Atg8 activating enzyme
G0:0071478	1	cellular response to radiation
G0:0001861	1	complement component C4b receptor activity
G0:2000703	1	negative regulation of fibroblast growth factor receptor signaling pathway involved in ureteric bud formation
G0:2000707	1	positive regulation of dense core granule biogenesis
G0:2000706	1	negative regulation of dense core granule biogenesis
G0:0070304	1	positive regulation of stress-activated protein kinase signaling cascade
G0:0070305	1	response to cGMP
G0:0035757	1	chemokine (C-C motif) ligand 19 binding
G0:0033382	1	maintenance of granzyme B location in T cell secretory granule
G0:0071651	1	positive regulation of chemokine (C-C motif) ligand 5 production
G0:0071650	1	negative regulation of chemokine (C-C motif) ligand 5 production
G0:2000568	1	positive regulation of memory T cell activation
G0:2000566	1	positive regulation of CD8-positive, alpha-beta T cell proliferation
G0:0035800	1	deubiquitinase activator activity
G0:2000564	1	regulation of CD8-positive, alpha-beta T cell proliferation
G0:0034401	1	regulation of transcription by chromatin organization
G0:2000562	1	negative regulation of CD4-positive, alpha-beta T cell proliferation
G0:0034402	1	recruitment of 3'-end processing factors to RNA polymerase II holoenzyme complex
G0:0035752	1	lysosomal lumen pH elevation
G0:0035750	1	protein localization to myelin sheath abaxonal region
G0:0030329	1	prenylcysteine metabolic process
G0:0035758	1	chemokine (C-C motif) ligand 21 binding
G0:0008437	1	thyrotropin-releasing hormone activity
G0:0030184	1	nitric oxide transmembrane transporter activity
G0:0017116	1	single-stranded DNA-dependent ATP-dependent DNA helicase activity
G0:0017113	1	dihydropyrimidine dehydrogenase (NADP+) activity
G0:0042228	1	interleukin-8 biosynthetic process
G0:0031058	1	positive regulation of histone modification
G0:0072239	1	metanephric glomerulus vasculature development
G0:0006557	1	S-adenosylmethioninamine biosynthetic process
G0:0043056	1	forward locomotion
G0:0033986	1	response to methanol
G0:0046690	1	response to tellurium ion
G0:0071955	1	recycling endosome to Golgi transport
G0:0000243	1	commitment complex
G0:0000246	1	delta24(24-1) sterol reductase activity
G0:0000248	1	C-5 sterol desaturase activity
G0:0072359	1	circulatory system development
G0:0047804	1	cysteine-S-conjugate beta-lyase activity
G0:0060082	1	eye blink reflex
G0:0072356	1	chromosome passenger complex localization to kinetochore
G0:0031583	1	phospholipase D-activating G-protein coupled receptor signaling pathway

GO:0031275 1 regulation of lateral pseudopodium assembly
 GO:0060668 1 regulation of branching involved in salivary gland morphogenesis by
 extracellular matrix-epithelial cell signaling
 GO:0031279 1 regulation of cyclase activity
 GO:0060659 1 nipple sheath formation
 GO:0002079 1 inner acrosomal membrane
 GO:0002071 1 glandular epithelial cell maturation
 GO:0035622 1 intrahepatic bile duct development
 GO:0022607 1 cellular component assembly
 GO:1990440 1 positive regulation of transcription from RNA polymerase II promoter in
 response to endoplasmic reticulum stress
 GO:0098599 1 palmitoyl hydrolase activity
 GO:0051102 1 DNA ligation involved in DNA recombination
 GO:0009063 1 cellular amino acid catabolic process
 GO:0034986 1 iron chaperone activity
 GO:0009069 1 serine family amino acid metabolic process
 GO:0010021 1 amylopectin biosynthetic process
 GO:0050512 1 lactosylceramide 4-alpha-galactosyltransferase activity
 GO:0034440 1 lipid oxidation
 GO:0004044 1 amidophosphoribosyltransferase activity
 GO:0004042 1 acetyl-CoA:L-glutamate N-acetyltransferase activity
 GO:0004043 1 L-aminoacidipate-semialdehyde dehydrogenase activity
 GO:0004040 1 amidase activity
 GO:0031715 1 C5L2 anaphylatoxin chemotactic receptor binding
 GO:0001674 1 female germ cell nucleus
 GO:0036054 1 protein-malonyllysine demalonylase activity
 GO:0034714 1 type III transforming growth factor beta receptor binding
 GO:0032805 1 positive regulation of low-density lipoprotein particle receptor catabolic
 process
 GO:0032804 1 negative regulation of low-density lipoprotein particle receptor catabolic
 process
 GO:1901208 1 negative regulation of heart looping
 GO:1901201 1 regulation of extracellular matrix assembly
 GO:1901203 1 positive regulation of extracellular matrix assembly
 GO:0032514 1 positive regulation of protein phosphatase type 2B activity
 GO:0008627 1 intrinsic apoptotic signaling pathway in response to osmotic stress
 GO:0043610 1 regulation of carbohydrate utilization
 GO:0043618 1 regulation of transcription from RNA polymerase II promoter in response to
 stress
 GO:0046092 1 deoxycytidine metabolic process
 GO:0098902 1 regulation of membrane depolarization during action potential
 GO:0070685 1 macropinocytic cup
 GO:0070684 1 seminal clot liquefaction
 GO:0071279 1 cellular response to cobalt ion
 GO:0097151 1 positive regulation of inhibitory postsynaptic membrane potential
 GO:0098901 1 regulation of cardiac muscle cell action potential
 GO:0004569 1 glycoprotein endo-alpha-1,2-mannosidase activity
 GO:0043812 1 phosphatidylinositol-4-phosphate phosphatase activity
 GO:0002066 1 columnar/cuboidal epithelial cell development
 GO:1900186 1 negative regulation of clathrin-mediated endocytosis
 GO:0045513 1 interleukin-27 binding
 GO:0070463 1 tubulin-dependent ATPase activity
 GO:0070462 1 plus-end specific microtubule depolymerization
 GO:0008650 1 rRNA (uridine-2'-O-)-methyltransferase activity
 GO:0043262 1 adenosine-diphosphatase activity
 GO:0003131 1 mesodermal-endodermal cell signaling
 GO:1900005 1 positive regulation of serine-type endopeptidase activity
 GO:0060879 1 semicircular canal fusion
 GO:0060873 1 anterior semicircular canal development
 GO:0060872 1 semicircular canal development
 GO:0060875 1 lateral semicircular canal development
 GO:0060876 1 semicircular canal formation
 GO:0008446 1 GDP-mannose 4,6-dehydratase activity
 GO:0034346 1 positive regulation of type III interferon production
 GO:0016723 1 oxidoreductase activity, oxidizing metal ions, NAD or NADP as acceptor
 GO:0003363 1 lamellipodium assembly involved in ameboidal cell migration
 GO:0097214 1 positive regulation of lysosomal membrane permeability
 GO:0044524 1 protein sulfhydration
 GO:0001075 1 RNA polymerase II core promoter sequence-specific DNA binding
 transcription factor activity involved in preinitiation complex assembly
 GO:0046222 1 aflatoxin metabolic process
 GO:0046223 1 aflatoxin catabolic process
 GO:0032996 1 Bcl3-Bcl10 complex
 GO:0002663 1 positive regulation of B cell tolerance induction
 GO:0002668 1 negative regulation of T cell anergy

G0:0048178	1	negative regulation of hepatocyte growth factor biosynthetic process
G0:1903200	1	positive regulation of L-dopa decarboxylase activity
G0:0071550	1	death-inducing signaling complex assembly
G0:1903209	1	positive regulation of oxidative stress-induced cell death
G0:0006769	1	nicotinamide metabolic process
G0:0001133	1	sequence-specific transcription regulatory region DNA binding RNA polymerase II transcription factor recruiting transcription factor activity
G0:0014029	1	neural crest formation
G0:0036261	1	7-methylguanosine cap hypermethylation
G0:0036269	1	swimming behavior
G0:0005231	1	excitatory extracellular ligand-gated ion channel activity
G0:0000035	1	acyl binding
G0:0014005	1	microglia development
G0:0005731	1	nucleolus organizer region
G0:0004728	1	receptor signaling protein tyrosine phosphatase activity
G0:0031644	1	regulation of neurological system process
G0:2000852	1	regulation of corticosterone secretion
G0:0003029	1	detection of hypoxic conditions in blood by carotid body chemoreceptor signaling
G0:1902847	1	regulation of neuronal signal transduction
G0:0042886	1	amide transport
G0:0003026	1	regulation of systemic arterial blood pressure by aortic arch baroreceptor feedback
G0:0003939	1	L-iditol 2-dehydrogenase activity
G0:0003285	1	septum secundum development
G0:1990258	1	histone glutamine methylation
G0:0002863	1	positive regulation of inflammatory response to antigenic stimulus
G0:0002866	1	positive regulation of acute inflammatory response to antigenic stimulus
G0:0019172	1	glyoxalase III activity
G0:0009720	1	detection of hormone stimulus
G0:0018009	1	N-terminal peptidyl-L-cysteine N-palmitoylation
G0:0019970	1	interleukin-11 binding
G0:0019203	1	carbohydrate phosphatase activity
G0:0001805	1	positive regulation of type III hypersensitivity
G0:0001806	1	type IV hypersensitivity
G0:2000765	1	regulation of cytoplasmic translation
G0:2000764	1	positive regulation of semaphorin-plexin signaling pathway involved in outflow tract morphogenesis
G0:2000767	1	positive regulation of cytoplasmic translation
G0:0001809	1	positive regulation of type IV hypersensitivity
G0:0001808	1	negative regulation of type IV hypersensitivity
G0:2000763	1	positive regulation of transcription from RNA polymerase II promoter involved in norepinephrine biosynthetic process
G0:0038052	1	estrogen-activated sequence-specific DNA binding RNA polymerase II transcription factor activity
G0:0034423	1	autophagic vacuole lumen
G0:0033342	1	negative regulation of collagen binding
G0:0002352	1	B cell negative selection
G0:0035826	1	rubidium ion transport
G0:0035827	1	rubidium ion transmembrane transporter activity
G0:0035770	1	ribonucleoprotein granule
G0:0035772	1	interleukin-13-mediated signaling pathway
G0:0003099	1	positive regulation of the force of heart contraction by chemical signal
G0:0003096	1	renal sodium ion transport
G0:0016517	1	interleukin-12 receptor activity
G0:0035444	1	nickel cation transmembrane transport
G0:0016515	1	interleukin-13 receptor activity
G0:0045703	1	ketoreductase activity
G0:0016519	1	gastric inhibitory peptide receptor activity
G0:0017177	1	glucosidase II complex
G0:0017174	1	glycine N-methyltransferase activity
G0:0017172	1	cysteine dioxygenase activity
G0:0006575	1	cellular modified amino acid metabolic process
G0:0005232	1	serotonin-activated cation-selective channel activity
G0:0072259	1	metanephric interstitial cell development
G0:0090232	1	positive regulation of spindle checkpoint
G0:0031073	1	cholesterol 26-hydroxylase activity
G0:0031071	1	cysteine desulfurase activity
G0:0002357	1	defense response to tumor cell
G0:0060064	1	Spemann organizer formation at the anterior end of the primitive streak
G0:0015993	1	molecular hydrogen transport
G0:0032817	1	regulation of natural killer cell proliferation
G0:0097001	1	ceramide binding
G0:0052899	1	N(1),N(12)-diacetylspermine:oxygen oxidoreductase (3-acetamidopropanal-forming) activity

G0:0098609	1	cell-cell adhesion
G0:0052894	1	norspermine:oxygen oxidoreductase activity
G0:0052895	1	N1-acetylspermine:oxygen oxidoreductase (N1-acetylspermidine-forming) activity
G0:0060606	1	tube closure
G0:0060602	1	branch elongation of an epithelium
G0:0035620	1	ceramide transporter activity
G0:0005009	1	insulin-activated receptor activity
G0:0005008	1	hepatocyte growth factor-activated receptor activity
G0:0002059	1	thymine binding
G0:0002058	1	uracil binding
G0:0051125	1	regulation of actin nucleation
G0:0051121	1	hepoxilin metabolic process
G0:0044819	1	mitotic G1/S transition checkpoint
G0:0030704	1	vitelline membrane formation
G0:1901211	1	negative regulation of cardiac chamber formation
G0:1901640	1	XTP binding
G0:0046880	1	regulation of follicle-stimulating hormone secretion
G0:2000384	1	negative regulation of ectoderm development
G0:0008655	1	pyrimidine-containing compound salvage
G0:0044795	1	trans-Golgi network to recycling endosome transport
G0:0032280	1	symmetric synapse
G0:0008609	1	alkylglycerone-phosphate synthase activity
G0:0008352	1	katanin complex
G0:0018969	1	thiocyanate metabolic process
G0:0045281	1	succinate dehydrogenase complex
G0:0070661	1	leukocyte proliferation
G0:0070662	1	mast cell proliferation
G0:0070664	1	negative regulation of leukocyte proliferation
G0:0070667	1	negative regulation of mast cell proliferation
G0:0004061	1	arylformamidase activity
G0:0004066	1	asparagine synthase (glutamine-hydrolyzing) activity
G0:0015432	1	bile acid-exporting ATPase activity
G0:0015439	1	heme-transporting ATPase activity
G0:0040017	1	positive regulation of locomotion
G0:0070407	1	oxidation-dependent protein catabolic process
G0:0070401	1	NADP+ binding
G0:0071880	1	adenylate cyclase-activating adrenergic receptor signaling pathway
G0:0033080	1	immature T cell proliferation in thymus
G0:0015734	1	taurine transport
G0:0060856	1	establishment of blood-brain barrier
G0:0034360	1	chylomicron remnant
G0:0034365	1	discoidal high-density lipoprotein particle
G0:0016160	1	amylase activity
G0:0051463	1	negative regulation of cortisol secretion
G0:0051460	1	negative regulation of corticotropin secretion
G0:0071209	1	U7 snRNA binding
G0:0071750	1	dimeric IgA immunoglobulin complex
G0:0071206	1	establishment of protein localization to juxtaparanode region of axon
G0:0001016	1	RNA polymerase III regulatory region DNA binding
G0:0046711	1	GDP biosynthetic process
G0:0046713	1	borate transport
G0:0008973	1	phosphopentomutase activity
G0:0008753	1	NADPH dehydrogenase (quinone) activity
G0:0035543	1	positive regulation of SNARE complex assembly
G0:0008750	1	NAD(P)+ transhydrogenase (AB-specific) activity
G0:0035545	1	determination of left/right asymmetry in nervous system
G0:0035544	1	negative regulation of SNARE complex assembly
G0:0061073	1	ciliary body morphogenesis
G0:0035548	1	negative regulation of interferon-beta secretion
G0:1903082	1	positive regulation of C-C chemokine receptor CCR7 signaling pathway
G0:0060479	1	lung cell differentiation
G0:0060473	1	cortical granule
G0:1990079	1	cartilage homeostasis
G0:0071477	1	cellular hypotonic salinity response
G0:0035511	1	oxidative DNA demethylation
G0:0006743	1	ubiquinone metabolic process
G0:0006742	1	NADP catabolic process
G0:0031626	1	beta-endorphin binding
G0:0031620	1	regulation of fever generation
G0:0031628	1	opioid receptor binding
G0:0005690	1	U4atac snRNP
G0:0022410	1	circadian sleep/wake cycle process
G0:0002842	1	positive regulation of T cell mediated immune response to tumor cell
G0:0010616	1	negative regulation of cardiac muscle adaptation

G0:0015228	1	coenzyme A transmembrane transporter activity
G0:0008297	1	single-stranded DNA exodeoxyribonuclease activity
G0:0008296	1	3'-5'-exodeoxyribonuclease activity
G0:0019732	1	antifungal humoral response
G0:0002590	1	negative regulation of antigen processing and presentation of peptide antigen via MHC class I
G0:0002591	1	positive regulation of antigen processing and presentation of peptide antigen via MHC class I
G0:0071926	1	endocannabinoid signaling pathway
G0:0070346	1	positive regulation of fat cell proliferation
G0:0007174	1	epidermal growth factor catabolic process
G0:0071691	1	cardiac muscle thin filament assembly
G0:0035847	1	uterine epithelium development
G0:0035844	1	cloaca development
G0:0035841	1	new growing cell tip
G0:0035849	1	nephric duct elongation
G0:0043540	1	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1 complex
G0:0003071	1	renal system process involved in regulation of systemic arterial blood pressure
G0:0043545	1	molybdopterin cofactor metabolic process
G0:0043549	1	regulation of kinase activity
G0:0016287	1	glycerone-phosphate 0-acyltransferase activity
G0:0045724	1	positive regulation of cilium assembly
G0:0045870	1	positive regulation of single stranded viral RNA replication via double stranded DNA intermediate
G0:0045872	1	positive regulation of rhodopsin gene expression
G0:0035803	1	egg coat formation
G0:0072273	1	metanephric nephron morphogenesis
G0:0072274	1	metanephric glomerular basement membrane development
G0:0072275	1	metanephric glomerulus morphogenesis
G0:0043090	1	amino acid import
G0:0043091	1	L-arginine import
G0:1900210	1	positive regulation of cardiolipin metabolic process
G0:1900746	1	regulation of vascular endothelial growth factor signaling pathway
G0:0035714	1	cellular response to nitrogen dioxide
G0:0035712	1	T-helper 2 cell activation
G0:0035713	1	response to nitrogen dioxide
G0:0035710	1	CD4-positive, alpha-beta T cell activation
G0:0030322	1	stabilization of membrane potential
G0:0035751	1	regulation of lysosomal lumen pH
G0:0060598	1	dichotomous subdivision of terminal units involved in mammary gland duct morphogenesis
G0:0060599	1	lateral sprouting involved in mammary gland duct morphogenesis
G0:0046380	1	N-acetylneuraminate biosynthetic process
G0:0097026	1	dendritic cell dendrite assembly
G0:0097022	1	lymphocyte migration into lymph node
G0:0060620	1	regulation of cholesterol import
G0:0060623	1	regulation of chromosome condensation
G0:0001226	1	RNA polymerase II transcription corepressor binding
G0:0001221	1	transcription cofactor binding
G0:0001223	1	transcription coactivator binding
G0:0005020	1	stem cell factor receptor activity
G0:0030497	1	fatty acid elongation
G0:0002037	1	negative regulation of L-glutamate transport
G0:0002036	1	regulation of L-glutamate transport
G0:0002030	1	inhibitory G-protein coupled receptor phosphorylation
G0:0002033	1	vasodilation by angiotensin involved in regulation of systemic arterial blood pressure
G0:0044388	1	small protein activating enzyme binding
G0:0032392	1	DNA geometric change
G0:0008995	1	ribonuclease E activity
G0:0032394	1	MHC class Ib receptor activity
G0:0004078	1	biotin-[methylcrotonoyl-CoA-carboxylase] ligase activity
G0:0015676	1	vanadium ion transport
G0:0098629	1	trans-Golgi network membrane organization
G0:0031773	1	kisspeptin receptor binding
G0:0036090	1	cleavage furrow ingression
G0:0008192	1	RNA guanylyltransferase activity
G0:0008193	1	tRNA guanylyltransferase activity
G0:0004883	1	glucocorticoid receptor activity
G0:0003851	1	2-hydroxyacylsphingosine 1-beta-galactosyltransferase activity
G0:0070646	1	protein modification by small protein removal
G0:0004080	1	biotin-[propionyl-CoA-carboxylase (ATP-hydrolyzing)] ligase activity
G0:0004081	1	bis(5'-nucleosyl)-tetraphosphatase (asymmetrical) activity
G0:0004087	1	carbamoyl-phosphate synthase (ammonia) activity

G0:0004085	1	butyryl-CoA dehydrogenase activity
G0:0004088	1	carbamoyl-phosphate synthase (glutamine-hydrolyzing) activity
G0:0016248	1	channel inhibitor activity
G0:2000486	1	negative regulation of glutamine transport
G0:0016530	1	metallochaperone activity
G0:0040031	1	snRNA modification
G0:0040034	1	regulation of development, heterochronic
G0:0034466	1	chromaffin granule lumen
G0:0070429	1	negative regulation of nucleotide-binding oligomerization domain
containing	1	signaling pathway
G0:0032738	1	positive regulation of interleukin-15 production
G0:0032730	1	positive regulation of interleukin-1 alpha production
G0:0032732	1	positive regulation of interleukin-1 production
G0:2000269	1	regulation of fibroblast apoptotic process
G0:2000266	1	regulation of blood coagulation, intrinsic pathway
G0:2000261	1	negative regulation of blood coagulation, common pathway
G0:0015149	1	hexose transmembrane transporter activity
G0:0060837	1	blood vessel endothelial cell differentiation
G0:0015141	1	succinate transmembrane transporter activity
G0:0050061	1	long-chain-aldehyde dehydrogenase activity
G0:0050113	1	inositol oxygenase activity
G0:0015142	1	tricarboxylic acid transmembrane transporter activity
G0:0050115	1	myosin-light-chain-phosphatase activity
G0:0015410	1	manganese-transporting ATPase activity
G0:0010816	1	calcitonin catabolic process
G0:1901979	1	regulation of inward rectifier potassium channel activity
G0:1901978	1	positive regulation of cell cycle checkpoint
G0:1901976	1	regulation of cell cycle checkpoint
G0:0042483	1	negative regulation of odontogenesis
G0:0030267	1	glyoxylate reductase (NADP) activity
G0:0051996	1	squalene synthase activity
G0:1901605	1	alpha-amino acid metabolic process
G0:0033989	1	3alpha,7alpha,12alpha-trihydroxy-5beta-cholest-24-enoyl-CoA hydratase activity
G0:0035039	1	male pronucleus assembly
G0:0035037	1	sperm entry
G0:0061502	1	early endosome to recycling endosome transport
G0:0030003	1	cellular cation homeostasis
G0:0061055	1	myotome development
G0:0035175	1	histone kinase activity (H3-S10 specific)
G0:0060454	1	positive regulation of gastric acid secretion
G0:0060453	1	regulation of gastric acid secretion
G0:0060450	1	positive regulation of hindgut contraction
G0:0003681	1	bent DNA binding
G0:0043375	1	CD8-positive, alpha-beta T cell lineage commitment
G0:0060459	1	left lung development
G0:0060458	1	right lung development
G0:0072237	1	metanephric proximal tubule development
G0:0006550	1	isoleucine catabolic process
G0:0004506	1	squalene monooxygenase activity
G0:0004504	1	peptidylglycine monooxygenase activity
G0:0004503	1	monophenol monooxygenase activity
G0:0004502	1	kynurenine 3-monooxygenase activity
G0:0004500	1	dopamine beta-monooxygenase activity
G0:0004509	1	steroid 21-monooxygenase activity
G0:2000791	1	negative regulation of mesenchymal cell proliferation involved in lung development
G0:0006014	1	D-ribose metabolic process
G0:1902118	1	calcidiol binding
G0:0030110	1	HLA-C specific inhibitory MHC class I receptor activity
G0:0048199	1	vesicle targeting, to, from or within Golgi
G0:0048668	1	collateral sprouting
G0:0014043	1	negative regulation of neuron maturation
G0:0042779	1	tRNA 3'-trailer cleavage
G0:0042772	1	DNA damage response, signal transduction resulting in transcription
G0:0072101	1	specification of ureteric bud anterior/posterior symmetry by BMP signaling pathway
G0:0072105	1	ureteric peristalsis
G0:0003418	1	growth plate cartilage chondrocyte differentiation
G0:0002828	1	regulation of type 2 immune response
G0:0007522	1	visceral muscle development
G0:0007527	1	adult somatic muscle development
G0:0010635	1	regulation of mitochondrial fusion
G0:0033505	1	floor plate morphogenesis
G0:0036371	1	protein localization to T-tubule

G0:0001596	1	angiotensin type I receptor activity
G0:0001595	1	angiotensin receptor activity
G0:0031052	1	chromosome breakage
G0:0003999	1	adenine phosphoribosyltransferase activity
G0:0047801	1	L-cysteine:2-oxoglutarate aminotransferase activity
G0:0047800	1	cysteamine dioxygenase activity
G0:0071909	1	determination of stomach left/right asymmetry
G0:0071908	1	determination of intestine left/right asymmetry
G0:2000016	1	negative regulation of determination of dorsal identity
G0:0072355	1	histone H3-T3 phosphorylation
G0:0032078	1	negative regulation of endodeoxyribonuclease activity
G0:0038018	1	Wnt receptor catabolic process
G0:0032077	1	positive regulation of deoxyribonuclease activity
G0:0032074	1	negative regulation of nuclease activity
G0:0032075	1	positive regulation of nuclease activity
G0:0003339	1	regulation of mesenchymal to epithelial transition involved in metanephros morphogenesis
G0:0035863	1	dITP catabolic process
G0:0052629	1	phosphatidylinositol-3,5-bisphosphate 3-phosphatase activity
G0:0035867	1	alpha-v-beta3 integrin-IGF-1-IGF1R complex
G0:0000972	1	transcription-dependent tethering of RNA polymerase II gene DNA at nuclear periphery
G0:0019242	1	methylglyoxal biosynthetic process
G0:0019243	1	methylglyoxal catabolic process to D-lactate
G0:0016554	1	cytidine to uridine editing
G0:0003058	1	hormonal regulation of the force of heart contraction
G0:0070361	1	mitochondrial light strand promoter anti-sense binding
G0:0070362	1	mitochondrial heavy strand promoter anti-sense binding
G0:0070364	1	mitochondrial heavy strand promoter sense binding
G0:0070367	1	negative regulation of hepatocyte differentiation
G0:0042282	1	hydroxymethylglutaryl-CoA reductase activity
G0:0047676	1	arachidonate-CoA ligase activity
G0:0033291	1	eukaryotic 80S initiation complex
G0:0019866	1	organelle inner membrane
G0:0035730	1	S-nitrosoglutathione binding
G0:0035731	1	dinitrosyl-iron complex binding
G0:0035732	1	nitric oxide storage
G0:0060025	1	regulation of synaptic activity
G0:0050907	1	detection of chemical stimulus involved in sensory perception
G0:0055094	1	response to lipoprotein particle
G0:0034545	1	fumarylpyruvate hydrolase activity
G0:0009229	1	thiamine diphosphate biosynthetic process
G0:0090096	1	positive regulation of metanephric cap mesenchymal cell proliferation
G0:0009225	1	nucleotide-sugar metabolic process
G0:0006463	1	steroid hormone receptor complex assembly
G0:0010387	1	COP9 signalosome assembly
G0:0001532	1	interleukin-21 receptor activity
G0:0046100	1	hypoxanthine metabolic process
G0:0048857	1	neural nucleus development
G0:0048850	1	hypophysis morphogenesis
G0:0009593	1	detection of chemical stimulus
G0:0009590	1	detection of gravity
G0:0035633	1	maintenance of blood-brain barrier
G0:0030748	1	amine N-methyltransferase activity
G0:1902499	1	positive regulation of protein autoubiquitination
G0:1902498	1	regulation of protein autoubiquitination
G0:0042643	1	actomyosin, actin portion
G0:0000150	1	recombinase activity
G0:0000153	1	cytoplasmic ubiquitin ligase complex
G0:0004312	1	fatty acid synthase activity
G0:0004313	1	[acyl-carrier-protein] S-acetyltransferase activity
G0:0004310	1	farnesyl-diphosphate farnesyltransferase activity
G0:0004316	1	3-oxoacyl-[acyl-carrier-protein] reductase (NADPH) activity
G0:0004317	1	3-hydroxypalmitoyl-[acyl-carrier-protein] dehydratase activity
G0:0004319	1	enoyl-[acyl-carrier-protein] reductase (NADPH, B-specific) activity
G0:0018924	1	mandelate metabolic process
G0:0003834	1	beta-carotene 15,15'-monooxygenase activity
G0:0003830	1	beta-1,4-mannosylglycoprotein 4-beta-N-acetylglucosaminyltransferase activity
G0:0006808	1	regulation of nitrogen utilization
G0:0019521	1	D-gluconate metabolic process
G0:0070626	1	(S)-2-(5-amino-1-(5-phospho-D-ribosyl)imidazole-4-carboxamido)succinate AMP-lyase (fumarate-forming) activity
G0:0070990	1	snRNP binding
G0:2000464	1	positive regulation of astrocyte chemotaxis

G0:2000465	1	regulation of glycogen (starch) synthase activity
G0:0070963	1	positive regulation of neutrophil mediated killing of gram-negative bacterium
G0:0070195	1	growth hormone receptor complex
G0:0070194	1	synaptonemal complex disassembly
G0:0070191	1	methionine-R-sulfoxide reductase activity
G0:0032244	1	positive regulation of nucleoside transport
G0:0033595	1	response to genistein
G0:0033040	1	sour taste receptor activity
G0:2000209	1	regulation of anoikis
G0:1900535	1	palmitic acid biosynthetic process
G0:0003867	1	4-aminobutyrate transaminase activity
G0:0060816	1	random inactivation of X chromosome
G0:0015166	1	polyol transmembrane transporter activity
G0:0015165	1	pyrimidine nucleotide-sugar transmembrane transporter activity
G0:0071575	1	integral component of external side of plasma membrane
G0:0071578	1	zinc ion transmembrane import
G0:0001787	1	natural killer cell proliferation
G0:0016121	1	carotene catabolic process
G0:0046469	1	platelet activating factor metabolic process
G0:0007034	1	vacuolar transport
G0:0007039	1	vacuolar protein catabolic process
G0:0015132	1	prostaglandin transmembrane transporter activity
G0:0071718	1	sodium-independent icosanoid transport
G0:0051058	1	negative regulation of small GTPase mediated signal transduction
G0:0071544	1	diphosphoinositol polyphosphate catabolic process
G0:1901627	1	negative regulation of postsynaptic membrane organization
G0:1901625	1	cellular response to ergosterol
G0:1901624	1	negative regulation of lymphocyte chemotaxis
G0:0097183	1	protein C inhibitor-coagulation factor XI complex
G0:0097182	1	protein C inhibitor-coagulation factor Xa complex
G0:0097181	1	protein C inhibitor-coagulation factor V complex
G0:0035509	1	negative regulation of myosin-light-chain-phosphatase activity
G0:0035505	1	positive regulation of myosin light chain kinase activity
G0:0036352	1	histone H2A-K15 ubiquitination
G0:0035501	1	MH1 domain binding
G0:0035500	1	MH2 domain binding
G0:0061526	1	acetylcholine secretion
G0:0090274	1	positive regulation of somatostatin secretion
G0:0031997	1	N-terminal myristoylation domain binding
G0:0031998	1	regulation of fatty acid beta-oxidation
G0:1990124	1	messenger ribonucleoprotein complex
G0:0006256	1	UDP catabolic process
G0:0006258	1	UDP-glucose catabolic process
G0:0042131	1	thiamine phosphate phosphatase activity
G0:0006789	1	bilirubin conjugation
G0:0042564	1	NLS-dependent protein nuclear import complex
G0:0006781	1	succinyl-CoA pathway
G0:0006780	1	uroporphyrinogen III biosynthetic process
G0:0003947	1	(N-acetylneuraminy)-galactosylglucosylceramide N-acetylglactosaminyltransferase activity
G0:0000097	1	sulfur amino acid biosynthetic process
G0:0004782	1	sulfinioalanine decarboxylase activity
G0:0072124	1	regulation of glomerular mesangial cell proliferation
G0:0010248	1	establishment or maintenance of transmembrane electrochemical gradient
G0:1902824	1	positive regulation of late endosome to lysosome transport
G0:0090271	1	positive regulation of fibroblast growth factor production
G0:0006121	1	mitochondrial electron transport, succinate to ubiquinone
G0:0005252	1	open rectifier potassium channel activity
G0:0005527	1	macrolide binding
G0:0004123	1	cystathionine gamma-lyase activity
G0:0004122	1	cystathionine beta-synthase activity
G0:1902532	1	negative regulation of intracellular signal transduction
G0:0010657	1	muscle cell apoptotic process
G0:1902530	1	positive regulation of protein linear polyubiquitination
G0:0009789	1	positive regulation of abscisic acid-activated signaling pathway
G0:0010650	1	positive regulation of cell communication by electrical coupling
G0:0010651	1	negative regulation of cell communication by electrical coupling
G0:0046901	1	tetrahydrofolylpolyglutamate biosynthetic process
G0:0036351	1	histone H2A-K13 ubiquitination
G0:0001575	1	globoside metabolic process
G0:0046904	1	calcium oxalate binding
G0:0046906	1	tetrapyrrole binding
G0:0071963	1	establishment or maintenance of cell polarity regulating cell shape
G0:0036053	1	glomerular endothelium fenestra

G0:0008783	1	agmatinase activity
G0:0008785	1	alkyl hydroperoxide reductase activity
G0:0043997	1	histone acetyltransferase activity (H4-K12 specific)
G0:0035042	1	fertilization, exchange of chromosomal proteins
G0:0038030	1	non-canonical Wnt signaling pathway via MAPK cascade
G0:0032500	1	muramyl dipeptide binding
G0:0038038	1	G-protein coupled receptor homodimeric complex
G0:0033037	1	polysaccharide localization
G0:0052600	1	propane-1,3-diamine oxidase activity
G0:0035886	1	vascular smooth muscle cell differentiation
G0:0004876	1	complement component C3a receptor activity
G0:0016717	1	oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water
G0:0016716	1	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, another compound as one donor, and incorporation of one atom of oxygen
G0:0016711	1	flavonoid 3'-monooxygenase activity
G0:0000957	1	mitochondrial RNA catabolic process
G0:0000958	1	mitochondrial mRNA catabolic process
G0:0071389	1	cellular response to mineralocorticoid stimulus
G0:0072721	1	cellular response to dithiothreitol
G0:0043509	1	activin A complex
G0:0043501	1	skeletal muscle adaptation
G0:0045769	1	negative regulation of asymmetric cell division
G0:1901185	1	negative regulation of ERBB signaling pathway
G0:0034590	1	L-hydroxyproline transmembrane transporter activity
G0:0034595	1	phosphatidylinositol phosphate 5-phosphatase activity
G0:0060552	1	positive regulation of fructose 1,6-bisphosphate metabolic process
G0:0060001	1	minus-end directed microfilament motor activity
G0:0060550	1	positive regulation of fructose 1,6-bisphosphate 1-phosphatase activity
G0:0060004	1	reflex
G0:0060558	1	regulation of calcidiol 1-monooxygenase activity
G0:0032773	1	positive regulation of monophenol monooxygenase activity
G0:0034047	1	regulation of protein phosphatase type 2A activity
G0:0034041	1	sterol-transporting ATPase activity
G0:0034040	1	lipid-transporting ATPase activity
G0:0050923	1	regulation of negative chemotaxis
G0:0050928	1	negative regulation of positive chemotaxis
G0:0034048	1	negative regulation of protein phosphatase type 2A activity
G0:0032802	1	low-density lipoprotein particle receptor catabolic process
G0:0045830	1	positive regulation of isotype switching
G0:0009204	1	deoxyribonucleoside triphosphate catabolic process
G0:0009200	1	deoxyribonucleoside triphosphate metabolic process
G0:0046122	1	purine deoxyribonucleoside metabolic process
G0:0046121	1	deoxyribonucleoside catabolic process
G0:0048532	1	anatomical structure arrangement
G0:0047298	1	(S)-3-amino-2-methylpropionate transaminase activity
G0:2001311	1	lysobisphosphatidic acid metabolic process
G0:0035312	1	5'-3' exodeoxyribonuclease activity
G0:0065005	1	protein-lipid complex assembly
G0:0052381	1	tRNA dimethylallyltransferase activity
G0:0048250	1	mitochondrial iron ion transport
G0:0048259	1	regulation of receptor-mediated endocytosis
G0:0000133	1	polarisome
G0:0045160	1	myosin I complex
G0:0070813	1	hydrogen sulfide metabolic process
G0:0070815	1	peptidyl-lysine 5-dioxygenase activity
G0:0004334	1	fumarylacetoacetase activity
G0:0004336	1	galactosylceramidase activity
G0:0004333	1	fumarate hydratase activity
G0:0009346	1	citrate lyase complex
G0:0004339	1	glucan 1,4-alpha-glucosidase activity
G0:0014058	1	negative regulation of acetylcholine secretion, neurotransmission
G0:0009712	1	catechol-containing compound metabolic process
G0:0006863	1	purine nucleobase transport
G0:0006860	1	extracellular amino acid transport
G0:0045221	1	negative regulation of FasL biosynthetic process
G0:0070976	1	TIR domain binding
G0:0042924	1	neuromedin U binding
G0:0042922	1	neuromedin U receptor binding
G0:2000194	1	regulation of female gonad development
G0:2000191	1	regulation of fatty acid transport
G0:0015913	1	short-chain fatty acid import
G0:0061000	1	negative regulation of dendritic spine development
G0:0032263	1	GMP salvage

G0:0032261	1	purine nucleotide salvage
G0:0015361	1	low affinity sodium:dicarboxylate symporter activity
G0:0015362	1	high affinity sodium:dicarboxylate symporter activity
G0:0015367	1	oxoglutarate:malate antiporter activity
G0:0021902	1	commitment of neuronal cell to specific neuron type in forebrain
G0:0061599	1	molybdopterin molybdotransferase activity
G0:0021905	1	forebrain-midbrain boundary formation
G0:0004476	1	mannose-6-phosphate isomerase activity
G0:0051545	1	negative regulation of elastin biosynthetic process
G0:0051541	1	elastin metabolic process
G0:0051542	1	elastin biosynthetic process
G0:0015105	1	arsenite transmembrane transporter activity
G0:0010464	1	regulation of mesenchymal cell proliferation
G0:0048284	1	organelle fusion
G0:0019101	1	female somatic sex determination
G0:0019103	1	pyrimidine nucleotide binding
G0:0019107	1	myristoyltransferase activity
G0:0005889	1	hydrogen:potassium-exchanging ATPase complex
G0:0021509	1	roof plate formation
G0:0032994	1	protein-lipid complex
G0:0032990	1	cell part morphogenesis
G0:0002014	1	vasoconstriction of artery involved in ischemic response to lowering of systemic arterial blood pressure
G0:0033028	1	myeloid cell apoptotic process
G0:0033025	1	regulation of mast cell apoptotic process
G0:2000224	1	regulation of testosterone biosynthetic process
G0:2000225	1	negative regulation of testosterone biosynthetic process
G0:2000227	1	negative regulation of pancreatic A cell differentiation
G0:0051041	1	positive regulation of calcium-independent cell-cell adhesion
G0:1901641	1	ITP binding
G0:0034696	1	response to prostaglandin F
G0:0034699	1	response to luteinizing hormone
G0:0008747	1	N-acetylneuraminase lyase activity
G0:0030594	1	neurotransmitter receptor activity
G0:0061011	1	hepatic duct development
G0:0061015	1	snRNA import into nucleus
G0:0042320	1	regulation of circadian sleep/wake cycle, REM sleep
G0:0015055	1	secretin receptor activity
G0:0015054	1	gastrin receptor activity
G0:0000305	1	response to oxygen radical
G0:0000301	1	retrograde transport, vesicle recycling within Golgi
G0:2001034	1	positive regulation of double-strand break repair via nonhomologous end joining
G0:1900117	1	regulation of execution phase of apoptosis
G0:1903135	1	cupric ion binding
G0:1903136	1	cuprous ion binding
G0:0031315	1	extrinsic component of mitochondrial outer membrane
G0:0072143	1	mesangial cell development
G0:2000386	1	positive regulation of ovarian follicle development
G0:0010266	1	response to vitamin B1
G0:0010265	1	SCF complex assembly
G0:0097309	1	cap1 mRNA methylation
G0:0002190	1	cap-independent translational initiation
G0:0097305	1	response to alcohol
G0:0002194	1	hepatocyte cell migration
G0:0061597	1	cyclic pyranopterins monophosphate synthase activity
G0:1901723	1	negative regulation of cell proliferation involved in kidney development
G0:0005503	1	all-trans retinal binding
G0:0004102	1	choline O-acetyltransferase activity
G0:0051394	1	regulation of nerve growth factor receptor activity
G0:0004108	1	citrate (Si)-synthase activity
G0:2001108	1	positive regulation of Rho guanyl-nucleotide exchange factor activity
G0:0071228	1	cellular response to tumor cell
G0:0046921	1	alpha-(1->6)-fucosyltransferase activity
G0:1902511	1	negative regulation of apoptotic DNA fragmentation
G0:0036337	1	Fas signaling pathway
G0:0043265	1	ectoplasm
G0:0071947	1	protein deubiquitination involved in ubiquitin-dependent protein catabolic process
G0:2000057	1	negative regulation of Wnt signaling pathway involved in digestive tract morphogenesis
G0:2000055	1	positive regulation of Wnt signaling pathway involved in dorsal/ventral axis specification
G0:2000052	1	positive regulation of non-canonical Wnt signaling pathway
G0:2000058	1	regulation of protein ubiquitination involved in ubiquitin-dependent

protein catabolic process

G0:0021985	1	neurohypophysis development
G0:0007136	1	meiotic prophase II
G0:0032528	1	microvillus organization
G0:0008455	1	alpha-1,6-mannosylglycoprotein 2-beta-N-acetylglucosaminyltransferase activity
G0:0003374	1	dynamin polymerization involved in mitochondrial fission
G0:0008456	1	alpha-N-acetylgalactosaminidase activity
G0:0008452	1	RNA ligase activity
G0:0008458	1	carnitine 0-octanoyltransferase activity
G0:0070012	1	oligopeptidase activity
G0:0047323	1	[3-methyl-2-oxobutanoate dehydrogenase (acetyl-transferring)] kinase activity
G0:0042134	1	rRNA primary transcript binding
G0:0047325	1	inositol tetrakisphosphate 1-kinase activity
G0:1901895	1	negative regulation of calcium-transporting ATPase activity
G0:1901896	1	positive regulation of calcium-transporting ATPase activity
G0:0003011	1	involuntary skeletal muscle contraction
G0:0016598	1	protein arginylation
G0:0072703	1	cellular response to methyl methanesulfonate
G0:0016590	1	ACF complex
G0:0016596	1	thienylcyclohexylpiperidine binding
G0:0021590	1	cerebellum maturation
G0:0021599	1	abducens nerve formation
G0:1900275	1	negative regulation of phospholipase C activity
G0:0031304	1	intrinsic component of mitochondrial inner membrane
G0:0002426	1	immunoglobulin production in mucosal tissue
G0:0031306	1	intrinsic component of mitochondrial outer membrane
G0:0032581	1	ER-dependent peroxisome organization
G0:0044783	1	G1 DNA damage checkpoint
G0:0015919	1	peroxisomal membrane transport
G0:0015917	1	aminophospholipid transport
G0:0015910	1	peroxisomal long-chain fatty acid import
G0:0046327	1	glycerol biosynthetic process from pyruvate
G0:0002761	1	regulation of myeloid leukocyte differentiation
G0:0002763	1	positive regulation of myeloid leukocyte differentiation
G0:0002764	1	immune response-regulating signaling pathway
G0:0002769	1	natural killer cell inhibitory signaling pathway
G0:0042696	1	menarche
G0:0006426	1	glycyl-tRNA aminoacylation
G0:0006425	1	glutamyl-tRNA aminoacylation
G0:0006422	1	aspartyl-tRNA aminoacylation
G0:0034342	1	response to type III interferon
G0:0046148	1	pigment biosynthetic process
G0:0061485	1	memory T cell proliferation
G0:0035332	1	positive regulation of hippo signaling
G0:0052816	1	long-chain acyl-CoA hydrolase activity
G0:0060689	1	cell differentiation involved in salivary gland development
G0:0060683	1	regulation of branching involved in salivary gland morphogenesis by epithelial-mesenchymal signaling
G0:0060681	1	branch elongation involved in ureteric bud branching
G0:0052814	1	medium-chain-aldehyde dehydrogenase activity
G0:0086039	1	calcium-transporting ATPase activity involved in regulation of cardiac muscle cell membrane potential
G0:0048237	1	rough endoplasmic reticulum lumen
G0:0048232	1	male gamete generation
G0:0000110	1	nucleotide-excision repair factor 1 complex
G0:0048239	1	negative regulation of DNA recombination at telomere
G0:0045145	1	single-stranded DNA 5'-3' exodeoxyribonuclease activity
G0:0070839	1	divalent metal ion export
G0:0070835	1	chromium ion transmembrane transporter activity
G0:0042492	1	gamma-delta T cell differentiation
G0:0072080	1	nephron tubule development
G0:0006842	1	tricarboxylic acid transport
G0:0006844	1	acyl carnitine transport
G0:0045203	1	integral component of cell outer membrane
G0:0045209	1	MAPK phosphatase export from nucleus, leptomycin B sensitive
G0:0070489	1	T cell aggregation
G0:0022004	1	midbrain-hindbrain boundary maturation during brain development
G0:0070481	1	nuclear-transcribed mRNA catabolic process, non-stop decay
G0:0060931	1	sinoatrial node cell development
G0:0036055	1	protein-succinyllysine desuccinylase activity
G0:0015126	1	canalicular bile acid transmembrane transporter activity
G0:0001681	1	sialate O-acetyltransferase activity
G0:0015874	1	norepinephrine transport

G0:2000426	1	negative regulation of apoptotic cell clearance
G0:2000425	1	regulation of apoptotic cell clearance
G0:2000420	1	negative regulation of eosinophil extravasation
G0:0070228	1	regulation of lymphocyte apoptotic process
G0:0015876	1	acetyl-CoA transport
G0:0070224	1	sulfide:quinone oxidoreductase activity
G0:0015870	1	acetylcholine transport
G0:0007072	1	positive regulation of transcription on exit from mitosis
G0:0071283	1	cellular response to iron(III) ion
G0:0019408	1	dolichol biosynthetic process
G0:1901407	1	regulation of phosphorylation of RNA polymerase II C-terminal domain
G0:0033552	1	response to vitamin B3
G0:0042497	1	triacyl lipopeptide binding
G0:0035921	1	desmosome disassembly
G0:0035927	1	RNA import into mitochondrion
G0:0035926	1	chemokine (C-C motif) ligand 2 secretion
G0:0030209	1	dermatan sulfate catabolic process
G0:0004350	1	glutamate-5-semialdehyde dehydrogenase activity
G0:1901668	1	regulation of superoxide dismutase activity
G0:1901666	1	positive regulation of NAD+ ADP-ribosyltransferase activity
G0:1901660	1	calcium ion export
G0:0016476	1	regulation of embryonic cell shape
G0:0050677	1	positive regulation of urothelial cell proliferation
G0:0047159	1	1-alkenylglycerophosphocholine O-acyltransferase activity
G0:0005590	1	collagen type VII trimer
G0:0072573	1	tolerance induction to lipopolysaccharide
G0:0072572	1	poly-ADP-D-ribose binding
G0:0072574	1	hepatocyte proliferation
G0:0005597	1	collagen type XVI trimer
G0:0000323	1	lytic vacuole
G0:0005596	1	collagen type XIV trimer
G0:0043381	1	negative regulation of memory T cell differentiation
G0:0002489	1	antigen processing and presentation of endogenous peptide antigen via MHC class Ib via ER pathway, TAP-dependent
G0:0071839	1	apoptotic process in bone marrow
G0:1900138	1	negative regulation of phospholipase A2 activity
G0:0008689	1	3-demethylubiquinone-9 3-O-methyltransferase activity
G0:1900134	1	negative regulation of renin secretion into blood stream
G0:1900131	1	negative regulation of lipid binding
G0:0031338	1	regulation of vesicle fusion
G0:0060746	1	parental behavior
G0:0060217	1	hemangioblast cell differentiation
G0:0072168	1	specification of anterior mesonephric tubule identity
G0:0001187	1	RNA polymerase I CORE element sequence-specific DNA binding transcription factor recruiting transcription factor activity
G0:0097326	1	melanocyte adhesion
G0:0048934	1	peripheral nervous system neuron differentiation
G0:0009438	1	methylglyoxal metabolic process
G0:2001113	1	negative regulation of cellular response to hepatocyte growth factor stimulus
G0:2001294	1	malonyl-CoA catabolic process
G0:0048685	1	negative regulation of collateral sprouting of intact axon in response to injury
G0:0005290	1	L-histidine transmembrane transporter activity
G0:0048683	1	regulation of collateral sprouting of intact axon in response to injury
G0:0005298	1	proline:sodium symporter activity
G0:0004164	1	diphthine synthase activity
G0:0004168	1	dolichol kinase activity
G0:1902159	1	regulation of cyclic nucleotide-gated ion channel activity
G0:0090149	1	membrane fission involved in mitochondrial fission
G0:0036317	1	tyrosyl-RNA phosphodiesterase activity
G0:0046947	1	hydroxylysine biosynthetic process
G0:0046940	1	nucleoside monophosphate phosphorylation
G0:0046942	1	carboxylic acid transport
G0:0050144	1	nucleoside deoxyribosyltransferase activity
G0:0055073	1	cadmium ion homeostasis
G0:0006984	1	ER-nucleus signaling pathway
G0:0030047	1	actin modification
G0:0030046	1	parallel actin filament bundle assembly
G0:0003359	1	noradrenergic neuron fate commitment
G0:0003356	1	regulation of cilium beat frequency
G0:0000915	1	actomyosin contractile ring assembly
G0:0045414	1	regulation of interleukin-8 biosynthetic process
G0:0002875	1	negative regulation of chronic inflammatory response to antigenic stimulus
G0:0070037	1	rRNA (pseudouridine) methyltransferase activity

G0:0047305	1	(R)-3-amino-2-methylpropionate-pyruvate transaminase activity
G0:1901879	1	regulation of protein depolymerization
G0:0032011	1	ARF protein signal transduction
G0:0032542	1	sulfiredoxin activity
G0:0034263	1	autophagy in response to ER overload
G0:0019809	1	spermidine binding
G0:0019807	1	aspartoacylase activity
G0:0030817	1	regulation of cAMP biosynthetic process
G0:0015660	1	formate efflux transmembrane transporter activity
G0:1900225	1	regulation of NLRP3 inflammasome complex assembly
G0:0016312	1	inositol bisphosphate phosphatase activity
G0:0051610	1	serotonin uptake
G0:0051615	1	histamine uptake
G0:0033275	1	actin-myosin filament sliding
G0:0071073	1	positive regulation of phospholipid biosynthetic process
G0:0071072	1	negative regulation of phospholipid biosynthetic process
G0:0046167	1	glycerol-3-phosphate biosynthetic process
G0:0046166	1	glyceraldehyde-3-phosphate biosynthetic process
G0:0046164	1	alcohol catabolic process
G0:0030412	1	formimidoyltetrahydrofolate cyclodeaminase activity
G0:1990172	1	G-protein coupled receptor catabolic process
G0:0035684	1	helper T cell extravasation
G0:0060516	1	primary prostatic bud elongation
G0:0060517	1	epithelial cell proliferation involved in prostatic bud elongation
G0:0044232	1	organelle membrane contact site
G0:0035350	1	FAD transmembrane transport
G0:0061605	1	molybdopterin-synthase adenylyltransferase activity
G0:0061604	1	molybdopterin-synthase sulfurtransferase activity
G0:0042512	1	negative regulation of tyrosine phosphorylation of Stat1 protein
G0:0042516	1	regulation of tyrosine phosphorylation of Stat3 protein
G0:0006409	1	tRNA export from nucleus
G0:0052830	1	inositol-1,3,4,6-tetrakisphosphate 6-phosphatase activity
G0:0052831	1	inositol-1,3,4,6-tetrakisphosphate 1-phosphatase activity
G0:0003430	1	growth plate cartilage chondrocyte growth
G0:0006404	1	RNA import into nucleus
G0:0006157	1	deoxyadenosine catabolic process
G0:0048749	1	compound eye development
G0:0008112	1	nicotinamide N-methyltransferase activity
G0:0008113	1	peptide-methionine (S)-S-oxide reductase activity
G0:0018478	1	malonate-semialdehyde dehydrogenase (acetylating) activity
G0:0008116	1	prostaglandin-I synthase activity
G0:0008117	1	sphinganine-1-phosphate aldolase activity
G0:0005175	1	CD27 receptor binding
G0:1990422	1	glyoxalase (glycolic acid-forming) activity
G0:0004371	1	glycerone kinase activity
G0:0004807	1	triose-phosphate isomerase activity
G0:0004378	1	GDP-Man:Man1GlcNAc2-PP-Dol alpha-1,3-mannosyltransferase activity
G0:0004809	1	tRNA (guanine-N2-)-methyltransferase activity
G0:0070859	1	positive regulation of bile acid biosynthetic process
G0:1902749	1	regulation of cell cycle G2/M phase transition
G0:1902961	1	positive regulation of aspartic-type endopeptidase activity involved in amyloid precursor protein catabolic process
G0:1902960	1	negative regulation of aspartic-type endopeptidase activity involved in amyloid precursor protein catabolic process
G0:0008802	1	betaine-aldehyde dehydrogenase activity
G0:0008803	1	bis(5'-nucleosyl)-tetrakisphosphate (symmetrical) activity
G0:0016938	1	kinesin I complex
G0:0090168	1	Golgi reassembly
G0:0031453	1	positive regulation of heterochromatin assembly
G0:0048371	1	lateral mesodermal cell differentiation
G0:0014835	1	myoblast differentiation involved in skeletal muscle regeneration
G0:0032430	1	positive regulation of phospholipase A2 activity
G0:0007440	1	foregut morphogenesis
G0:0044214	1	fully spanning plasma membrane
G0:0015326	1	cationic amino acid transmembrane transporter activity
G0:0015320	1	phosphate ion carrier activity
G0:0018455	1	alcohol dehydrogenase [NAD(P)+] activity
G0:0001716	1	L-amino-acid oxidase activity
G0:0014810	1	positive regulation of skeletal muscle contraction by regulation of release of sequestered calcium ion
G0:0014812	1	muscle cell migration
G0:0014813	1	skeletal muscle satellite cell commitment
G0:0051580	1	regulation of neurotransmitter uptake
G0:0051585	1	negative regulation of dopamine uptake involved in synaptic transmission
G0:0051589	1	negative regulation of neurotransmitter transport

G0:0015495	1	gamma-aminobutyric acid:proton symporter activity
G0:0050197	1	phytanate-CoA ligase activity
G0:1990441	1	negative regulation of transcription from RNA polymerase II promoter in response to endoplasmic reticulum stress
G0:0015499	1	formate transmembrane transporter activity
G0:0036105	1	peroxisome membrane class-1 targeting sequence binding
G0:2000402	1	negative regulation of lymphocyte migration
G0:2000151	1	negative regulation of planar cell polarity pathway involved in cardiac muscle tissue morphogenesis
G0:2000156	1	regulation of retrograde vesicle-mediated transport, Golgi to ER
G0:2000157	1	negative regulation of ubiquitin-specific protease activity
G0:0090534	1	calcium ion-transporting ATPase complex
G0:0019145	1	aminobutyraldehyde dehydrogenase activity
G0:0005237	1	inhibitory extracellular ligand-gated ion channel activity
G0:0032957	1	inositol trisphosphate metabolic process
G0:0007057	1	spindle assembly involved in female meiosis I
G0:0050178	1	phenylpyruvate tautomerase activity
G0:0035907	1	dorsal aorta development
G0:0035904	1	aorta development
G0:0035112	1	genitalia morphogenesis
G0:0030887	1	positive regulation of myeloid dendritic cell activation
G0:0030883	1	endogenous lipid antigen binding
G0:0030882	1	lipid antigen binding
G0:0000036	1	ACP phosphopantetheine attachment site binding involved in fatty acid biosynthetic process
G0:0070001	1	aspartic-type peptidase activity
G0:1901684	1	arsenate ion transmembrane transport
G0:0043487	1	regulation of RNA stability
G0:0033682	1	ATP-dependent 5'-3' DNA/RNA helicase activity
G0:0016410	1	N-acyltransferase activity
G0:0045623	1	negative regulation of T-helper cell differentiation
G0:0045624	1	positive regulation of T-helper cell differentiation
G0:0047173	1	phosphatidylcholine-retinol O-acyltransferase activity
G0:0006233	1	dTDP biosynthetic process
G0:0004729	1	oxygen-dependent protoporphyrinogen oxidase activity
G0:1900483	1	regulation of protein targeting to vacuolar membrane
G0:0004724	1	magnesium-dependent protein serine/threonine phosphatase activity
G0:0042599	1	lamellar body
G0:1900155	1	negative regulation of bone trabecula formation
G0:1900158	1	negative regulation of bone mineralization involved in bone maturation
G0:1900159	1	positive regulation of bone mineralization involved in bone maturation
G0:0031682	1	G-protein gamma-subunit binding
G0:0031686	1	A1 adenosine receptor binding
G0:0090317	1	negative regulation of intracellular protein transport
G0:0050754	1	positive regulation of fractalkine biosynthetic process
G0:0005767	1	secondary lysosome
G0:0022851	1	GABA-gated chloride ion channel activity
G0:0097343	1	riposome assembly
G0:0051800	1	phosphatidylinositol-3,4-bisphosphate 3-phosphatase activity
G0:0004494	1	methylmalonyl-CoA mutase activity
G0:0004496	1	mevalonate kinase activity
G0:0004491	1	methylmalonate-semialdehyde dehydrogenase (acylating) activity
G0:0004490	1	methylglutaconyl-CoA hydratase activity
G0:0007618	1	mating
G0:0004492	1	methylmalonyl-CoA decarboxylase activity
G0:0004498	1	calcidiol 1-monooxygenase activity
G0:2000755	1	positive regulation of sphingomyelin catabolic process
G0:1902081	1	negative regulation of calcium ion import into sarcoplasmic reticulum
G0:0030620	1	U2 snRNA binding
G0:1902559	1	3'-phospho-5'-adenylyl sulfate transmembrane transport
G0:1902227	1	negative regulation of macrophage colony-stimulating factor signaling pathway
G0:0046964	1	3'-phosphoadenosine 5'-phosphosulfate transmembrane transporter activity
G0:0046963	1	3'-phosphoadenosine 5'-phosphosulfate transport
G0:0001512	1	dihydropyrimidinamide riboside quinone reductase activity
G0:0004835	1	tubulin-tyrosine ligase activity
G0:0036047	1	peptidyl-lysine demalonylation
G0:0048002	1	antigen processing and presentation of peptide antigen
G0:0036414	1	histone citrullination
G0:0048006	1	antigen processing and presentation, endogenous lipid antigen via MHC class Ib
G0:0000701	1	purine-specific mismatch base pair DNA N-glycosylase activity
G0:0000703	1	oxidized pyrimidine nucleobase lesion DNA N-glycosylase activity
G0:0004639	1	phosphoribosylaminoimidazolesuccinocarboxamide synthase activity
G0:0004638	1	phosphoribosylaminoimidazole carboxylase activity

G0:0004149	1	dihydrolipoyllysine-residue succinyltransferase activity
G0:0004148	1	dihydrolipoyl dehydrogenase activity
G0:0004631	1	phosphomevalonate kinase activity
G0:0004633	1	phosphopantothenoylcysteine decarboxylase activity
G0:0004637	1	phosphoribosylamine-glycine ligase activity
G0:0033557	1	Slx1-Slx4 complex
G0:0008495	1	protoheme IX farnesyltransferase activity
G0:0060980	1	cell migration involved in coronary vasculogenesis
G0:1903073	1	negative regulation of death-inducing signaling complex assembly
G0:0001971	1	negative regulation of activation of membrane attack complex
G0:0070055	1	HAC1-type intron splice site recognition and cleavage
G0:0060987	1	lipid tube
G0:2000368	1	positive regulation of acrosomal vesicle exocytosis
G0:1901856	1	negative regulation of cellular respiration
G0:2000363	1	positive regulation of prostaglandin-E synthase activity
G0:0051248	1	negative regulation of protein metabolic process
G0:0051249	1	regulation of lymphocyte activation
G0:0072061	1	inner medullary collecting duct development
G0:0032561	1	guanyl ribonucleotide binding
G0:0050038	1	L-xylulose reductase (NADP+) activity
G0:0010769	1	regulation of cell morphogenesis involved in differentiation
G0:0032567	1	dGTP binding
G0:0010760	1	negative regulation of macrophage chemotaxis
G0:0010767	1	regulation of transcription from RNA polymerase II promoter in response to
UV-induced	DNA damage	
G0:0034243	1	regulation of transcription elongation from RNA polymerase II promoter
G0:0033746	1	histone demethylase activity (H3-R2 specific)
G0:0033961	1	cis-stilbene-oxide hydrolase activity
G0:0034240	1	negative regulation of macrophage fusion
G0:0033749	1	histone demethylase activity (H4-R3 specific)
G0:0021771	1	lateral geniculate nucleus development
G0:0021779	1	oligodendrocyte cell fate commitment
G0:0002460	1	adaptive immune response based on somatic recombination of immune
receptors built from	immunoglobulin superfamily domains	
G0:0015684	1	ferrous iron transport
G0:0047369	1	succinate-hydroxymethylglutarate CoA-transferase activity
G0:0071893	1	BMP signaling pathway involved in nephric duct formation
G0:0071894	1	histone H2B conserved C-terminal lysine ubiquitination
G0:0016332	1	establishment or maintenance of polarity of embryonic epithelium
G0:0046368	1	GDP-L-fucose metabolic process
G0:0051639	1	actin filament network formation
G0:0002729	1	positive regulation of natural killer cell cytokine production
G0:0002721	1	regulation of B cell cytokine production
G0:0038184	1	cell surface bile acid receptor signaling pathway
G0:0038185	1	intracellular bile acid receptor signaling pathway
G0:0038186	1	lithocholic acid receptor activity
G0:0038182	1	G-protein coupled bile acid receptor activity
G0:0038183	1	bile acid signaling pathway
G0:1901142	1	insulin metabolic process
G0:1901143	1	insulin catabolic process
G0:0042356	1	GDP-4-dehydro-D-rhamnose reductase activity
G0:0048520	1	positive regulation of behavior
G0:0043299	1	leukocyte degranulation
G0:0060534	1	trachea cartilage development
G0:0060537	1	muscle tissue development
G0:0006393	1	termination of mitochondrial transcription
G0:0035378	1	carbon dioxide transmembrane transport
G0:0035379	1	carbon dioxide transmembrane transporter activity
G0:0035373	1	chondroitin sulfate proteoglycan binding
G0:0035375	1	zymogen binding
G0:0035377	1	transepithelial water transport
G0:0061627	1	S-methylmethionine-homocysteine S-methyltransferase activity
G0:0061626	1	pharyngeal arch artery morphogenesis
G0:0042534	1	regulation of tumor necrosis factor biosynthetic process
G0:0009841	1	mitochondrial endopeptidase Clp complex
G0:0044726	1	protection of DNA demethylation of female pronucleus
G0:0006178	1	guanine salvage
G0:0006173	1	dADP biosynthetic process
G0:0005157	1	macrophage colony-stimulating factor receptor binding
G0:0045185	1	maintenance of protein location
G0:0045183	1	translation factor activity, non-nucleic acid binding
G0:0032344	1	regulation of aldosterone metabolic process
G0:0042450	1	arginine biosynthetic process via ornithine
G0:0047977	1	hepoxilin-epoxide hydrolase activity
G0:0045189	1	connective tissue growth factor biosynthetic process

G0:0004824	1	lysine-tRNA ligase activity
G0:0004820	1	glycine-tRNA ligase activity
G0:0060390	1	regulation of SMAD protein import into nucleus
G0:1902943	1	positive regulation of voltage-gated chloride channel activity
G0:1902947	1	regulation of tau-protein kinase activity
G0:1902946	1	protein localization to early endosome
G0:1902949	1	positive regulation of tau-protein kinase activity
G0:1902948	1	negative regulation of tau-protein kinase activity
G0:0042988	1	Xll-like protein binding
G0:0042984	1	regulation of amyloid precursor protein biosynthetic process
G0:0046909	1	intermembrane transport
G0:0090107	1	regulation of high-density lipoprotein particle assembly
G0:0090101	1	negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway
G0:0090108	1	positive regulation of high-density lipoprotein particle assembly
G0:0051033	1	RNA transmembrane transporter activity
G0:0051036	1	regulation of endosome size
G0:0051039	1	positive regulation of transcription during meiosis
G0:0050201	1	fucokinase activity
G0:0036292	1	DNA rewinding
G0:0060896	1	neural plate pattern specification
G0:0010481	1	epidermal cell division
G0:0001704	1	formation of primary germ layer
G0:0070092	1	regulation of glucagon secretion
G0:2000176	1	positive regulation of pro-T cell differentiation
G0:2000172	1	regulation of branching morphogenesis of a nerve
G0:0070265	1	necrotic cell death
G0:0070091	1	glucagon secretion
G0:0070260	1	5'-tyrosyl-DNA phosphodiesterase activity
G0:0070262	1	peptidyl-serine dephosphorylation
G0:0032972	1	regulation of muscle filament sliding speed
G0:0070268	1	cornification
G0:0006660	1	phosphatidylserine catabolic process
G0:0070094	1	positive regulation of glucagon secretion
G0:1901339	1	regulation of store-operated calcium channel activity
G0:2000287	1	positive regulation of myotome development
G0:0033514	1	L-lysine catabolic process to acetyl-CoA via L-pipecolate
G0:0008531	1	riboflavin kinase activity
G0:0035967	1	cellular response to topologically incorrect protein
G0:0006214	1	thymidine catabolic process
G0:0032600	1	chemokine receptor transport out of membrane raft
G0:0032607	1	interferon-alpha production
G0:0043311	1	positive regulation of eosinophil degranulation
G0:0043310	1	negative regulation of eosinophil degranulation
G0:0043461	1	proton-transporting ATP synthase complex assembly
G0:0072684	1	mitochondrial tRNA 3'-trailer cleavage, endonucleolytic
G0:0072687	1	meiotic spindle
G0:0045601	1	regulation of endothelial cell differentiation
G0:0045607	1	regulation of auditory receptor cell differentiation
G0:0005310	1	dicarboxylic acid transmembrane transporter activity
G0:0045609	1	positive regulation of auditory receptor cell differentiation
G0:0048075	1	positive regulation of eye pigmentation
G0:0071133	1	alpha9-beta1 integrin-ADAM8 complex
G0:0047117	1	enoyl-[acyl-carrier-protein] reductase (NADPH, A-specific) activity
G0:0000823	1	inositol-1,4,5-trisphosphate 6-kinase activity
G0:0005316	1	high affinity inorganic phosphate:sodium symporter activity
G0:0071418	1	cellular response to amine stimulus
G0:0000435	1	positive regulation of transcription from RNA polymerase II promoter by galactose
G0:0031118	1	rRNA pseudouridine synthesis
G0:0034766	1	negative regulation of ion transmembrane transport
G0:0034767	1	positive regulation of ion transmembrane transport
G0:0034763	1	negative regulation of transmembrane transport
G0:0097102	1	endothelial tip cell fate specification
G0:0097101	1	blood vessel endothelial cell fate specification
G0:0097100	1	supercoiled DNA binding
G0:1900175	1	regulation of nodal signaling pathway involved in determination of lateral mesoderm left/right asymmetry
G0:0035581	1	sequestering of extracellular ligand from receptor
G0:0051796	1	negative regulation of catagen
G0:0051790	1	short-chain fatty acid biosynthetic process
G0:0051793	1	medium-chain fatty acid catabolic process
G0:0060709	1	glycogen cell differentiation involved in embryonic placenta development
G0:0010972	1	negative regulation of G2/M transition of mitotic cell cycle
G0:0010970	1	microtubule-based transport

G0:0046645	1	positive regulation of gamma-delta T cell activation
G0:0097369	1	sodium ion import
G0:0097368	1	establishment of Sertoli cell barrier
G0:2000761	1	positive regulation of N-terminal peptidyl-lysine acetylation
G0:0097362	1	MCM8-MCM9 complex
G0:0051866	1	general adaptation syndrome
G0:0051867	1	general adaptation syndrome, behavioral process
G0:0090071	1	negative regulation of ribosome biogenesis
G0:0007634	1	optokinetic behavior
G0:0006617	1	SRP-dependent cotranslational protein targeting to membrane, signal
sequence recognition		
G0:0006616	1	SRP-dependent cotranslational protein targeting to membrane, translocation
G0:0036468	1	L-dopa decarboxylase activity
G0:1902204	1	positive regulation of hepatocyte growth factor receptor signaling pathway
G0:0048392	1	intermediate mesodermal cell differentiation
G0:0047016	1	cholest-5-ene-3-beta,7-alpha-diol 3-beta-dehydrogenase activity
G0:0045048	1	protein insertion into ER membrane
G0:0045041	1	protein import into mitochondrial intermembrane space
G0:0043916	1	DNA-7-methylguanine glycosylase activity
G0:0006948	1	induction by virus of host cell-cell fusion
G0:0000725	1	recombinational repair
G0:0004610	1	phosphoacetylglucosamine mutase activity
G0:0004617	1	phosphoglycerate dehydrogenase activity
G0:0018171	1	peptidyl-cysteine oxidation
G0:0060562	1	epithelial tube morphogenesis
G0:0070072	1	vacuolar proton-transporting V-type ATPase complex assembly
G0:0070076	1	histone lysine demethylation
G0:0006175	1	dATP biosynthetic process
G0:0070078	1	histone H3-R2 demethylation
G0:0070079	1	histone H4-R3 demethylation
G0:0034971	1	histone H3-R17 methylation
G0:1900133	1	regulation of renin secretion into blood stream
G0:2000340	1	positive regulation of chemokine (C-X-C motif) ligand 1 production
G0:2000615	1	regulation of histone H3-K9 acetylation
G0:2000617	1	positive regulation of histone H3-K9 acetylation
G0:0021572	1	rhombomere 6 development
G0:2000348	1	regulation of CD40 signaling pathway
G0:0051264	1	mono-olein transacylation activity
G0:0051265	1	diolein transacylation activity
G0:0051267	1	CP2 mannose-ethanolamine phosphotransferase activity
G0:0042214	1	terpene metabolic process
G0:0010747	1	positive regulation of plasma membrane long-chain fatty acid transport
G0:2000584	1	negative regulation of platelet-derived growth factor receptor-alpha
signaling pathway		
G0:0021758	1	putamen development
G0:0021757	1	caudate nucleus development
G0:0002448	1	mast cell mediated immunity
G0:0002443	1	leukocyte mediated immunity
G0:0060847	1	endothelial cell fate specification
G0:0071301	1	cellular response to vitamin B1
G0:0060212	1	negative regulation of nuclear-transcribed mRNA poly(A) tail shortening
G0:0046341	1	CDP-diacylglycerol metabolic process
G0:0046439	1	L-cysteine metabolic process
G0:0080146	1	L-cysteine desulphydrase activity
G0:0072169	1	specification of posterior mesonephric tubule identity
G0:0051656	1	establishment of organelle localization
G0:0051651	1	maintenance of location in cell
G0:0034516	1	response to vitamin B6
G0:1990134	1	epithelial cell apoptotic process involved in palatal shelf morphogenesis
G0:1990136	1	linoleate 9S-lipoxygenase activity
G0:0001189	1	RNA polymerase I transcriptional preinitiation complex assembly at the
promoter for the nuclear large rRNA transcript		
G0:0048560	1	establishment of anatomical structure orientation
G0:0035397	1	helper T cell enhancement of adaptive immune response
G0:0017005	1	3'-tyrosyl-DNA phosphodiesterase activity
G0:0033233	1	regulation of protein sumoylation
G0:0086023	1	adrenergic receptor signaling pathway involved in heart process
G0:0052872	1	tocotrienol omega-hydroxylase activity
G0:0086024	1	adrenergic receptor signaling pathway involved in positive regulation of
heart rate		
G0:0042558	1	pteridine-containing compound metabolic process
G0:0042559	1	pteridine-containing compound biosynthetic process
G0:0006117	1	acetaldehyde metabolic process
G0:0005136	1	interleukin-4 receptor binding
G0:0005139	1	interleukin-7 receptor binding

G0:0070892	1	lipoteichoic acid receptor activity
G0:0047915	1	ganglioside galactosyltransferase activity
G0:0042431	1	indole metabolic process
G0:0090296	1	regulation of mitochondrial DNA replication
G0:0090297	1	positive regulation of mitochondrial DNA replication
G0:0050659	1	N-acetylgalactosamine 4-sulfate 6-O-sulfotransferase activity
G0:0039702	1	viral budding via host ESCRT complex
G0:0090298	1	negative regulation of mitochondrial DNA replication
G0:0050655	1	dermatan sulfate proteoglycan metabolic process
G0:2000313	1	regulation of fibroblast growth factor receptor signaling pathway involved in neural plate anterior/posterior pattern formation
G0:0090128	1	regulation of synapse maturation
G0:0008554	1	sodium-exporting ATPase activity, phosphorylative mechanism
G0:0009399	1	nitrogen fixation
G0:0009398	1	FMN biosynthetic process
G0:2001202	1	negative regulation of transforming growth factor-beta secretion
G0:0008555	1	chloride-transporting ATPase activity
G0:0003944	1	N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase activity
G0:0051012	1	microtubule sliding
G0:0008123	1	cholesterol 7-alpha-monooxygenase activity
G0:0005165	1	neurotrophin receptor binding
G0:0007400	1	neuroblast fate determination
G0:0018364	1	peptidyl-glutamine methylation
G0:0050046	1	lathosterol oxidase activity
G0:0008109	1	N-acetylglucosaminide beta-1,6-N-acetylglucosaminyltransferase activity
G0:0010714	1	positive regulation of collagen metabolic process
G0:0010711	1	negative regulation of collagen catabolic process
G0:0015182	1	L-asparagine transmembrane transporter activity
G0:0036146	1	cellular response to mycotoxin
G0:0036143	1	kringle domain binding
G0:0036140	1	peptidyl-asparagine 3-dioxygenase activity
G0:0036141	1	L-phenylalanine-oxaloacetate transaminase activity
G0:0015052	1	beta3-adrenergic receptor activity
G0:0032919	1	spermine acetylation
G0:0032916	1	positive regulation of transforming growth factor beta3 production
G0:0032913	1	negative regulation of transforming growth factor beta3 production
G0:0004349	1	glutamate 5-kinase activity
G0:0018585	1	fluorene oxygenase activity
G0:0016638	1	oxidoreductase activity, acting on the CH-NH2 group of donors
G0:0008513	1	secondary active organic cation transmembrane transporter activity
G0:0014858	1	positive regulation of skeletal muscle cell proliferation
G0:0014853	1	regulation of excitatory postsynaptic membrane potential involved in skeletal muscle contraction
G0:0004347	1	glucose-6-phosphate isomerase activity
G0:0014856	1	skeletal muscle cell proliferation
G0:0015728	1	mevalonate transport
G0:0032621	1	interleukin-18 production
G0:0032620	1	interleukin-17 production
G0:0047757	1	chondroitin-glucuronate 5-epimerase activity
G0:0015724	1	formate transport
G0:0047280	1	nicotinamide phosphoribosyltransferase activity
G0:0047288	1	monosialoganglioside sialyltransferase activity
G0:0016189	1	synaptic vesicle to endosome fusion
G0:0047710	1	bis(5'-adenosyl)-triphosphatase activity
G0:0002676	1	regulation of chronic inflammatory response
G0:0070247	1	regulation of natural killer cell apoptotic process
G0:0047134	1	protein-disulfide reductase activity
G0:0071110	1	histone biotinylation
G0:0072254	1	metanephric glomerular mesangial cell differentiation
G0:0047131	1	saccharopine dehydrogenase (NAD+, L-glutamate-forming) activity
G0:0047130	1	saccharopine dehydrogenase (NADP+, L-lysine-forming) activity
G0:0072255	1	metanephric glomerular mesangial cell development
G0:0034164	1	negative regulation of toll-like receptor 9 signaling pathway
G0:0070176	1	DRM complex
G0:2000802	1	positive regulation of endocardial cushion to mesenchymal transition involved in heart valve formation
G0:0019983	1	interleukin-9 binding
G0:0019982	1	interleukin-7 binding
G0:0030845	1	phospholipase C-inhibiting G-protein coupled receptor signaling pathway
G0:0030844	1	positive regulation of intermediate filament depolymerization
G0:0050823	1	peptide antigen stabilization
G0:0034705	1	potassium channel complex
G0:0034702	1	ion channel complex
G0:0050827	1	toxin receptor binding

G0:0046080	1	dUTP metabolic process
G0:0050828	1	regulation of liquid surface tension
G0:0046083	1	adenine metabolic process
G0:0050221	1	prostaglandin-E2 9-reductase activity
G0:0046086	1	adenosine biosynthetic process
G0:0004163	1	diphosphomevalonate decarboxylase activity
G0:1900195	1	positive regulation of oocyte maturation
G0:0097165	1	nuclear stress granule
G0:0097161	1	DH domain binding
G0:0097162	1	MADS box domain binding
G0:0061090	1	positive regulation of sequestering of zinc ion
G0:0007321	1	sperm displacement
G0:0090350	1	negative regulation of cellular organofluorine metabolic process
G0:0006585	1	dopamine biosynthetic process from tyrosine
G0:0097383	1	dIDP diphosphatase activity
G0:0022894	1	Intermediate conductance calcium-activated potassium channel activity
G0:0002114	1	interleukin-33 receptor activity
G0:0071378	1	cellular response to growth hormone stimulus
G0:0009134	1	nucleoside diphosphate catabolic process
G0:0046949	1	fatty-acyl-CoA biosynthetic process
G0:1901751	1	leukotriene A4 metabolic process
G0:1902044	1	regulation of Fas signaling pathway
G0:1902045	1	negative regulation of Fas signaling pathway
G0:0006639	1	acylglycerol metabolic process
G0:0016971	1	flavin-linked sulfhydryl oxidase activity
G0:0036444	1	calcium ion import into mitochondrion
G0:0005585	1	collagen type II trimer
G0:0005582	1	collagen type XV trimer
G0:0032408	1	MutSbeta complex binding
G0:0046943	1	carboxylic acid transmembrane transporter activity
G0:0031393	1	negative regulation of prostaglandin biosynthetic process
G0:2001186	1	negative regulation of CD8-positive, alpha-beta T cell activation
G0:1902261	1	positive regulation of delayed rectifier potassium channel activity
G0:0060699	1	regulation of endoribonuclease activity
G0:1902598	1	creatine transmembrane transport
G0:1902268	1	negative regulation of polyamine transmembrane transport
G0:0031074	1	nucleocytoplasmic shuttling complex
G0:0045062	1	extrathymic T cell selection
G0:0000296	1	spermine transport
G0:0045065	1	cytotoxic T cell differentiation
G0:0004454	1	ketohexokinase activity
G0:0004457	1	lactate dehydrogenase activity
G0:0004458	1	D-lactate dehydrogenase (cytochrome) activity
G0:0048040	1	UDP-glucuronate decarboxylase activity
G0:0086094	1	positive regulation of ryanodine-sensitive calcium-release channel activity by adrenergic receptor signaling pathway involved in positive regulation of cardiac muscle contraction
G0:0031531	1	thyrotropin-releasing hormone receptor binding
G0:0004676	1	3-phosphoinositide-dependent protein kinase activity
G0:0004671	1	protein C-terminal S-isoprenylcysteine carboxyl O-methyltransferase activity
G0:0004673	1	protein histidine kinase activity
G0:0018114	1	threonine racemase activity
G0:0018117	1	protein adenylation
G0:2000845	1	positive regulation of testosterone secretion
G0:0034959	1	endothelin maturation
G0:2000327	1	positive regulation of ligand-dependent nuclear receptor transcription coactivator activity
G0:2000326	1	negative regulation of ligand-dependent nuclear receptor transcription coactivator activity
G0:2000320	1	negative regulation of T-helper 17 cell differentiation
G0:0021511	1	spinal cord patterning
G0:0021512	1	spinal cord anterior/posterior patterning
G0:0060912	1	cardiac cell fate specification
G0:0051204	1	protein insertion into mitochondrial membrane
G0:0090435	1	protein localization to nuclear envelope
G0:0010725	1	regulation of primitive erythrocyte differentiation
G0:0010722	1	regulation of ferrochelatase activity
G0:0010721	1	negative regulation of cell development
G0:0010729	1	positive regulation of hydrogen peroxide biosynthetic process
G0:0019646	1	aerobic electron transport chain
G0:0060690	1	epithelial cell differentiation involved in salivary gland development
G0:0002932	1	tendon sheath development
G0:0007371	1	ventral midline determination
G0:0071329	1	cellular response to sucrose stimulus

G0:0044708	1	single-organism behavior
G0:0001912	1	positive regulation of leukocyte mediated cytotoxicity
G0:2000639	1	negative regulation of SREBP signaling pathway
G0:0001910	1	regulation of leukocyte mediated cytotoxicity
G0:0001914	1	regulation of T cell mediated cytotoxicity
G0:0001918	1	farnesylated protein binding
G0:0051673	1	membrane disruption in other organism
G0:0030802	1	regulation of cyclic nucleotide biosynthetic process
G0:2000513	1	positive regulation of granzyme A production
G0:0035150	1	regulation of tube size
G0:0035623	1	renal glucose absorption
G0:0030472	1	mitotic spindle organization in nucleus
G0:0035621	1	ER to Golgi ceramide transport
G0:0035627	1	ceramide transport
G0:0035624	1	receptor transactivation
G0:0061400	1	positive regulation of transcription from RNA polymerase II promoter in response to calcium ion
G0:0003186	1	tricuspid valve morphogenesis
G0:0003185	1	sinoatrial valve morphogenesis
G0:0060601	1	lateral sprouting from an epithelium
G0:0017020	1	myosin phosphatase regulator activity
G0:0033878	1	hormone-sensitive lipase activity
G0:0086007	1	voltage-gated calcium channel activity involved in cardiac muscle cell action potential
G0:0033871	1	[heparan sulfate]-glucosamine 3-sulfotransferase 2 activity
G0:0043167	1	ion binding
G0:0016232	1	HNK-1 sulfotransferase activity
G0:1903052	1	positive regulation of proteolysis involved in cellular protein catabolic process
G0:1903056	1	regulation of melanosome organization
G0:0031703	1	type 2 angiotensin receptor binding
G0:0042414	1	epinephrine metabolic process
G0:0042413	1	carnitine catabolic process
G0:0072003	1	kidney rudiment formation
G0:0031708	1	endothelin B receptor binding
G0:0047939	1	L-glucuronate reductase activity
G0:0050674	1	urothelial cell proliferation
G0:0015887	1	pantothenate transmembrane transport
G0:0015881	1	creatine transport
G0:0060138	1	fetal process involved in parturition
G0:0002329	1	pre-B cell differentiation
G0:0005115	1	receptor tyrosine kinase-like orphan receptor binding
G0:0002327	1	immature B cell differentiation
G0:0002055	1	adenine binding
G0:0001698	1	gastrin-induced gastric acid secretion
G0:0009115	1	xanthine catabolic process
G0:0001011	1	sequence-specific DNA binding RNA polymerase recruiting transcription factor activity
G0:0008479	1	queuine tRNA-ribosyltransferase activity
G0:0008478	1	pyridoxal kinase activity
G0:0001743	1	optic placode formation
G0:2000137	1	negative regulation of cell proliferation involved in heart morphogenesis
G0:0043890	1	N-acetylgalactosamine-6-sulfatase activity
G0:0005221	1	intracellular cyclic nucleotide activated cation channel activity
G0:0008120	1	ceramide glucosyltransferase activity
G0:0008470	1	isovaleryl-CoA dehydrogenase activity
G0:0032423	1	regulation of mismatch repair
G0:0032425	1	positive regulation of mismatch repair
G0:0032396	1	inhibitory MHC class I receptor activity
G0:0032399	1	HECT domain binding
G0:0032938	1	negative regulation of translation in response to oxidative stress
G0:1901373	1	lipid hydroperoxide transport
G0:0003213	1	cardiac right atrium morphogenesis
G0:0016618	1	hydroxypyruvate reductase activity
G0:0000917	1	barrier septum assembly
G0:0008579	1	JUN kinase phosphatase activity
G0:1990442	1	intrinsic apoptotic signaling pathway in response to nitrosative stress
G0:0019343	1	cysteine biosynthetic process via cystathionine
G0:0019341	1	dibenzo-p-dioxin catabolic process
G0:0015707	1	nitrite transport
G0:0015706	1	nitrate transport
G0:0045932	1	negative regulation of muscle contraction
G0:2000798	1	negative regulation of amniotic stem cell differentiation
G0:1990256	1	signal clustering
G0:2000795	1	negative regulation of epithelial cell proliferation involved in lung

morphogenesis		
G0:0043423	1	3-phosphoinositide-dependent protein kinase binding
G0:2000793	1	cell proliferation involved in heart valve development
G0:0001697	1	histamine-induced gastric acid secretion
G0:0052884	1	all-trans-retinyl-palmitate hydrolase, 11-cis retinol forming activity
G0:0045645	1	positive regulation of eosinophil differentiation
G0:0070512	1	positive regulation of histone H4-K20 methylation
G0:0004731	1	purine-nucleoside phosphorylase activity
G0:0021650	1	vestibulocochlear nerve formation
G0:0034148	1	negative regulation of toll-like receptor 5 signaling pathway
G0:1900425	1	negative regulation of defense response to bacterium
G0:0030865	1	cortical cytoskeleton organization
G0:1990259	1	histone-glutamine methyltransferase activity
G0:0034728	1	nucleosome organization
G0:0050809	1	diazepam binding
G0:1901873	1	regulation of post-translational protein modification
G0:0034722	1	gamma-glutamyl-peptidase activity
G0:0086075	1	gap junction channel activity involved in cardiac conduction electrical coupling
G0:0002196	1	Ser-tRNA(Ala) hydrolase activity
G0:0097350	1	neutrophil clearance
G0:0002154	1	thyroid hormone mediated signaling pathway
G0:0097141	1	BIM-BCL-2 complex
G0:0097140	1	BIM-BCL-xl complex
G0:0010939	1	regulation of necrotic cell death
G0:0010934	1	macrophage cytokine production
G0:0010933	1	positive regulation of macrophage tolerance induction
G0:0046604	1	positive regulation of mitotic centrosome separation
G0:0046605	1	regulation of centrosome cycle
G0:0046601	1	positive regulation of centriole replication
G0:0033823	1	procollagen glucosyltransferase activity
G0:0002135	1	CTP binding
G0:0030393	1	fructoselysine metabolic process
G0:2001213	1	negative regulation of vasculogenesis
G0:0032945	1	negative regulation of mononuclear cell proliferation
G0:1903190	1	glyoxal catabolic process
G0:1903197	1	positive regulation of L-dopa biosynthetic process
G0:0036393	1	thiocyanate peroxidase activity
G0:0036399	1	TCR signalosome assembly
G0:0036398	1	TCR signalosome
G0:0045004	1	DNA replication proofreading
G0:0004479	1	methionyl-tRNA formyltransferase activity
G0:0005308	1	creatine transmembrane transporter activity
G0:0005309	1	creatine:sodium symporter activity
G0:0005302	1	L-tyrosine transmembrane transporter activity
G0:0008963	1	phospho-N-acetylmuramoyl-pentapeptide-transferase activity
G0:0008746	1	NAD(P)+ transhydrogenase activity
G0:0008967	1	phosphoglycolate phosphatase activity
G0:0042602	1	riboflavin reductase (NADPH) activity
G0:0004657	1	proline dehydrogenase activity
G0:0031515	1	tRNA (m1A) methyltransferase complex
G0:0004655	1	porphobilinogen synthase activity
G0:0004654	1	polyribonucleotide nucleotidyltransferase activity
G0:0031510	1	SUMO activating enzyme complex
G0:0045660	1	positive regulation of neutrophil differentiation
G0:0031700	1	adrenomedullin receptor binding
G0:0044356	1	clearance of foreign intracellular DNA by conversion of DNA cytidine to uridine
G0:0061149	1	BMP signaling pathway involved in ureter morphogenesis
G0:0021935	1	cerebellar granule cell precursor tangential migration
G0:0019088	1	immortalization of host cell by virus
G0:0019089	1	transmission of virus
G0:0021534	1	cell proliferation in hindbrain
G0:0021539	1	subthalamus development
G0:0006304	1	DNA modification
G0:0090416	1	nicotinate transporter activity
G0:0032097	1	positive regulation of response to food
G0:0007231	1	osmosensory signaling pathway
G0:0001682	1	tRNA 5'-leader removal
G0:0001680	1	tRNA 3'-terminal CCA addition
G0:0019883	1	antigen processing and presentation of endogenous antigen
G0:0019884	1	antigen processing and presentation of exogenous antigen
G0:0019888	1	protein phosphatase regulator activity
G0:0070164	1	negative regulation of adiponectin secretion
G0:0002485	1	antigen processing and presentation of endogenous peptide antigen via MHC

class I via ER pathway, TAP-dependent

G0:0044729 1 hemi-methylated DNA-binding

G0:0044721 1 protein import into peroxisome matrix, substrate release

G0:0044727 1 DNA demethylation of male pronucleus

G0:1901296 1 negative regulation of canonical Wnt signaling pathway involved in cardiac muscle cell fate commitment

G0:1901740 1 negative regulation of myoblast fusion

G0:2000308 1 negative regulation of tumor necrosis factor (ligand) superfamily member 11 production

G0:2000655 1 negative regulation of cellular response to testosterone stimulus

G0:2000657 1 negative regulation of apolipoprotein binding

G0:2000303 1 regulation of ceramide biosynthetic process

G0:2000302 1 positive regulation of synaptic vesicle exocytosis

G0:0038121 1 C-C motif chemokine 21 receptor activity

G0:1901128 1 gentamycin metabolic process

G0:0005673 1 transcription factor TFIIE complex

G0:0051958 1 methotrexate transport

G0:0033273 1 response to vitamin

G0:0043269 1 regulation of ion transport

G0:0021793 1 chemorepulsion of branchiomotor axon

G0:0097476 1 spinal cord motor neuron migration

G0:0035604 1 fibroblast growth factor receptor signaling pathway involved in positive regulation of cell proliferation in bone marrow

G0:0035605 1 peptidyl-cysteine S-nitrosylase activity

G0:0035606 1 peptidyl-cysteine S-trans-nitrosylation

G0:0061469 1 regulation of type B pancreatic cell proliferation

G0:0035602 1 fibroblast growth factor receptor signaling pathway involved in negative regulation of apoptotic process in bone marrow

G0:0035603 1 fibroblast growth factor receptor signaling pathway involved in hemopoiesis

G0:0061467 1 basolateral protein localization

G0:0014734 1 skeletal muscle hypertrophy

G0:0014737 1 positive regulation of muscle atrophy

G0:0018964 1 propylene metabolic process

G0:0046479 1 glycosphingolipid catabolic process

G0:0046473 1 phosphatidic acid metabolic process

G0:0017045 1 corticotropin-releasing hormone activity

G0:0045924 1 regulation of female receptivity

G0:0086066 1 atrial cardiac muscle cell to AV node cell communication

G0:0086065 1 cell communication involved in cardiac conduction

G0:0086062 1 voltage-gated sodium channel activity involved in Purkinje myocyte action potential

G0:0043181 1 vacuolar sequestering

G0:0033858 1 N-acetylgalactosamine kinase activity

G0:1901228 1 positive regulation of transcription from RNA polymerase II promoter involved in heart development

G0:1903078 1 positive regulation of protein localization to plasma membrane

G0:0031723 1 CXCR4 chemokine receptor binding

G0:0031721 1 hemoglobin alpha binding

G0:0031724 1 CXCR5 chemokine receptor binding

G0:0060332 1 positive regulation of response to interferon-gamma

G0:0060330 1 regulation of response to interferon-gamma

G0:0090251 1 protein localization involved in establishment of planar polarity

G0:0060481 1 lobar bronchus epithelium development

G0:0060482 1 lobar bronchus development

G0:0050614 1 delta24-sterol reductase activity

G0:0050613 1 delta14-sterol reductase activity

G0:0046293 1 formaldehyde biosynthetic process

G0:0046295 1 glycolate biosynthetic process

G0:0046296 1 glycolate catabolic process

G0:0048523 1 negative regulation of cellular process

G0:0050961 1 detection of temperature stimulus involved in sensory perception

G0:0015211 1 purine nucleoside transmembrane transporter activity

G0:0060159 1 regulation of dopamine receptor signaling pathway

G0:0002085 1 inhibition of neuroepithelial cell differentiation

G0:0048297 1 negative regulation of isotype switching to IgA isotypes

G0:0005461 1 UDP-glucuronic acid transmembrane transporter activity

G0:0048291 1 isotype switching to IgG isotypes

G0:0001760 1 aminocarboxymuconate-semialdehyde decarboxylase activity

G0:0046491 1 L-methylmalonyl-CoA metabolic process

G0:0005412 1 glucose:sodium symporter activity

G0:0031769 1 glucagon receptor binding

G0:0002081 1 outer acrosomal membrane

G0:0003948 1 N4-(beta-N-acetylglucosaminyl)-L-asparaginase activity

G0:0046490 1 isopentenyl diphosphate metabolic process

G0:1901350	1	cell-cell signaling involved in cell-cell junction organization
G0:0003940	1	L-iduronidase activity
G0:0008227	1	G-protein coupled amine receptor activity
G0:0035984	1	cellular response to trichostatin A
G0:0006227	1	dUDP biosynthetic process
G0:0014895	1	smooth muscle hypertrophy
G0:0014896	1	muscle hypertrophy
G0:0014891	1	striated muscle atrophy
G0:0047714	1	galactolipase activity
G0:0015761	1	mannose transport
G0:0072663	1	establishment of protein localization to peroxisome
G0:0072660	1	maintenance of protein location in plasma membrane
G0:0043404	1	corticotropin-releasing hormone receptor activity
G0:0043402	1	glucocorticoid mediated signaling pathway
G0:0043400	1	cortisol secretion
G0:0016496	1	substance P receptor activity
G0:0016497	1	substance K receptor activity
G0:0016495	1	C-X3-C chemokine receptor activity
G0:0000415	1	negative regulation of histone H3-K36 methylation
G0:0008761	1	UDP-N-acetylglucosamine 2-epimerase activity
G0:0070287	1	ferritin receptor activity
G0:0061445	1	endocardial cushion cell fate commitment
G0:0070576	1	vitamin D 24-hydroxylase activity
G0:0070573	1	metalloprotease activity
G0:0032406	1	MutLbeta complex binding
G0:0046782	1	regulation of viral transcription
G0:2000518	1	negative regulation of T-helper 1 cell activation
G0:0072599	1	establishment of protein localization to endoplasmic reticulum
G0:0034126	1	positive regulation of MyD88-dependent toll-like receptor signaling pathway
G0:2000516	1	positive regulation of CD4-positive, alpha-beta T cell activation
G0:0021679	1	cerebellar molecular layer development
G0:0000831	1	inositol hexakisphosphate 6-kinase activity
G0:0002541	1	activation of plasma proteins involved in acute inflammatory response
G0:0030801	1	positive regulation of cyclic nucleotide metabolic process
G0:0019694	1	alkanesulfonate metabolic process
G0:0050865	1	regulation of cell activation
G0:0050864	1	regulation of B cell activation
G0:0016230	1	sphingomyelin phosphodiesterase activator activity
G0:2001145	1	negative regulation of phosphatidylinositol-3,4,5-trisphosphate 5-phosphatase activity
G0:0046041	1	ITP metabolic process
G0:0051733	1	polydeoxyribonucleotide kinase activity
G0:0051731	1	polynucleotide 5'-hydroxyl-kinase activity
G0:0051736	1	ATP-dependent polyribonucleotide 5'-hydroxyl-kinase activity
G0:0046168	1	glycerol-3-phosphate catabolic process
G0:0071159	1	NF-kappaB complex
G0:2000753	1	positive regulation of glucosylceramide catabolic process
G0:0070539	1	linoleic acid binding
G0:0071622	1	regulation of granulocyte chemotaxis
G0:0001164	1	RNA polymerase I CORE element sequence-specific DNA binding
G0:0035299	1	inositol pentakisphosphate 2-kinase activity
G0:0002155	1	regulation of thyroid hormone mediated signaling pathway
G0:0002152	1	bile acid conjugation
G0:0002153	1	steroid receptor RNA activator RNA binding
G0:0051885	1	positive regulation of anagen
G0:0051882	1	mitochondrial depolarization
G0:1901227	1	negative regulation of transcription from RNA polymerase II promoter involved in heart development
G0:0036403	1	arachidonate 8(S)-lipoxygenase activity
G0:2001233	1	regulation of apoptotic signaling pathway
G0:0008890	1	glycine C-acetyltransferase activity
G0:0061140	1	lung secretory cell differentiation
G0:0061141	1	lung ciliated cell differentiation
G0:0005098	1	Ran GTPase activator activity
G0:0045025	1	mitochondrial degradosome
G0:0004419	1	hydroxymethylglutaryl-CoA lyase activity
G0:0004418	1	hydroxymethylbilane synthase activity
G0:0047874	1	dolichyldiphosphatase activity
G0:0004411	1	homogentisate 1,2-dioxygenase activity
G0:0006679	1	glucosylceramide biosynthetic process
G0:0006677	1	glycosylceramide metabolic process
G0:0008941	1	nitric oxide dioxygenase activity
G0:0043973	1	histone H3-K4 acetylation
G0:0048087	1	positive regulation of developmental pigmentation

G0:0001135	1	RNA polymerase II transcription factor recruiting transcription factor activity
G0:0005325	1	peroxisomal fatty-acyl-CoA transporter activity
G0:0008768	1	UDP-sugar diphosphatase activity
G0:0000789	1	cytoplasmic chromatin
G0:0042624	1	ATPase activity, uncoupled
G0:0035437	1	maintenance of protein localization in endoplasmic reticulum
G0:0010092	1	specification of organ identity
G0:0018738	1	S-formylglutathione hydrolase activity
G0:0018733	1	3,4-dihydrocoumarin hydrolase activity
G0:0019061	1	uncoating of virus
G0:0072677	1	eosinophil migration
G0:0015578	1	mannose transmembrane transporter activity
G0:0019605	1	butyrate metabolic process
G0:0070145	1	mitochondrial asparaginyl-tRNA aminoacylation
G0:0032138	1	single base insertion or deletion binding
G0:0070140	1	SUMO-specific isopeptidase activity
G0:0070143	1	mitochondrial alanyl-tRNA aminoacylation
G0:0032875	1	regulation of DNA endoreduplication
G0:0031856	1	parathyroid hormone receptor binding
G0:1901725	1	regulation of histone deacetylase activity
G0:2000677	1	regulation of transcription regulatory region DNA binding
G0:0060735	1	regulation of eIF2 alpha phosphorylation by dsRNA
G0:0060220	1	camera-type eye photoreceptor cell fate commitment
G0:0015878	1	biotin transport
G0:0033882	1	choloyl-CoA hydrolase activity
G0:0009441	1	glycolate metabolic process
G0:0038106	1	choriogonadotropin hormone binding
G0:0038100	1	nodal binding
G0:0033885	1	10-hydroxy-9-(phosphonooxy)octadecanoate phosphatase activity
G0:0060229	1	lipase activator activity
G0:0045990	1	carbon catabolite regulation of transcription
G0:1901899	1	positive regulation of relaxation of cardiac muscle
G0:0050746	1	regulation of lipoprotein metabolic process
G0:0034369	1	plasma lipoprotein particle remodeling
G0:0045560	1	regulation of TRAIL receptor biosynthetic process
G0:0061444	1	endocardial cushion cell development
G0:0042022	1	interleukin-12 receptor complex
G0:0042023	1	DNA endoreduplication
G0:0072434	1	signal transduction involved in mitotic G2 DNA damage checkpoint
G0:0072432	1	response to G1 DNA damage checkpoint signaling
G0:0003144	1	embryonic heart tube formation
G0:0072431	1	signal transduction involved in mitotic G1 DNA damage checkpoint
G0:0046456	1	icosanoid biosynthetic process
G0:0046452	1	dihydrofolate metabolic process
G0:0043060	1	meiotic metaphase I plate congression
G0:0060345	1	spleen trabecula formation
G0:0086042	1	cardiac muscle cell-cardiac muscle cell adhesion
G0:0086047	1	membrane depolarization during Purkinje myocyte cell action potential
G0:0052835	1	inositol-3,4,6-trisphosphate 1-kinase activity
G0:0097260	1	eoxin A4 synthase activity
G0:0035669	1	TRAM-dependent toll-like receptor 4 signaling pathway
G0:0035665	1	TIRAP-dependent toll-like receptor 4 signaling pathway
G0:0035663	1	Toll-like receptor 2 binding
G0:0005754	1	mitochondrial proton-transporting ATP synthase, catalytic core
G0:0072047	1	proximal/distal pattern formation involved in nephron development
G0:0060311	1	negative regulation of elastin catabolic process
G0:0090272	1	negative regulation of fibroblast growth factor production
G0:0090273	1	regulation of somatostatin secretion
G0:0017061	1	S-methyl-5-thioadenosine phosphorylase activity
G0:0043105	1	negative regulation of GTP cyclohydrolase I activity
G0:0017064	1	fatty acid amide hydrolase activity
G0:0017065	1	single-strand selective uracil DNA N-glycosylase activity
G0:0051946	1	regulation of glutamate uptake involved in transmission of nerve impulse
G0:0008111	1	alpha-methylacyl-CoA racemase activity
G0:0060175	1	brain-derived neurotrophic factor-activated receptor activity
G0:0060177	1	regulation of angiotensin metabolic process
G0:0009645	1	response to low light intensity stimulus
G0:0008115	1	sarcosine oxidase activity
G0:0001315	1	age-dependent response to reactive oxygen species
G0:0035087	1	siRNA loading onto RISC involved in RNA interference
G0:0002367	1	cytokine production involved in immune response
G0:0009159	1	deoxyribonucleoside monophosphate catabolic process
G0:0009154	1	purine ribonucleotide catabolic process
G0:0009152	1	purine ribonucleotide biosynthetic process

G0:0048211	1	Golgi vesicle docking
G0:0048210	1	Golgi vesicle fusion to target membrane
G0:0015855	1	pyrimidine nucleobase transport
G0:0045844	1	positive regulation of striated muscle tissue development
G0:0000041	1	transition metal ion transport
G0:0004750	1	ribulose-phosphate 3-epimerase activity
G0:0004751	1	ribose-5-phosphate isomerase activity
G0:0004757	1	sepiapterin reductase activity
G0:0015295	1	solute:proton symporter activity
G0:0052565	1	response to defense-related host nitric oxide production
G0:0046715	1	borate transmembrane transporter activity
G0:0003968	1	RNA-directed RNA polymerase activity
G0:0001010	1	sequence-specific DNA binding transcription factor recruiting transcription factor activity
G0:0003964	1	RNA-directed DNA polymerase activity
G0:0045352	1	interleukin-1 Type I receptor antagonist activity
G0:0070773	1	protein-N-terminal glutamine amidohydrolase activity
G0:0045358	1	negative regulation of interferon-beta biosynthetic process
G0:0019477	1	L-lysine catabolic process
G0:0070774	1	phytoceramidase activity
G0:0060731	1	positive regulation of intestinal epithelial structure maintenance
G0:0048692	1	negative regulation of axon extension involved in regeneration
G0:0072608	1	interleukin-10 secretion
G0:0071494	1	cellular response to UV-C
G0:0070702	1	inner mucus layer
G0:0072600	1	establishment of protein localization to Golgi
G0:0000433	1	negative regulation of transcription from RNA polymerase II promoter by glucose
G0:0045687	1	positive regulation of glial cell differentiation
G0:0005924	1	cell-substrate adherens junction
G0:0045685	1	regulation of glial cell differentiation
G0:0002605	1	negative regulation of dendritic cell antigen processing and presentation
G0:0030283	1	testosterone dehydrogenase [NAD(P)] activity
G0:0070553	1	nicotinic acid receptor activity
G0:0070551	1	endoribonuclease activity, cleaving siRNA-paired mRNA
G0:0032468	1	Golgi calcium ion homeostasis
G0:0033484	1	nitric oxide homeostasis
G0:2000536	1	negative regulation of entry of bacterium into host cell
G0:0097451	1	glial limiting end-foot
G0:0019290	1	siderophore biosynthetic process
G0:0030827	1	negative regulation of cGMP biosynthetic process
G0:0030826	1	regulation of cGMP biosynthetic process
G0:1902742	1	apoptotic process involved in development
G0:0015742	1	alpha-ketoglutarate transport
G0:0010517	1	regulation of phospholipase activity
G0:0006581	1	acetylcholine catabolic process
G0:0051717	1	inositol-1,3,4,5-tetrakisphosphate 3-phosphatase activity
G0:0048773	1	erythrophore differentiation
G0:0044557	1	relaxation of smooth muscle
G0:0031370	1	eukaryotic initiation factor 4G binding
G0:0071608	1	macrophage inflammatory protein-1 alpha production
G0:0071609	1	chemokine (C-C motif) ligand 5 production
G0:0071602	1	phytosphingosine biosynthetic process
G0:0005289	1	high affinity arginine transmembrane transporter activity
G0:0032536	1	regulation of cell projection size
G0:1900281	1	positive regulation of CD4-positive, alpha-beta T cell costimulation
G0:0035270	1	endocrine system development
G0:0035272	1	exocrine system development
G0:0030354	1	melanin-concentrating hormone activity
G0:0043754	1	dihydrolipoyllysine-residue (2-methylpropanoyl)transferase activity
G0:0022865	1	transmembrane electron transfer carrier
G0:0030683	1	evasion or tolerance by virus of host immune response
G0:0097090	1	presynaptic membrane organization
G0:0030684	1	preribosome
G0:0030171	1	voltage-gated proton channel activity
G0:0061162	1	establishment of monopolar cell polarity
G0:0015039	1	NADPH-adrenodoxin reductase activity
G0:0042253	1	granulocyte macrophage colony-stimulating factor biosynthetic process
G0:0043028	1	cysteine-type endopeptidase regulator activity involved in apoptotic process
G0:0060785	1	regulation of apoptosis involved in tissue homeostasis
G0:0060784	1	regulation of cell proliferation involved in tissue homeostasis
G0:0060783	1	mesenchymal smoothened signaling pathway involved in prostate gland development
G0:0060782	1	regulation of mesenchymal cell proliferation involved in prostate gland

development

G0:0048313	1	Golgi inheritance
G0:0000235	1	astral microtubule
G0:0004921	1	interleukin-11 receptor activity
G0:0031087	1	deadenylation-independent decapping of nuclear-transcribed mRNA
G0:0004925	1	prolactin receptor activity
G0:0043969	1	histone H2B acetylation
G0:0061078	1	positive regulation of prostaglandin secretion involved in immune response
G0:0060072	1	large conductance calcium-activated potassium channel activity
G0:2001253	1	regulation of histone H3-K36 trimethylation
G0:2001250	1	positive regulation of ammonia assimilation cycle
G0:0005347	1	ATP transmembrane transporter activity
G0:0005345	1	purine nucleobase transmembrane transporter activity
G0:0005343	1	organic acid:sodium symporter activity
G0:0004348	1	glucosylceramidase activity
G0:0034012	1	FAD-AMP lyase (cyclizing) activity
G0:0090044	1	positive regulation of tubulin deacetylation
G0:0090049	1	regulation of cell migration involved in sprouting angiogenesis
G0:0034130	1	toll-like receptor 1 signaling pathway
G0:0044316	1	cone cell pedicle
G0:0044313	1	protein K6-linked deubiquitination
G0:0072078	1	nephron tubule morphogenesis
G0:0090450	1	inosine-diphosphatase activity
G0:0036029	1	protein C inhibitor-KLK3 complex
G0:0036028	1	protein C inhibitor-thrombin complex
G0:0046814	1	coreceptor-mediated virion attachment to host cell
G0:0036025	1	protein C inhibitor-TMPRSS11E complex
G0:0036024	1	protein C inhibitor-TMPRSS7 complex
G0:0036027	1	protein C inhibitor-PLAU complex
G0:0036026	1	protein C inhibitor-PLAT complex
G0:0018094	1	protein polyglycylation
G0:0070126	1	mitochondrial translational termination
G0:0070127	1	tRNA aminoacylation for mitochondrial protein translation
G0:0070123	1	transforming growth factor beta receptor activity, type III
G0:0070121	1	Kupffer's vesicle development
G0:0032852	1	positive regulation of Ral GTPase activity
G0:0002578	1	negative regulation of antigen processing and presentation
G0:1901250	1	negative regulation of lung goblet cell differentiation
G0:1901251	1	positive regulation of lung goblet cell differentiation
G0:1901255	1	nucleotide-excision repair involved in interstrand cross-link repair
G0:1901258	1	positive regulation of macrophage colony-stimulating factor production
G0:0008541	1	proteasome regulatory particle, lid subcomplex
G0:0061158	1	3'-UTR-mediated mRNA destabilization
G0:0072531	1	pyrimidine-containing compound transmembrane transport
G0:0032144	1	4-aminobutyrate transaminase complex
G0:0016028	1	rhabdomere
G0:0010509	1	polyamine homeostasis
G0:0016005	1	phospholipase A2 activator activity
G0:0015037	1	peptide disulfide oxidoreductase activity
G0:0042008	1	interleukin-18 receptor activity
G0:0032222	1	regulation of synaptic transmission, cholinergic
G0:0003167	1	atrioventricular bundle cell differentiation
G0:0003163	1	sinoatrial node development
G0:0003168	1	Purkinje myocyte differentiation
G0:0015755	1	fructose transport
G0:0015327	1	cystine:glutamate antiporter activity
G0:0016229	1	steroid dehydrogenase activity
G0:0060491	1	regulation of cell projection assembly
G0:0014719	1	skeletal muscle satellite cell activation
G0:0034663	1	endoplasmic reticulum chaperone complex
G0:0033814	1	propanoyl-CoA C-acyltransferase activity
G0:0006193	1	ITP catabolic process
G0:0033126	1	positive regulation of GTP catabolic process
G0:0004158	1	dihydroorotate oxidase activity
G0:0061441	1	renal artery morphogenesis
G0:0050857	1	positive regulation of antigen receptor-mediated signaling pathway
G0:0035642	1	histone methyltransferase activity (H3-R17 specific)
G0:0035643	1	L-DOPA receptor activity
G0:0035644	1	phosphoanandamide dephosphorylation
G0:0035645	1	enteric smooth muscle cell differentiation
G0:0061310	1	canonical Wnt signaling pathway involved in cardiac neural crest cell differentiation involved in heart development
G0:0046051	1	UTP metabolic process
G0:0016222	1	procollagen-proline 4-dioxygenase complex
G0:0031947	1	negative regulation of glucocorticoid biosynthetic process

G0:0031946	1	regulation of glucocorticoid biosynthetic process
G0:0060377	1	negative regulation of mast cell differentiation
G0:0060375	1	regulation of mast cell differentiation
G0:0015822	1	ornithine transport
G0:0015826	1	threonine transport
G0:0015827	1	tryptophan transport
G0:0021658	1	rhombomere 3 morphogenesis
G0:0010855	1	adenylate cyclase inhibitor activity
G0:0015828	1	tyrosine transport
G0:0046054	1	dGMP metabolic process
G0:0060496	1	mesenchymal-epithelial cell signaling involved in lung development
G0:0001087	1	TFIIB-class binding transcription factor activity
G0:0004621	1	glycosylphosphatidylinositol phospholipase D activity
G0:0001080	1	nitrogen catabolite activation of transcription from RNA polymerase II promoter
G0:0052927	1	CTP:tRNA cytidyltransferase activity
G0:0052925	1	dol-P-Man:Man(5)GlcNAc(2)-PP-Dol alpha-1,3-mannosyltransferase activity
G0:0052928	1	CTP:3'-cytidine-tRNA cytidyltransferase activity
G0:0030548	1	acetylcholine receptor regulator activity
G0:0030549	1	acetylcholine receptor activator activity
G0:0048787	1	presynaptic active zone membrane
G0:1903038	1	negative regulation of leukocyte cell-cell adhesion
G0:0047743	1	chlordecone reductase activity
G0:0003142	1	cardiogenic plate morphogenesis
G0:1902616	1	acyl carnitine transmembrane transport
G0:2001065	1	mannan binding
G0:0036233	1	glycine import
G0:2001069	1	glycogen binding
G0:0004598	1	peptidylamidoglycolate lyase activity
G0:0006037	1	cell wall chitin metabolic process
G0:0004590	1	orotidine-5'-phosphate decarboxylase activity
G0:0004591	1	oxoglutarate dehydrogenase (succinyl-transferring) activity
G0:0004595	1	pantetheine-phosphate adenylyltransferase activity
G0:0004597	1	peptide-aspartate beta-dioxygenase activity
G0:0043843	1	ADP-specific glucokinase activity
G0:0008049	1	male courtship behavior
G0:0016844	1	strictosidine synthase activity
G0:0016846	1	carbon-sulfur lyase activity
G0:0016841	1	ammonia-lyase activity
G0:0000066	1	mitochondrial ornithine transport
G0:0070899	1	mitochondrial tRNA wobble uridine modification
G0:0004777	1	succinate-semialdehyde dehydrogenase (NAD+) activity
G0:0004773	1	sterol-sulfatase activity
G0:0052547	1	regulation of peptidase activity
G0:0008267	1	poly-glutamine tract binding
G0:0003905	1	alkylbase DNA N-glycosylase activity
G0:0008262	1	importin-alpha export receptor activity
G0:0043849	1	Ras palmitoyltransferase activity
G0:0060367	1	sagittal suture morphogenesis
G0:0003908	1	methylated-DNA-[protein]-cysteine S-methyltransferase activity
G0:0015491	1	cation:cation antiporter activity
G0:0070715	1	sodium-dependent organic cation transport
G0:0034899	1	trimethylamine monooxygenase activity
G0:0071140	1	resolution of mitotic recombination intermediates
G0:2000734	1	negative regulation of glial cell-derived neurotrophic factor receptor signaling pathway involved in ureteric bud formation
G0:2000739	1	regulation of mesenchymal stem cell differentiation
G0:2000080	1	negative regulation of canonical Wnt signaling pathway involved in controlling type B pancreatic cell proliferation
G0:2000081	1	positive regulation of canonical Wnt signaling pathway involved in controlling type B pancreatic cell proliferation
G0:0000453	1	enzyme-directed rRNA 2'-O-methylation
G0:0051365	1	cellular response to potassium ion starvation
G0:0071548	1	response to dexamethasone
G0:0050379	1	UDP-glucuronate 5'-epimerase activity
G0:0032440	1	2-alkenal reductase [NAD(P)] activity
G0:2000404	1	regulation of T cell migration
G0:0008039	1	synaptic target recognition
G0:0032448	1	DNA hairpin binding
G0:0060299	1	negative regulation of sarcomere organization
G0:0034477	1	U6 snRNA 3'-end processing
G0:0035852	1	horizontal cell localization
G0:0002506	1	polysaccharide assembly with MHC class II protein complex
G0:0002502	1	peptide antigen assembly with MHC class I protein complex
G0:0002508	1	central tolerance induction

G0:0071422	1	succinate transmembrane transport
G0:0071442	1	positive regulation of histone H3-K14 acetylation
G0:0002149	1	hypochlorous acid biosynthetic process
G0:0015019	1	heparan-alpha-glucosaminide N-acetyltransferase activity
G0:0001856	1	complement component C5a binding
G0:0016277	1	[myelin basic protein]-arginine N-methyltransferase activity
G0:0046554	1	malate dehydrogenase (NADP+) activity
G0:0030348	1	syntaxin-3 binding
G0:0007108	1	cytokinesis, initiation of separation
G0:0071664	1	catenin-TCF7L2 complex
G0:0071665	1	gamma-catenin-TCF7L2 complex
G0:0071663	1	positive regulation of granzyme B production
G0:0030378	1	serine racemase activity
G0:0030372	1	high molecular weight B cell growth factor receptor binding
G0:0035787	1	cell migration involved in kidney development
G0:0060658	1	nipple morphogenesis
G0:0018773	1	acetylpyruvate hydrolase activity
G0:0035783	1	CD4-positive, alpha-beta T cell costimulation
G0:0035782	1	mature natural killer cell chemotaxis
G0:0035789	1	metanephric mesenchymal cell migration
G0:0032482	1	Rab protein signal transduction
G0:0060751	1	branch elongation involved in mammary gland duct branching
G0:0035438	1	cyclic-di-GMP binding
G0:0032484	1	Ral protein signal transduction
G0:0061106	1	negative regulation of stomach neuroendocrine cell differentiation
G0:0061102	1	stomach neuroendocrine cell differentiation
G0:0061103	1	carotid body glomus cell differentiation
G0:0061100	1	lung neuroendocrine cell differentiation
G0:0061108	1	seminal vesicle epithelium development
G0:0021897	1	forebrain astrocyte development
G0:0042276	1	error-prone translesion synthesis
G0:0042278	1	purine nucleoside metabolic process
G0:0043000	1	Golgi to plasma membrane CFTR protein transport
G0:0006505	1	GPI anchor metabolic process
G0:0048337	1	positive regulation of mesodermal cell fate specification
G0:0000210	1	NAD+ diphosphatase activity
G0:0000215	1	tRNA 2'-phosphotransferase activity
G0:0004903	1	growth hormone receptor activity
G0:0004900	1	erythropoietin receptor activity
G0:0004904	1	interferon receptor activity
G0:0072362	1	regulation of glycolytic process by negative regulation of transcription from RNA polymerase II promoter
G0:0072363	1	regulation of glycolytic by positive regulation of transcription from RNA polymerase II promoter
G0:0072366	1	regulation of cellular ketone metabolic process by positive regulation of transcription from RNA polymerase II promoter
G0:0072365	1	regulation of cellular ketone metabolic process by negative regulation of transcription from RNA polymerase II promoter
G0:2001273	1	regulation of glucose import in response to insulin stimulus
G0:0042661	1	regulation of mesodermal cell fate specification
G0:0042666	1	negative regulation of ectodermal cell fate specification
G0:0042667	1	auditory receptor cell fate specification
G0:0090025	1	regulation of monocyte chemotaxis
G0:0033577	1	protein glycosylation in endoplasmic reticulum
G0:0031741	1	type B gastrin/cholecystokinin receptor binding
G0:0051174	1	regulation of phosphorus metabolic process
G0:0051171	1	regulation of nitrogen compound metabolic process
G0:0050560	1	aspartate-tRNA(Asn) ligase activity
G0:0050561	1	glutamate-tRNA(Gln) ligase activity
G0:0010878	1	cholesterol storage
G0:0005368	1	taurine transmembrane transporter activity
G0:0005369	1	taurine:sodium symporter activity
G0:0008907	1	integrase activity
G0:0005362	1	low-affinity glucose:sodium symporter activity
G0:0004018	1	N6-(1,2-dicarboxyethyl)AMP AMP-lyase (fumarate-forming) activity
G0:0060313	1	negative regulation of blood vessel remodeling
G0:0051282	1	regulation of sequestering of calcium ion
G0:0004014	1	adenosylmethionine decarboxylase activity
G0:1902409	1	mitotic cytokinetic cell separation
G0:0034255	1	regulation of urea metabolic process
G0:0001621	1	ADP receptor activity
G0:0036004	1	GAF domain binding
G0:0010876	1	lipid localization
G0:0030362	1	protein phosphatase type 4 regulator activity
G0:0061157	1	mRNA destabilization

G0:0032788	1	saturated monocarboxylic acid metabolic process
G0:0032789	1	unsaturated monocarboxylic acid metabolic process
G0:0032782	1	bile acid secretion
G0:0001999	1	renal response to blood flow involved in circulatory renin-angiotensin regulation of systemic arterial blood pressure
G0:0001998	1	angiotensin mediated vasoconstriction involved in regulation of systemic arterial blood pressure
G0:0001993	1	regulation of systemic arterial blood pressure by norepinephrine-epinephrine
G0:0052739	1	phosphatidylserine 1-acylhydrolase activity
G0:1901189	1	positive regulation of ephrin receptor signaling pathway
G0:1901186	1	positive regulation of ERBB signaling pathway
G0:0055100	1	adiponectin binding
G0:1901184	1	regulation of ERBB signaling pathway
G0:0052732	1	phosphoethanolamine phosphatase activity
G0:0052731	1	phosphocholine phosphatase activity
G0:0033783	1	25-hydroxycholesterol 7alpha-hydroxylase activity
G0:0033782	1	24-hydroxycholesterol 7alpha-hydroxylase activity
G0:0033781	1	cholesterol 24-hydroxylase activity
G0:0016046	1	detection of fungus
G0:0070459	1	prolactin secretion
G0:0045523	1	interleukin-27 receptor binding
G0:0070105	1	positive regulation of interleukin-6-mediated signaling pathway
G0:0036222	1	XTP diphosphatase activity
G0:0047012	1	sterol-4-alpha-carboxylate 3-dehydrogenase (decarboxylating) activity
G0:0071275	1	cellular response to aluminum ion
G0:0047015	1	3-hydroxy-2-methylbutyryl-CoA dehydrogenase activity
G0:0003108	1	negative regulation of the force of heart contraction by chemical signal
G0:0003106	1	negative regulation of glomerular filtration by angiotensin
G0:0043257	1	laminin-8 complex
G0:0046434	1	organophosphate catabolic process
G0:1901989	1	positive regulation of cell cycle phase transition
G0:0060843	1	venous endothelial cell differentiation
G0:1900053	1	negative regulation of retinoic acid biosynthetic process
G0:0030369	1	ICAM-3 receptor activity
G0:0044088	1	regulation of vacuole organization
G0:0043482	1	cellular pigment accumulation
G0:0034645	1	cellular macromolecule biosynthetic process
G0:0034649	1	histone demethylase activity (H3-monomethyl-K4 specific)
G0:0097226	1	sperm mitochondrial sheath
G0:0008613	1	diuretic hormone activity
G0:0097224	1	sperm connecting piece
G0:0097222	1	mitochondrial mRNA polyadenylation
G0:0043622	1	cortical microtubule organization
G0:0061379	1	inferior colliculus development
G0:0090187	1	positive regulation of pancreatic juice secretion
G0:0061374	1	mammillothalamic axonal tract development
G0:0061377	1	mammary gland lobule development
G0:0060422	1	peptidyl-dipeptidase inhibitor activity
G0:0060355	1	positive regulation of cell adhesion molecule production
G0:0060356	1	leucine import
G0:0090237	1	regulation of arachidonic acid secretion
G0:0060359	1	response to ammonium ion
G0:0010836	1	negative regulation of protein ADP-ribosylation
G0:0010835	1	regulation of protein ADP-ribosylation
G0:0047312	1	L-phenylalanine:pyruvate aminotransferase activity
G0:0045622	1	regulation of T-helper cell differentiation
G0:0005998	1	xylulose catabolic process
G0:0005996	1	monosaccharide metabolic process
G0:0015227	1	acyl carnitine transmembrane transporter activity
G0:0005993	1	trehalose catabolic process
G0:0045940	1	positive regulation of steroid metabolic process
G0:0051903	1	S-(hydroxymethyl)glutathione dehydrogenase activity
G0:0051908	1	double-stranded DNA 5'-3' exodeoxyribonuclease activity
G0:0009996	1	negative regulation of cell fate specification
G0:0006714	1	sesquiterpenoid metabolic process
G0:0006710	1	androgen catabolic process
G0:0006711	1	estrogen catabolic process
G0:0006713	1	glucocorticoid catabolic process
G0:0030526	1	granulocyte macrophage colony-stimulating factor receptor complex
G0:0061598	1	molybdopterin adenylyltransferase activity
G0:0046016	1	positive regulation of transcription by glucose
G0:0005199	1	structural constituent of cell wall
G0:0047860	1	diiodophenylpyruvate reductase activity
G0:2001045	1	negative regulation of integrin-mediated signaling pathway

G0:0004422	1	hypoxanthine phosphoribosyltransferase activity
G0:0036250	1	peroxisome transport along microtubule
G0:2001040	1	positive regulation of cellular response to drug
G0:1990009	1	retinal cell apoptotic process
G0:0004423	1	iduronate-2-sulfatase activity
G0:1990001	1	inhibition of cysteine-type endopeptidase activity involved in apoptotic process
G0:1990005	1	granular vesicle
G0:0097242	1	beta-amyloid clearance
G0:0004573	1	mannosyl-oligosaccharide glucosidase activity
G0:0004577	1	N-acetylglucosaminyl diphosphodolichol N-acetylglucosaminyltransferase activity
G0:0004574	1	oligo-1,6-glucosidase activity
G0:0004575	1	sucrose alpha-glucosidase activity
G0:0004578	1	chitobiosyl diphosphodolichol beta-mannosyltransferase activity
G0:0052904	1	N1-acetylspermidine:oxygen oxidoreductase (3-acetamidopropanal-forming) activity
G0:0052906	1	tRNA (guanine(37)-N(1))-methyltransferase activity
G0:0016262	1	protein N-acetylglucosaminyltransferase activity
G0:0016860	1	intramolecular oxidoreductase activity
G0:0000003	1	reproduction
G0:0014038	1	regulation of Schwann cell differentiation
G0:0000009	1	alpha-1,6-mannosyltransferase activity
G0:0072198	1	mesenchymal cell proliferation involved in ureter development
G0:0009191	1	ribonucleoside diphosphate catabolic process
G0:0072192	1	ureter epithelial cell differentiation
G0:0072195	1	kidney smooth muscle cell differentiation
G0:0018032	1	protein amidation
G0:0003921	1	GMP synthase activity
G0:0003922	1	GMP synthase (glutamine-hydrolyzing) activity
G0:0072517	1	host cell viral assembly compartment
G0:0017186	1	peptidyl-pyroglutamic acid biosynthetic process, using glutaminy-peptide cyclotransferase
G0:0070736	1	protein-glycine ligase activity, initiating
G0:0070735	1	protein-glycine ligase activity
G0:0070733	1	protein adenylyltransferase activity
G0:0006231	1	dTMP biosynthetic process
G0:0046204	1	nor-spermidine metabolic process
G0:0042851	1	L-alanine metabolic process
G0:0002368	1	B cell cytokine production
G0:0050353	1	trimethyllysine dioxygenase activity
G0:0050355	1	triphosphatase activity
G0:0016784	1	3-mercaptopyruvate sulfurtransferase activity
G0:0016785	1	transferase activity, transferring selenium-containing groups
G0:0015086	1	cadmium ion transmembrane transporter activity
G0:0015087	1	cobalt ion transmembrane transporter activity
G0:0002528	1	regulation of vascular permeability involved in acute inflammatory response
G0:0015782	1	CMP-N-acetylneuramate transport
G0:0015781	1	pyrimidine nucleotide-sugar transport
G0:0015787	1	UDP-glucuronic acid transport
G0:0015785	1	UDP-galactose transport
G0:0010557	1	positive regulation of macromolecule biosynthetic process
G0:0071461	1	cellular response to redox state
G0:0047220	1	galactosylxylosylprotein 3-beta-galactosyltransferase activity
G0:0001874	1	(1->3)-beta-D-glucan receptor activity
G0:0071469	1	cellular response to alkalinity
G0:0046577	1	long-chain-alcohol oxidase activity
G0:0046570	1	methylthioribulose 1-phosphate dehydratase activity
G0:0051754	1	meiotic sister chromatid cohesion, centromeric
G0:0051758	1	homologous chromosome movement towards spindle pole involved in homologous chromosome segregation
G0:0071641	1	negative regulation of macrophage inflammatory protein 1 alpha production
G0:0044599	1	AP-5 adaptor complex
G0:0034417	1	bisphosphoglycerate 3-phosphatase activity
G0:2000572	1	positive regulation of interleukin-4-dependent isotype switching to IgE isotypes
G0:0045815	1	positive regulation of gene expression, epigenetic
G0:0033373	1	maintenance of protease location in mast cell secretory granule
G0:2000576	1	positive regulation of microtubule motor activity
G0:0033371	1	T cell secretory granule organization
G0:0035238	1	vitamin A biosynthetic process
G0:0030311	1	poly-N-acetylactosamine biosynthetic process
G0:0042292	1	URM1 activating enzyme activity
G0:0061296	1	negative regulation of mesenchymal cell apoptotic process involved in

mesonephric nephron morphogenesis
G0:0035693 1 NOS2-CD74 complex
G0:0033193 1 Lsd1/2 complex
G0:0002083 1 4-hydroxybenzoate decaprenyltransferase activity
G0:0016250 1 N-sulfoglucosamine sulfohydrolase activity
G0:0016521 1 pituitary adenylate cyclase activating polypeptide activity
G0:0016256 1 N-glycan processing to lysosome
G0:0017125 1 deoxycytidyl transferase activity
G0:0017126 1 nucleogenesis
G0:0045887 1 positive regulation of synaptic growth at neuromuscular junction
G0:1990081 1 trimethylamine receptor activity
G0:0006529 1 asparagine biosynthetic process
G0:0072200 1 negative regulation of mesenchymal cell proliferation involved in ureter development
G0:0043062 1 extracellular structure organization
G0:0046687 1 response to chromate
G0:0046680 1 response to DDT
G0:0000271 1 polysaccharide biosynthetic process
G0:0045083 1 negative regulation of interleukin-12 biosynthetic process
G0:0043783 1 oxidoreductase activity, oxidizing metal ions with flavin as acceptor
G0:0004964 1 luteinizing hormone receptor activity
G0:0004961 1 thromboxane A2 receptor activity
G0:0004960 1 thromboxane receptor activity
G0:0004963 1 follicle-stimulating hormone receptor activity
G0:0072347 1 response to anesthetic
G0:0072340 1 cellular lactam catabolic process
G0:0031260 1 pseudopodium membrane
G0:0031268 1 pseudopodium organization
G0:0031704 1 apelin receptor binding
G0:0048352 1 paraxial mesoderm structural organization
G0:0031707 1 endothelin A receptor binding
G0:0004381 1 fucosylgalactoside 3-alpha-galactosyltransferase activity
G0:0004380 1 glycoprotein-fucosylgalactoside alpha-N-acetylglactosaminyltransferase activity
G0:0004382 1 guanosine-diphosphatase activity
G0:0009074 1 aromatic amino acid family catabolic process
G0:0010034 1 response to acetate
G0:0018208 1 peptidyl-proline modification
G0:0003069 1 vasodilation by acetylcholine involved in regulation of systemic arterial blood pressure
G0:0004037 1 allantoicase activity
G0:0004034 1 aldose 1-epimerase activity
G0:0097185 1 cellular response to azide
G0:0001605 1 adrenomedullin receptor activity
G0:0001604 1 urotensin II receptor activity
G0:0036060 1 slit diaphragm assembly
G0:0016896 1 exoribonuclease activity, producing 5'-phosphomonoesters
G0:0060823 1 canonical Wnt signaling pathway involved in neural plate anterior/posterior pattern formation
G0:0032762 1 mast cell cytokine production
G0:0032812 1 positive regulation of epinephrine secretion
G0:0032814 1 regulation of natural killer cell activation
G0:0031860 1 telomeric 3' overhang formation
G0:0032769 1 negative regulation of monooxygenase activity
G0:0031861 1 prolactin-releasing peptide receptor binding
G0:0071877 1 regulation of adrenergic receptor signaling pathway
G0:0071874 1 cellular response to norepinephrine stimulus
G0:0071878 1 negative regulation of adrenergic receptor signaling pathway
G0:0008653 1 lipopolysaccharide metabolic process
G0:0043189 1 H4/H2A histone acetyltransferase complex
G0:2000388 1 positive regulation of antral ovarian follicle growth
G0:0021683 1 cerebellar granular layer morphogenesis
G0:0021682 1 nerve maturation
G0:0070694 1 deoxyribonucleoside 5'-monophosphate N-glycosidase activity
G0:0015440 1 peptide-transporting ATPase activity
G0:0042941 1 D-alanine transport
G0:0033677 1 DNA/RNA helicase activity
G0:0045503 1 dynein light chain binding
G0:0070471 1 uterine smooth muscle contraction
G0:0047560 1 3-dehydrosphinganine reductase activity
G0:0071250 1 cellular response to nitrite
G0:0042044 1 fluid transport
G0:0071259 1 cellular response to magnetism
G0:2000331 1 regulation of terminal button organization
G0:1900038 1 negative regulation of cellular response to hypoxia

G0:1900035	1	negative regulation of cellular response to heat
G0:1900037	1	regulation of cellular response to hypoxia
G0:0032223	1	negative regulation of synaptic transmission, cholinergic
G0:0052822	1	DNA-3-methylguanine glycosylase activity
G0:0052821	1	DNA-7-methyladenine glycosylase activity
G0:0035992	1	tendon formation
G0:0047389	1	glycerophosphocholine phosphodiesterase activity
G0:0034334	1	adherens junction maintenance
G0:2000740	1	negative regulation of mesenchymal stem cell differentiation
G0:0097200	1	cysteine-type endopeptidase activity involved in execution phase of apoptosis
G0:0005816	1	spindle pole body
G0:0061354	1	planar cell polarity pathway involved in pericardium morphogenesis
G0:0061350	1	planar cell polarity pathway involved in cardiac muscle tissue morphogenesis
G0:0061358	1	negative regulation of Wnt protein secretion
G0:0060405	1	regulation of penile erection
G0:0060407	1	negative regulation of penile erection
G0:0060400	1	negative regulation of growth hormone receptor signaling pathway
G0:0015868	1	purine ribonucleotide transport
G0:0015865	1	purine nucleotide transport
G0:0015862	1	uridine transport
G0:0015860	1	purine nucleoside transmembrane transport
G0:0046210	1	nitric oxide catabolic process
G0:0001042	1	RNA polymerase I core binding
G0:0046745	1	viral capsid secondary envelopment
G0:0019185	1	snRNA-activating protein complex
G0:0002651	1	positive regulation of tolerance induction to self antigen
G0:1902164	1	positive regulation of DNA damage response, signal transduction by p53 class mediator resulting in transcription of p21 class mediator
G0:1902167	1	positive regulation of intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator
G0:0035573	1	N-terminal peptidyl-serine trimethylation
G0:0002380	1	immunoglobulin secretion involved in immune response
G0:0004493	1	methylmalonyl-CoA epimerase activity
G0:0046525	1	xylosylprotein 4-beta-galactosyltransferase activity
G0:0016920	1	pyroglutamyl-peptidase activity
G0:1902307	1	positive regulation of sodium ion transmembrane transport
G0:0046521	1	sphingoid catabolic process
G0:1902303	1	negative regulation of potassium ion export
G0:0009452	1	7-methylguanosine RNA capping
G0:0046520	1	sphingoid biosynthetic process
G0:1902309	1	negative regulation of peptidyl-serine dephosphorylation
G0:0045353	1	interleukin-1 Type II receptor antagonist activity
G0:0045355	1	negative regulation of interferon-alpha biosynthetic process
G0:1990029	1	vasomotion
G0:0008108	1	UDP-glucose:hexose-1-phosphate uridylyltransferase activity
G0:0000390	1	spliceosomal complex disassembly
G0:0045720	1	negative regulation of integrin biosynthetic process
G0:0004555	1	alpha,alpha-trehalase activity
G0:0072707	1	cellular response to sodium dodecyl sulfate
G0:0043874	1	acireductone synthase activity
G0:0048160	1	primary follicle stage
G0:0000023	1	maltose metabolic process
G0:0000026	1	alpha-1,2-mannosyltransferase activity
G0:0014016	1	neuroblast differentiation
G0:0014013	1	regulation of gliogenesis
G0:0004730	1	pseudouridylate synthase activity
G0:0031673	1	H zone
G0:0004733	1	pyridoxamine-phosphate oxidase activity
G0:0004736	1	pyruvate carboxylase activity
G0:0004810	1	tRNA adenylyltransferase activity
G0:0004363	1	glutathione synthase activity
G0:0071449	1	cellular response to lipid hydroperoxide
G0:0002897	1	positive regulation of central B cell tolerance induction
G0:0051322	1	anaphase
G0:0050333	1	thiamin-triphosphatase activity
G0:0018012	1	N-terminal peptidyl-alanine trimethylation
G0:0018016	1	N-terminal peptidyl-proline dimethylation
G0:0010577	1	metalloenzyme activator activity
G0:0071404	1	cellular response to low-density lipoprotein particle stimulus
G0:0044772	1	mitotic cell cycle phase transition
G0:0071401	1	cellular response to triglyceride
G0:0002143	1	tRNA wobble position uridine thiolation
G0:0070315	1	G1 to G0 transition involved in cell differentiation

G0:0032594	1	protein transport within lipid bilayer
G0:0032597	1	B cell receptor transport into membrane raft
G0:1901532	1	regulation of hematopoietic progenitor cell differentiation
G0:1901536	1	negative regulation of DNA demethylation
G0:0045686	1	negative regulation of glial cell differentiation
G0:2000590	1	negative regulation of metanephric mesenchymal cell migration
G0:2000591	1	positive regulation of metanephric mesenchymal cell migration
G0:1901021	1	positive regulation of calcium ion transmembrane transporter activity
G0:2000597	1	positive regulation of optic nerve formation
G0:0030337	1	DNA polymerase processivity factor activity
G0:0035743	1	CD4-positive, alpha-beta T cell cytokine production
G0:0035745	1	T-helper 2 cell cytokine production
G0:0035717	1	chemokine (C-C motif) ligand 7 binding
G0:1901739	1	regulation of myoblast fusion
G0:0071821	1	FANCM-MHF complex
G0:1902514	1	regulation of generation of L-type calcium current
G0:0042182	1	ketone catabolic process
G0:0046514	1	ceramide catabolic process
G0:0008424	1	glycoprotein 6-alpha-L-fucosyltransferase activity
G0:0072234	1	metanephric nephron tubule development
G0:0042231	1	interleukin-13 biosynthetic process
G0:0072227	1	metanephric macula densa development
G0:0043049	1	otic placode formation
G0:0043048	1	dolichyl monophosphate biosynthetic process
G0:0072229	1	metanephric proximal convoluted tubule development
G0:0072235	1	metanephric distal tubule development
G0:0000257	1	nitrilase activity
G0:0000256	1	allantoin catabolic process
G0:0000254	1	C-4 methylsterol oxidase activity
G0:0000250	1	lanosterol synthase activity
G0:0004943	1	C3a anaphylatoxin receptor activity
G0:0004941	1	beta2-adrenergic receptor activity
G0:0004940	1	beta1-adrenergic receptor activity
G0:0060096	1	serotonin secretion, neurotransmission
G0:0039008	1	pronephric nephron tubule morphogenesis
G0:0010446	1	response to alkalinity
G0:0060592	1	mammary gland formation
G0:0031240	1	external side of cell outer membrane
G0:0060677	1	ureteric bud elongation
G0:0033488	1	cholesterol biosynthetic process via 24,25-dihydrolanosterol
G0:0060678	1	dichotomous subdivision of terminal units involved in ureteric bud branching
G0:0010370	1	perinucleolar chromocenter
G0:0048370	1	lateral mesoderm formation
G0:2000534	1	positive regulation of renal albumin absorption
G0:0005017	1	platelet-derived growth factor-activated receptor activity
G0:2000535	1	regulation of entry of bacterium into host cell
G0:0005018	1	platelet-derived growth factor alpha-receptor activity
G0:0002041	1	intussusceptive angiogenesis
G0:0051134	1	negative regulation of NK T cell activation
G0:0051139	1	metal ion:proton antiporter activity
G0:0009013	1	succinate-semialdehyde dehydrogenase [NAD(P)+] activity
G0:0050528	1	acyloxyacyl hydrolase activity
G0:2000533	1	negative regulation of renal albumin absorption
G0:0009019	1	tRNA (guanine-N1-)-methyltransferase activity
G0:0004055	1	argininosuccinate synthase activity
G0:2000405	1	negative regulation of T cell migration
G0:0004057	1	arginyltransferase activity
G0:0004056	1	argininosuccinate lyase activity
G0:0004051	1	arachidonate 5-lipoxygenase activity
G0:0004059	1	aralkylamine N-acetyltransferase activity
G0:0004058	1	aromatic-L-amino-acid decarboxylase activity
G0:0036049	1	peptidyl-lysine desuccinylation
G0:0036048	1	protein desuccinylation
G0:0036041	1	long-chain fatty acid binding
G0:0022613	1	ribonucleoprotein complex biogenesis
G0:0022616	1	DNA strand elongation
G0:0022615	1	protein to membrane docking
G0:0060448	1	dichotomous subdivision of terminal units involved in lung branching
G0:0045299	1	otolith mineralization
G0:0090235	1	regulation of metaphase plate congression
G0:0043603	1	cellular amide metabolic process
G0:0043602	1	nitrate catabolic process
G0:0003912	1	DNA nucleotidylexotransferase activity
G0:0070673	1	response to interleukin-18

G0:0042954	1	lipoprotein transporter activity
G0:0051025	1	negative regulation of immunoglobulin secretion
G0:0070853	1	myosin VI binding
G0:0023035	1	CD40 signaling pathway
G0:0051445	1	regulation of meiotic cell cycle
G0:0000291	1	nuclear-transcribed mRNA catabolic process, exonucleolytic
G0:0030281	1	structural constituent of cutaneous appendage
G0:0016034	1	maleylacetoacetate isomerase activity
G0:0000822	1	inositol hexakisphosphate binding
G0:0040001	1	establishment of mitotic spindle localization
G0:0000824	1	inositol tetrakisphosphate 3-kinase activity
G0:0090346	1	cellular organofluorine metabolic process
G0:0005307	1	choline:sodium symporter activity
G0:1901491	1	negative regulation of lymphangiogenesis
G0:1901492	1	positive regulation of lymphangiogenesis
G0:0021999	1	neural plate anterior/posterior regionalization
G0:0021998	1	neural plate mediolateral regionalization
G0:0021990	1	neural plate formation
G0:0021993	1	initiation of neural tube closure
G0:0021997	1	neural plate axis specification
G0:1900015	1	regulation of cytokine production involved in inflammatory response
G0:0015744	1	succinate transport
G0:1900011	1	negative regulation of corticotropin-releasing hormone receptor activity
G0:0060844	1	arterial endothelial cell fate commitment
G0:0044089	1	positive regulation of cellular component biogenesis
G0:0032127	1	dense core granule membrane
G0:0034359	1	mature chylomicron
G0:0034358	1	plasma lipoprotein particle
G0:0017089	1	glycolipid transporter activity
G0:0034356	1	NAD biosynthesis via nicotinamide riboside salvage pathway
G0:0034602	1	oxoglutarate dehydrogenase (NAD+) activity
G0:0034353	1	RNA pyrophosphohydrolase activity
G0:0051490	1	negative regulation of filopodium assembly
G0:0015849	1	organic acid transport
G0:0030298	1	receptor signaling protein tyrosine kinase activator activity
G0:0002678	1	positive regulation of chronic inflammatory response
G0:0002673	1	regulation of acute inflammatory response
G0:0097484	1	dendrite extension
G0:0030294	1	receptor signaling protein tyrosine kinase inhibitor activity
G0:0005956	1	protein kinase CK2 complex
G0:0004632	1	phosphopantothenate--cysteine ligase activity
G0:0004142	1	diacylglycerol cholinephosphotransferase activity
G0:0016247	1	channel regulator activity
G0:0004140	1	dephospho-CoA kinase activity
G0:0016246	1	RNA interference
G0:1903094	1	negative regulation of protein K48-linked deubiquitination
G0:0010813	1	neuropeptide catabolic process
G0:0060464	1	lung lobe formation
G0:0060461	1	right lung morphogenesis
G0:0010814	1	substance P catabolic process
G0:1902121	1	lithocholic acid binding
G0:0004534	1	5'-3' exoribonuclease activity
G0:0004530	1	deoxyribonuclease I activity
G0:0006751	1	glutathione catabolic process
G0:0048638	1	regulation of developmental growth
G0:0048145	1	regulation of fibroblast proliferation
G0:0048632	1	negative regulation of skeletal muscle tissue growth
G0:0005224	1	ATP-binding and phosphorylation-dependent chloride channel activity
G0:0014076	1	response to fluoxetine
G0:0042720	1	mitochondrial inner membrane peptidase complex
G0:0031651	1	negative regulation of heat generation
G0:0060280	1	negative regulation of ovulation
G0:0031658	1	negative regulation of cyclin-dependent protein serine/threonine kinase activity involved in G1/S transition of mitotic cell cycle
G0:0060284	1	regulation of cell development
G0:1902857	1	positive regulation of nonmotile primary cilium assembly
G0:0042892	1	chloramphenicol transport
G0:0042840	1	D-glucuronate catabolic process
G0:0047191	1	1-alkylglycerophosphocholine O-acyltransferase activity
G0:0022406	1	membrane docking
G0:0022402	1	cell cycle process
G0:0002878	1	negative regulation of acute inflammatory response to non-antigenic stimulus
G0:0032353	1	negative regulation of hormone biosynthetic process
G0:0007576	1	nucleolar fragmentation

GO:0015217 1 ADP transmembrane transporter activity
 GO:0015216 1 purine nucleotide transmembrane transporter activity
 GO:0050313 1 sulfur dioxygenase activity
 GO:2000143 1 negative regulation of DNA-templated transcription, initiation
 GO:2000412 1 positive regulation of thymocyte migration
 GO:0019742 1 pentacyclic triterpenoid metabolic process
 GO:0019964 1 interferon-gamma binding
 GO:0019747 1 regulation of isoprenoid metabolic process
 GO:0019962 1 type I interferon binding
 GO:0019969 1 interleukin-10 binding
 GO:0070086 1 ubiquitin-dependent endocytosis
 GO:0019730 1 antimicrobial humoral response
 GO:0071936 1 coreceptor activity involved in Wnt signaling pathway
 GO:2000751 1 histone H3-T3 phosphorylation involved in chromosome passenger complex localization to kinetochore
 GO:2000027 1 regulation of organ morphogenesis
 GO:2000758 1 positive regulation of peptidyl-lysine acetylation
 GO:0023057 1 negative regulation of signaling
 GO:0070335 1 aspartate binding
 GO:0038042 1 dimeric G-protein coupled receptor signaling pathway
 GO:0038047 1 morphine receptor activity
 GO:0038046 1 enkephalin receptor activity
 GO:0038049 1 ligand-activated RNA polymerase II transcription factor binding
 transcription factor activity
 GO:0038048 1 dynorphin receptor activity
 GO:0016223 1 beta-alanine-pyruvate transaminase activity
 GO:0052657 1 guanine phosphoribosyltransferase activity
 GO:0052652 1 cyclic purine nucleotide metabolic process
 GO:0021697 1 cerebellar cortex formation
 GO:0021691 1 cerebellar Purkinje cell layer maturation
 GO:0021881 1 Wnt-activated signaling pathway involved in forebrain neuron fate commitment
 GO:0046534 1 positive regulation of photoreceptor cell differentiation
 GO:0046538 1 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase activity
 GO:0046539 1 histamine N-methyltransferase activity
 GO:0045713 1 low-density lipoprotein particle receptor biosynthetic process
 GO:0017168 1 5-oxoprolinase (ATP-hydrolyzing) activity
 GO:0047621 1 acylpyruvate hydrolase activity
 GO:0047620 1 acylglycerol kinase activity
 GO:1902732 1 positive regulation of chondrocyte proliferation
 GO:0086103 1 G-protein coupled receptor signaling pathway involved in heart process
 GO:0018395 1 peptidyl-lysine hydroxylation to 5-hydroxy-L-lysine
 GO:0006566 1 threonine metabolic process
 GO:0072240 1 metanephric DCT cell differentiation
 GO:0035769 1 B cell chemotaxis across high endothelial venule
 GO:0035768 1 endothelial cell chemotaxis to fibroblast growth factor
 GO:1900758 1 negative regulation of D-amino-acid oxidase activity
 GO:1900451 1 positive regulation of glutamate receptor signaling pathway
 GO:0031001 1 response to brefeldin A
 GO:0072303 1 positive regulation of glomerular metanephric mesangial cell proliferation
 GO:0039020 1 pronephric nephron tubule development
 GO:0039023 1 pronephric duct morphogenesis
 GO:0034014 1 response to triglyceride
 GO:0015980 1 energy derivation by oxidation of organic compounds
 GO:0046390 1 ribose phosphate biosynthetic process
 GO:0097013 1 phagocytic vesicle lumen
 GO:0035491 1 positive regulation of leukotriene production involved in inflammatory response
 GO:0052599 1 methylputrescine oxidase activity
 GO:0035493 1 SNARE complex assembly
 GO:0008403 1 25-hydroxycholecalciferol-24-hydroxylase activity
 GO:0052885 1 all-trans-retinyl-ester hydrolase, 11-cis retinol forming activity
 GO:1903007 1 positive regulation of Lys63-specific deubiquitinase activity
 GO:0060611 1 mammary gland fat development
 GO:0010768 1 negative regulation of transcription from RNA polymerase II promoter in response to UV-induced DNA damage
 GO:0005034 1 osmosensor activity
 GO:0048822 1 enucleate erythrocyte development
 GO:0060301 1 positive regulation of cytokine activity
 GO:0033182 1 regulation of histone ubiquitination
 GO:0044829 1 positive regulation by host of viral genome replication
 GO:0060300 1 regulation of cytokine activity
 GO:0044393 1 microspike
 GO:0044390 1 small protein conjugating enzyme binding
 GO:1903008 1 organelle disassembly

GO:0060305 1 regulation of cell diameter
 GO:0060304 1 regulation of phosphatidylinositol dephosphorylation
 GO:0030719 1 P granule organization
 GO:0050031 1 L-pipecolate oxidase activity
 GO:0000173 1 inactivation of MAPK activity involved in osmosensory signaling pathway
 GO:0035410 1 dihydrotestosterone 17-beta-dehydrogenase activity
 GO:1902462 1 positive regulation of mesenchymal stem cell proliferation
 GO:1902463 1 protein localization to cell leading edge
 GO:0045127 1 N-acetylglucosamine kinase activity
 GO:0033214 1 iron assimilation by chelation and transport
 GO:0018979 1 trichloroethylene metabolic process
 GO:0008349 1 MAP kinase kinase kinase activity
 GO:0008617 1 guanosine metabolic process
 GO:0043626 1 PCNA complex
 GO:0043624 1 cellular protein complex disassembly
 GO:0045272 1 plasma membrane respiratory chain complex I
 GO:0045273 1 respiratory chain complex II
 GO:0045271 1 respiratory chain complex I
 GO:0019518 1 L-threonine catabolic process to glycine
 GO:0019516 1 lactate oxidation
 GO:0004079 1 biotin-[methylmalonyl-CoA-carboxytransferase] ligase activity
 GO:0004077 1 biotin-[acetyl-CoA-carboxylase] ligase activity
 GO:0004070 1 aspartate carbamoyltransferase activity
 GO:0052798 1 beta-galactoside alpha-2,3-sialyltransferase activity
 GO:0031883 1 taste receptor binding
 GO:0070438 1 mTOR-FKBP12-rapamycin complex
 GO:0070430 1 positive regulation of nucleotide-binding oligomerization domain
 containing 1 signaling pathway
 GO:0070433 1 negative regulation of nucleotide-binding oligomerization domain
 containing 2 signaling pathway
 GO:0070434 1 positive regulation of nucleotide-binding oligomerization domain
 containing 2 signaling pathway
 GO:0002685 1 regulation of leukocyte migration
 GO:0032723 1 positive regulation of connective tissue growth factor production
 GO:2000255 1 negative regulation of male germ cell proliferation
 GO:2000254 1 regulation of male germ cell proliferation
 GO:0033091 1 positive regulation of immature T cell proliferation
 GO:2000256 1 positive regulation of male germ cell proliferation
 GO:0060825 1 fibroblast growth factor receptor signaling pathway involved in neural
 plate anterior/posterior pattern formation
 GO:0015152 1 glucose-6-phosphate transmembrane transporter activity
 GO:0050104 1 L-gulonate 3-dehydrogenase activity
 GO:0060829 1 negative regulation of canonical Wnt signaling pathway involved in neural
 plate anterior/posterior pattern formation
 GO:0033897 1 ribonuclease T2 activity
 GO:0034373 1 intermediate-density lipoprotein particle remodeling
 GO:0005854 1 nascent polypeptide-associated complex
 GO:0060169 1 negative regulation of adenosine receptor signaling pathway
 GO:0009309 1 amine biosynthetic process
 GO:0009305 1 protein biotinylation
 GO:0046705 1 CDP biosynthetic process
 GO:0070649 1 formin-nucleated actin cable assembly
 GO:0030272 1 5-formyltetrahydrofolate cyclo-ligase activity
 GO:0030273 1 melanin-concentrating hormone receptor activity
 GO:0034511 1 U3 snoRNA binding
 GO:0090193 1 positive regulation of glomerulus development
 GO:0002412 1 antigen transcytosis by M cells in mucosal-associated lymphoid tissue
 GO:0035864 1 response to potassium ion
 GO:0001581 1 detection of chemical stimulus involved in sensory perception of sour
 taste
 GO:1901612 1 cardiolipin binding
 GO:1901611 1 phosphatidylglycerol binding
 GO:0061061 1 muscle structure development
 GO:0035538 1 carbohydrate response element binding
 GO:0042376 1 phyloquinone catabolic process
 GO:0072161 1 mesenchymal cell differentiation involved in kidney development
 GO:0043369 1 CD4-positive or CD8-positive, alpha-beta T cell lineage commitment
 GO:0060446 1 branching involved in open tracheal system development
 GO:0003692 1 left-handed Z-DNA binding
 GO:0002358 1 B cell homeostatic proliferation
 GO:0004511 1 tyrosine 3-monooxygenase activity
 GO:0004513 1 neolactotetraosylceramide alpha-2,3-sialyltransferase activity
 GO:0004516 1 nicotinate phosphoribosyltransferase activity
 GO:0072163 1 mesonephric epithelium development
 GO:0031081 1 nuclear pore distribution

G0:0042489	1	negative regulation of odontogenesis of dentin-containing tooth
G0:0008616	1	queuosine biosynthetic process
G0:1902122	1	chenodeoxycholic acid binding
G0:0048613	1	embryonic ectodermal digestive tract morphogenesis
G0:0042703	1	menstruation
G0:0042706	1	eye photoreceptor cell fate commitment
G0:0031635	1	adenylate cyclase-inhibiting opioid receptor signaling pathway
G0:0039532	1	negative regulation of viral-induced cytoplasmic pattern recognition receptor signaling pathway
G0:2001251	1	negative regulation of chromosome organization
G0:0035718	1	macrophage migration inhibitory factor binding
G0:0002851	1	positive regulation of peripheral T cell tolerance induction
G0:0040032	1	post-embryonic body morphogenesis
G0:2001142	1	nicotinate transport
G0:0010603	1	regulation of cytoplasmic mRNA processing body assembly
G0:0015234	1	thiamine transmembrane transporter activity
G0:0015230	1	FAD transmembrane transporter activity
G0:0010609	1	mRNA localization resulting in posttranscriptional regulation of gene expression
G0:0001587	1	Gq/11-coupled serotonin receptor activity
G0:0003983	1	UTP:glucose-1-phosphate uridylyltransferase activity
G0:0002581	1	negative regulation of antigen processing and presentation of peptide or polysaccharide antigen via MHC class II
G0:0015099	1	nickel cation transmembrane transporter activity
G0:0015093	1	ferrous iron transmembrane transporter activity
G0:0044029	1	hypomethylation of CpG island
G0:0015094	1	lead ion transmembrane transporter activity
G0:2000005	1	negative regulation of metanephric S-shaped body morphogenesis
G0:2000007	1	negative regulation of metanephric comma-shaped body morphogenesis
G0:2000003	1	positive regulation of DNA damage checkpoint
G0:0070350	1	regulation of white fat cell proliferation
G0:0070352	1	positive regulation of white fat cell proliferation
G0:0038066	1	p38MAPK cascade
G0:0036312	1	phosphatidylinositol 3-kinase regulatory subunit binding
G0:0004692	1	cGMP-dependent protein kinase activity
G0:0003322	1	pancreatic A cell development
G0:0003327	1	type B pancreatic cell fate commitment
G0:0008404	1	arachidonic acid 14,15-epoxygenase activity
G0:0008405	1	arachidonic acid 11,12-epoxygenase activity
G0:0035851	1	Krueppel-associated box domain binding
G0:0016768	1	spermine synthase activity
G0:0047391	1	alkylglycerophosphoethanolamine phosphodiesterase activity
G0:0047390	1	glycerophosphocholine cholinephosphodiesterase activity
G0:0047394	1	glycerophosphoinositol inositolphosphodiesterase activity
G0:0003061	1	positive regulation of the force of heart contraction by norepinephrine
G0:0043553	1	negative regulation of phosphatidylinositol 3-kinase activity
G0:0002095	1	caveolar macromolecular signaling complex
G0:0045735	1	nutrient reservoir activity
G0:0045738	1	negative regulation of DNA repair
G0:0008321	1	Ral guanyl-nucleotide exchange factor activity
G0:0002295	1	T-helper cell lineage commitment
G0:0071000	1	response to magnetism
G0:0071004	1	U2-type prespliceosome
G0:0072268	1	pattern specification involved in metanephros development
G0:0072264	1	metanephric glomerular endothelium development
G0:1900737	1	negative regulation of phospholipase C-activating G-protein coupled receptor signaling pathway
G0:0035709	1	memory T cell activation
G0:1900223	1	positive regulation of beta-amyloid clearance
G0:0035705	1	T-helper 17 cell chemotaxis
G0:0035445	1	borate transmembrane transport
G0:1900738	1	positive regulation of phospholipase C-activating G-protein coupled receptor signaling pathway
G0:0031021	1	interphase microtubule organizing center
G0:0060051	1	negative regulation of protein glycosylation
G0:0060587	1	regulation of lipoprotein lipid oxidation
G0:0034038	1	deoxyhypusine synthase activity
G0:0060580	1	ventral spinal cord interneuron fate determination
G0:0060588	1	negative regulation of lipoprotein lipid oxidation
G0:0097031	1	mitochondrial respiratory chain complex I biogenesis
G0:0097037	1	heme export
G0:0061189	1	positive regulation of sclerotome development
G0:0061187	1	regulation of chromatin silencing at rDNA
G0:0061185	1	negative regulation of dermatome development
G0:0061181	1	regulation of chondrocyte development

G0:0009234	1	menaquinone biosynthetic process
G0:0009231	1	riboflavin biosynthetic process
G0:0046111	1	xanthine biosynthetic process
G0:0005053	1	peroxisome matrix targeting signal-2 binding
G0:0072302	1	negative regulation of metanephric glomerular mesangial cell proliferation
G0:0009585	1	red, far-red light phototransduction
G0:1902997	1	negative regulation of neurofibrillary tangle assembly
G0:0009589	1	detection of UV
G0:0060538	1	skeletal muscle organ development
G0:0031501	1	mannosyltransferase complex
G0:0030731	1	guanidinoacetate N-methyltransferase activity
G0:0003188	1	heart valve formation
G0:0034242	1	negative regulation of syncytium formation by plasma membrane fusion
G0:0036088	1	D-serine catabolic process
G0:0031695	1	alpha-2B adrenergic receptor binding
G0:0048269	1	methionine adenosyltransferase complex
G0:0008187	1	poly-pyrimidine tract binding
G0:0031629	1	synaptic vesicle fusion to presynaptic membrane
G0:0045137	1	development of primary sexual characteristics
G0:0035853	1	chromosome passenger complex localization to spindle midzone
G0:0050543	1	icosatetraenoic acid binding
G0:0018917	1	fluorene metabolic process
G0:0003844	1	1,4-alpha-glucan branching enzyme activity
G0:0060717	1	chorion development
G0:0015143	1	urate transmembrane transporter activity
G0:0071593	1	lymphocyte aggregation
G0:0070980	1	biphenyl catabolic process
G0:0070981	1	L-asparagine biosynthetic process
G0:0070634	1	transepithelial ammonium transport
G0:0004092	1	carnitine O-acetyltransferase activity
G0:0042910	1	xenobiotic transporter activity
G0:0004096	1	catalase activity
G0:0045989	1	positive regulation of striated muscle contraction
G0:0040040	1	thermosensory behavior
G0:0070181	1	small ribosomal subunit rRNA binding
G0:0070184	1	mitochondrial tyrosyl-tRNA aminoacylation
G0:0032701	1	negative regulation of interleukin-18 production
G0:0050290	1	sphingomyelin phosphodiesterase D activity
G0:1902904	1	negative regulation of fibril organization
G0:2000277	1	positive regulation of oxidative phosphorylation uncoupler activity
G0:0033609	1	oxalate metabolic process
G0:0060809	1	mesodermal to mesenchymal transition involved in gastrulation
G0:0004742	1	dihydrolipoyllysine-residue acetyltransferase activity
G0:0042790	1	transcription of nuclear large rRNA transcript from RNA polymerase I promoter
G0:0060802	1	epiblast cell-extraembryonic ectoderm cell signaling involved in anterior/posterior axis specification
G0:0060804	1	positive regulation of Wnt signaling pathway by BMP signaling pathway
G0:0051531	1	NFAT protein import into nucleus
G0:0060806	1	negative regulation of cell differentiation involved in embryonic placenta development
G0:1900276	1	regulation of proteinase activated receptor activity
G0:0071585	1	detoxification of cadmium ion
G0:0071584	1	negative regulation of zinc ion transmembrane import
G0:0016153	1	urocanate hydratase activity
G0:0016150	1	translation release factor activity, codon nonspecific
G0:0016154	1	pyrimidine-nucleoside phosphorylase activity
G0:0051459	1	regulation of corticotropin secretion
G0:0051458	1	corticotropin secretion
G0:0051452	1	intracellular pH reduction
G0:0005873	1	plus-end kinesin complex
G0:0072016	1	glomerular parietal epithelial cell development
G0:0044610	1	FMN transmembrane transporter activity
G0:0043128	1	positive regulation of 1-phosphatidylinositol 4-kinase activity
G0:0046272	1	stilbene catabolic process
G0:1901628	1	positive regulation of postsynaptic membrane organization
G0:0002637	1	regulation of immunoglobulin production
G0:0030251	1	guanylate cyclase inhibitor activity
G0:0003065	1	positive regulation of heart rate by epinephrine
G0:0003972	1	RNA ligase (ATP) activity
G0:0003977	1	UDP-N-acetylglucosamine diphosphorylase activity
G0:1901630	1	negative regulation of presynaptic membrane organization
G0:0003976	1	UDP-N-acetylglucosamine-lysosomal-enzyme N-acetylglucosaminephosphotransferase activity
G0:0097198	1	histone H3-K36 trimethylation

GO:0003975 1 UDP-N-acetylglucosamine-dolichyl-phosphate N-acetylglucosaminophosphotransferase activity
 GO:0035048 1 splicing factor protein import into nucleus
 GO:1990264 1 peptidyl-tyrosine dephosphorylation involved in inactivation of protein kinase activity
 GO:1990266 1 neutrophil migration
 GO:1990261 1 pre-mRNA catabolic process
 GO:0035516 1 oxidative DNA demethylase activity
 GO:0030037 1 actin filament reorganization involved in cell cycle
 GO:0061043 1 regulation of vascular wound healing
 GO:0060978 1 angiogenesis involved in coronary vascular morphogenesis
 GO:0003952 1 NAD+ synthase (glutamine-hydrolyzing) activity
 GO:0061518 1 microglial cell proliferation
 GO:0061048 1 negative regulation of branching involved in lung morphogenesis
 GO:0003979 1 UDP-glucose 6-dehydrogenase activity
 GO:0003978 1 UDP-glucose 4-epimerase activity
 GO:0042357 1 thiamine diphosphate metabolic process
 GO:0047936 1 glucose 1-dehydrogenase [NAD(P)] activity
 GO:0006240 1 dCDP biosynthetic process
 GO:0030628 1 pre-mRNA 3'-splice site binding
 GO:0003955 1 NAD(P)H dehydrogenase (quinone) activity
 GO:0000379 1 tRNA-type intron splice site recognition and cleavage
 GO:0009917 1 sterol 5-alpha reductase activity
 GO:0009914 1 hormone transport
 GO:0046817 1 chemokine receptor antagonist activity
 GO:0006060 1 sorbitol metabolic process
 GO:0048677 1 axon extension involved in regeneration
 GO:0005260 1 channel-conductance-controlling ATPase activity
 GO:0047933 1 glucose-1,6-bisphosphate synthase activity
 GO:0004798 1 thymidylate kinase activity
 GO:0042766 1 nucleosome mobilization
 GO:0004790 1 thioether S-methyltransferase activity
 GO:0072110 1 glomerular mesangial cell proliferation
 GO:0050720 1 interleukin-1 beta biosynthetic process
 GO:0010255 1 glucose mediated signaling pathway
 GO:0072060 1 outer medullary collecting duct development
 GO:0035846 1 oviduct epithelium development
 GO:0060398 1 regulation of growth hormone receptor signaling pathway
 GO:0050462 1 N-acetylneuraminase synthase activity
 GO:0030264 1 nuclear fragmentation involved in apoptotic nuclear change
 GO:0004138 1 deoxyguanosine kinase activity
 GO:0004139 1 deoxyribose-phosphate aldolase activity
 GO:0002839 1 positive regulation of immune response to tumor cell
 GO:0030621 1 U4 snRNA binding
 GO:0004132 1 dCMP deaminase activity
 GO:0004133 1 glycogen debranching enzyme activity
 GO:0004134 1 4-alpha-glucanotransferase activity
 GO:0004135 1 amylo-alpha-1,6-glucosidase activity
 GO:0072267 1 metanephric capsule specification
 GO:0007538 1 primary sex determination
 GO:0010625 1 positive regulation of Schwann cell proliferation
 GO:0001560 1 regulation of cell growth by extracellular stimulus
 GO:0046911 1 metal chelating activity
 GO:0001567 1 cholesterol 25-hydroxylase activity
 GO:0046915 1 transition metal ion transmembrane transporter activity
 GO:0017071 1 intracellular cyclic nucleotide activated cation channel complex
 GO:0030623 1 U5 snRNA binding
 GO:0071971 1 extracellular vesicular exosome assembly
 GO:0008792 1 arginine decarboxylase activity
 GO:0008796 1 bis(5'-nucleosyl)-tetraphosphatase activity
 GO:2000063 1 positive regulation of ureter smooth muscle cell differentiation
 GO:0002223 1 stimulatory C-type lectin receptor signaling pathway
 GO:0032850 1 positive regulation of ARF GTPase activity
 GO:0038009 1 regulation of signal transduction by receptor internalization
 GO:0008425 1 2-polyprenyl-6-methoxy-1,4-benzoquinone methyltransferase activity
 GO:0035874 1 cellular response to copper ion starvation
 GO:0000962 1 positive regulation of mitochondrial RNA catabolic process
 GO:0055103 1 ligase regulator activity
 GO:0000964 1 mitochondrial RNA 5'-end processing
 GO:0000966 1 RNA 5'-end processing
 GO:0047408 1 alkenylglycerophosphocholine hydrolase activity
 GO:2000688 1 positive regulation of rubidium ion transmembrane transporter activity
 GO:0043578 1 nuclear matrix organization
 GO:2000682 1 positive regulation of rubidium ion transport
 GO:2000683 1 regulation of cellular response to X-ray

G0:2000680	1	regulation of rubidium ion transport
G0:2000685	1	positive regulation of cellular response to X-ray
G0:0003963	1	RNA-3'-phosphate cyclase activity
G0:0035701	1	hematopoietic stem cell migration
G0:0045751	1	negative regulation of Toll signaling pathway
G0:0033981	1	D-dopachrome decarboxylase activity
G0:0071025	1	RNA surveillance
G0:0031477	1	myosin VII complex
G0:0034230	1	enkephalin processing
G0:0034231	1	islet amyloid polypeptide processing
G0:0072285	1	mesenchymal to epithelial transition involved in metanephric renal vesicle formation
G0:0034589	1	hydroxyproline transport
G0:0072287	1	metanephric distal tubule morphogenesis
G0:0072286	1	metanephric connecting tubule development
G0:0033919	1	glucan 1,3-alpha-glucosidase activity
G0:1900245	1	positive regulation of MDA-5 signaling pathway
G0:1900242	1	regulation of synaptic vesicle endocytosis
G0:0010698	1	acetyltransferase activator activity
G0:0072141	1	renal interstitial cell development
G0:0035727	1	lysophosphatidic acid binding
G0:0035723	1	interleukin-15-mediated signaling pathway
G0:0060035	1	notochord cell development
G0:0015942	1	formate metabolic process
G0:0022829	1	wide pore channel activity
G0:0034050	1	host programmed cell death induced by symbiont
G0:0097057	1	TRAF2-GSTP1 complex
G0:0097051	1	establishment of protein localization to endoplasmic reticulum membrane
G0:2000808	1	negative regulation of synaptic vesicle clustering
G0:0061501	1	cyclic-GMP-AMP synthase activity
G0:0033593	1	BRCA2-MAGE-D1 complex
G0:0034039	1	8-oxo-7,8-dihydroguanine DNA N-glycosylase activity
G0:0090085	1	regulation of protein deubiquitination
G0:0090081	1	regulation of heart induction by regulation of canonical Wnt signaling pathway
G0:2000521	1	negative regulation of immunological synapse formation
G0:2000526	1	positive regulation of glycoprotein biosynthetic process involved in immunological synapse formation
G0:0061050	1	regulation of cell growth involved in cardiac muscle cell development
G0:1902715	1	positive regulation of interferon-gamma secretion
G0:2001306	1	lipoxin B4 biosynthetic process
G0:0032145	1	succinate-semialdehyde dehydrogenase binding
G0:0035472	1	choriogonadotropin hormone receptor activity
G0:0065010	1	extracellular membrane-bounded organelle
G0:0048244	1	phytanoyl-CoA dioxygenase activity
G0:1900477	1	negative regulation of G1/S transition of mitotic cell cycle by negative regulation of transcription from RNA polymerase II promoter
G0:0048242	1	epinephrine secretion
G0:0045113	1	regulation of integrin biosynthetic process
G0:0045112	1	integrin biosynthetic process
G0:0060456	1	positive regulation of digestive system process
G0:0004304	1	estrone sulfotransferase activity
G0:0004306	1	ethanolamine-phosphate cytidylyltransferase activity
G0:0018931	1	naphthalene metabolic process
G0:0003827	1	alpha-1,3-mannosylglycoprotein 2-beta-N-acetylglucosaminyltransferase activity
G0:0045239	1	tricarboxylic acid cycle enzyme complex
G0:0045234	1	protein palmitoylation
G0:0008309	1	double-stranded DNA exodeoxyribonuclease activity
G0:0042938	1	dipeptide transport
G0:0070611	1	histone methyltransferase activity (H3-R2 specific)
G0:0070612	1	histone methyltransferase activity (H2A-R3 specific)
G0:0070615	1	nucleosome-dependent ATPase activity
G0:0070618	1	Grb2-Sos complex
G0:0042931	1	enterobactin transporter activity
G0:0042936	1	dipeptide transporter activity
G0:0061507	1	cyclic-GMP-AMP binding
G0:2000479	1	regulation of cAMP-dependent protein kinase activity
G0:2000478	1	positive regulation of metanephric glomerular visceral epithelial cell development
G0:0051089	1	constitutive protein ectodomain proteolysis
G0:0031283	1	negative regulation of guanylate cyclase activity
G0:0051083	1	'de novo' cotranslational protein folding
G0:0032277	1	negative regulation of gonadotropin secretion
G0:0032272	1	negative regulation of protein polymerization

G0:0032273	1	positive regulation of protein polymerization
G0:0015378	1	sodium:chloride symporter activity
G0:2000213	1	positive regulation of glutamate metabolic process
G0:2000212	1	negative regulation of glutamate metabolic process
G0:0070486	1	leukocyte aggregation
G0:0090500	1	endocardial cushion to mesenchymal transition
G0:0033494	1	ferulate metabolic process
G0:0050146	1	nucleoside phosphotransferase activity
G0:0050145	1	nucleoside phosphate kinase activity
G0:0015112	1	nitrate transmembrane transporter activity
G0:0015002	1	heme-copper terminal oxidase activity
G0:0071566	1	UFM1 activating enzyme activity
G0:0019627	1	urea metabolic process
G0:0016137	1	glycoside metabolic process
G0:0019119	1	phenanthrene-9,10-epoxide hydrolase activity
G0:0019115	1	benzaldehyde dehydrogenase activity
G0:0003874	1	6-pyruvoyltetrahydropterin synthase activity
G0:0005895	1	interleukin-5 receptor complex
G0:0051435	1	BH4 domain binding
G0:0005898	1	interleukin-13 receptor complex
G0:0046038	1	GMP catabolic process
G0:0032980	1	keratinocyte activation
G0:0045128	1	negative regulation of reciprocal meiotic recombination
G0:0033059	1	cellular pigmentation
G0:1900387	1	negative regulation of cell-cell adhesion by negative regulation of
transcription from		RNA polymerase II promoter
G0:0008398	1	sterol 14-demethylase activity
G0:0030237	1	female sex determination
G0:0030233	1	deoxynucleotide transmembrane transporter activity
G0:0046030	1	inositol trisphosphate phosphatase activity
G0:0008397	1	sterol 12-alpha-hydroxylase activity
G0:1901652	1	response to peptide
G0:0002001	1	renin secretion into blood stream
G0:0010428	1	methyl-CpNpG binding
G0:0035063	1	nuclear speck organization
G0:0030586	1	[methionine synthase] reductase activity
G0:0061026	1	cardiac muscle tissue regeneration
G0:0004508	1	steroid 17-alpha-monooxygenase activity
G0:0031983	1	vesicle lumen
G0:0072542	1	protein phosphatase activator activity
G0:0072541	1	peroxynitrite reductase activity
G0:0006049	1	UDP-N-acetylglucosamine catabolic process
G0:0010743	1	regulation of macrophage derived foam cell differentiation
G0:0044111	1	development involved in symbiotic interaction
G0:0006040	1	amino sugar metabolic process
G0:0006042	1	glucosamine biosynthetic process
G0:0006043	1	glucosamine catabolic process
G0:0044546	1	NLRP3 inflammasome complex assembly
G0:0005277	1	acetylcholine transmembrane transporter activity
G0:1903122	1	negative regulation of TRAIL-activated apoptotic signaling pathway
G0:1903126	1	negative regulation of centriole-centriole cohesion
G0:0042747	1	circadian sleep/wake cycle, REM sleep
G0:0060434	1	bronchus morphogenesis
G0:0042748	1	circadian sleep/wake cycle, non-REM sleep
G0:0050706	1	regulation of interleukin-1 beta secretion
G0:0050701	1	interleukin-1 secretion
G0:0010273	1	detoxification of copper ion
G0:0031403	1	lithium ion binding
G0:1900076	1	regulation of cellular response to insulin stimulus
G0:0001401	1	mitochondrial sorting and assembly machinery complex
G0:0048640	1	negative regulation of developmental growth
G0:0004113	1	2',3'-cyclic-nucleotide 3'-phosphodiesterase activity
G0:0090246	1	convergent extension involved in somitogenesis
G0:1902523	1	positive regulation of protein K63-linked ubiquitination
G0:0010646	1	regulation of cell communication
G0:1902524	1	positive regulation of protein K48-linked ubiquitination
G0:1902527	1	positive regulation of protein monoubiquitination
G0:0036326	1	VEGF-A-activated receptor activity
G0:0015100	1	vanadium ion transmembrane transporter activity
G0:0014048	1	regulation of glutamate secretion
G0:0016992	1	lipoate synthase activity
G0:0071951	1	conversion of methionyl-tRNA to N-formyl-methionyl-tRNA
G0:0055082	1	cellular chemical homeostasis
G0:2000042	1	negative regulation of double-strand break repair via homologous
recombination		

G0:2000043	1	regulation of cardiac cell fate specification
G0:0038089	1	positive regulation of cell migration by vascular endothelial growth factor signaling pathway
G0:0030366	1	molybdopterin synthase activity
G0:0038024	1	cargo receptor activity
G0:0032048	1	cardiolipin metabolic process
G0:0008445	1	D-aspartate oxidase activity
G0:0008442	1	3-hydroxyisobutyrate dehydrogenase activity
G0:0008443	1	phosphofructokinase activity
G0:0008441	1	3'(2'),5'-bisphosphate nucleotidase activity
G0:0015633	1	zinc transporting ATPase activity
G0:0042108	1	positive regulation of cytokine biosynthetic process
G0:0047464	1	heparosan-N-sulfate-glucuronate 5-epimerase activity
G0:0042107	1	cytokine metabolic process
G0:0043519	1	regulation of myosin II filament organization
G0:0072734	1	cellular response to staurosporine
G0:0003025	1	regulation of systemic arterial blood pressure by baroreceptor feedback
G0:0021586	1	pons maturation
G0:0021588	1	cerebellum formation
G0:0003062	1	regulation of heart rate by chemical signal
G0:0071042	1	nuclear polyadenylation-dependent mRNA catabolic process
G0:0071048	1	nuclear retention of unspliced pre-mRNA at the site of transcription
G0:0034213	1	quinolinate catabolic process
G0:0021723	1	medullary reticular formation development
G0:0019859	1	thymine metabolic process
G0:0060016	1	granulosa cell development
G0:0060010	1	Sertoli cell fate commitment
G0:0015961	1	diadenosine polyphosphate catabolic process
G0:0046331	1	lateral inhibition
G0:0046485	1	ether lipid metabolic process
G0:0002779	1	antibacterial peptide secretion
G0:0008532	1	N-acetylactosaminide beta-1,3-N-acetylglucosaminyltransferase activity
G0:0044691	1	tooth eruption
G0:0003251	1	positive regulation of cell proliferation involved in heart valve morphogenesis
G0:0009892	1	negative regulation of metabolic process
G0:0048262	1	determination of dorsal/ventral asymmetry
G0:0031764	1	type 1 galanin receptor binding
G0:0008534	1	oxidized purine nucleobase lesion DNA N-glycosylase activity
G0:1990182	1	exosomal secretion
G0:0030999	1	linear element assembly
G0:0035964	1	COPI-coated vesicle budding
G0:0090219	1	negative regulation of lipid kinase activity
G0:0060376	1	positive regulation of mast cell differentiation
G0:0090214	1	spongiotrophoblast layer developmental growth
G0:1902731	1	negative regulation of chondrocyte proliferation
G0:0048621	1	post-embryonic digestive tract morphogenesis
G0:0090212	1	negative regulation of establishment of blood-brain barrier
G0:0090210	1	regulation of establishment of blood-brain barrier
G0:0031768	1	ghrelin receptor binding
G0:0035306	1	positive regulation of dephosphorylation
G0:0034127	1	regulation of MyD88-independent toll-like receptor signaling pathway
G0:0042835	1	BRE binding
G0:0045130	1	keratan sulfotransferase activity
G0:0051050	1	positive regulation of transport
G0:0045338	1	farnesyl diphosphate metabolic process
G0:0045136	1	development of secondary sexual characteristics
G0:0000126	1	transcription factor TFIIIB complex
G0:0004321	1	fatty-acyl-CoA synthase activity
G0:0004326	1	tetrahydrofolylpolyglutamate synthase activity
G0:0004325	1	ferrochelatase activity
G0:0004324	1	ferredoxin-NADP+ reductase activity
G0:0072097	1	negative regulation of branch elongation involved in ureteric bud branching by BMP signaling pathway
G0:0072092	1	ureteric bud invasion
G0:0001544	1	initiation of primordial ovarian follicle growth
G0:0008859	1	exoribonuclease II activity
G0:0006876	1	cellular cadmium ion homeostasis
G0:0043682	1	copper-transporting ATPase activity
G0:0045210	1	FasL biosynthetic process
G0:0045212	1	neurotransmitter receptor biosynthetic process
G0:0045218	1	zonula adherens maintenance
G0:0032606	1	type I interferon production
G0:0001545	1	primary ovarian follicle growth
G0:0042269	1	regulation of natural killer cell mediated cytotoxicity

G0:0070946	1	neutrophil mediated killing of gram-positive bacterium
G0:0070947	1	neutrophil mediated killing of fungus
G0:0031429	1	box H/ACA snoRNP complex
G0:0031895	1	V1B vasopressin receptor binding
G0:0097487	1	multivesicular body, internal vesicle
G0:2000187	1	positive regulation of phosphate transmembrane transport
G0:0031896	1	V2 vasopressin receptor binding
G0:0034120	1	positive regulation of erythrocyte aggregation
G0:0070495	1	negative regulation of thrombin receptor signaling pathway
G0:0002695	1	negative regulation of leukocyte activation
G0:0009631	1	cold acclimation
G0:0009637	1	response to blue light
G0:0032210	1	regulation of telomere maintenance via telomerase
G0:0051960	1	regulation of nervous system development
G0:0015350	1	methotrexate transporter activity
G0:0018400	1	peptidyl-proline hydroxylation to 3-hydroxy-L-proline
G0:0018406	1	protein C-linked glycosylation via 2'-alpha-mannosyl-L-tryptophan
G0:0010189	1	vitamin E biosynthetic process
G0:0021910	1	smoothed signaling pathway involved in ventral spinal cord patterning
G0:0021912	1	regulation of transcription from RNA polymerase II promoter involved in spinal cord motor neuron fate specification
G0:0021919	1	BMP signaling pathway involved in spinal cord dorsal/ventral patterning
G0:0021918	1	regulation of transcription from RNA polymerase II promoter involved in somatic motor neuron fate commitment
G0:0042163	1	interleukin-12 beta subunit binding
G0:0010987	1	negative regulation of high-density lipoprotein particle clearance
G0:0090527	1	actin filament reorganization
G0:0003842	1	1-pyrroline-5-carboxylate dehydrogenase activity
G0:0015130	1	mevalonate transmembrane transporter activity
G0:0010455	1	positive regulation of cell fate commitment
G0:0015136	1	sialic acid transmembrane transporter activity
G0:0043012	1	regulation of fusion of sperm to egg plasma membrane
G0:2000452	1	regulation of CD8-positive, alpha-beta cytotoxic T cell extravasation
G0:2000451	1	positive regulation of CD8-positive, alpha-beta T cell extravasation
G0:2000454	1	positive regulation of CD8-positive, alpha-beta cytotoxic T cell extravasation
G0:0034104	1	negative regulation of tissue remodeling
G0:0052926	1	dol-P-Man:Man(6)GlcNAc(2)-PP-Dol alpha-1,2-mannosyltransferase activity
G0:0070237	1	positive regulation of activation-induced cell death of T cells
G0:0070235	1	regulation of activation-induced cell death of T cells
G0:0035932	1	aldosterone secretion
G0:0033034	1	positive regulation of myeloid cell apoptotic process
G0:0033030	1	negative regulation of neutrophil apoptotic process
G0:2000231	1	positive regulation of pancreatic stellate cell proliferation
G0:2000982	1	positive regulation of inner ear receptor cell differentiation
G0:0052929	1	ATP:3'-cytidine-cytidine-tRNA adenylyltransferase activity
G0:1901671	1	positive regulation of superoxide dismutase activity
G0:1901673	1	regulation of spindle assembly involved in mitosis
G0:1901675	1	negative regulation of histone H3-K27 acetylation
G0:1901676	1	positive regulation of histone H3-K27 acetylation
G0:0016119	1	carotene metabolic process
G0:0016116	1	carotenoid metabolic process
G0:0070985	1	TFIIK complex
G0:0042313	1	protein kinase C deactivation
G0:0043397	1	regulation of corticotropin-releasing hormone secretion
G0:0046355	1	mannan catabolic process
G0:0042164	1	interleukin-12 alpha subunit binding
G0:0072560	1	type B pancreatic cell maturation
G0:0000334	1	3-hydroxyanthranilate 3,4-dioxygenase activity
G0:0010578	1	regulation of adenylate cyclase activity involved in G-protein coupled receptor signaling pathway
G0:0004098	1	cerebroside-sulfatase activity
G0:0048789	1	cytoskeletal matrix organization at active zone
G0:0009957	1	epidermal cell fate specification
G0:0009956	1	radial pattern formation
G0:0050894	1	determination of affect
G0:0002347	1	response to tumor cell
G0:0044258	1	intestinal lipid catabolic process
G0:1900107	1	regulation of nodal signaling pathway
G0:0031098	1	stress-activated protein kinase signaling cascade
G0:0090327	1	negative regulation of locomotion involved in locomotory behavior
G0:0031302	1	intrinsic component of endosome membrane
G0:0050760	1	negative regulation of thymidylate synthase biosynthetic process
G0:1902036	1	regulation of hematopoietic stem cell differentiation
G0:2000826	1	regulation of heart morphogenesis

G0:0097338	1	response to clozapine
G0:2000824	1	negative regulation of androgen receptor activity
G0:2000825	1	positive regulation of androgen receptor activity
G0:0038193	1	thromboxane A2 signaling pathway
G0:0009403	1	toxin biosynthetic process
G0:0048790	1	maintenance of presynaptic active zone structure
G0:0045517	1	interleukin-20 receptor binding
G0:0005519	1	cytoskeletal regulatory protein binding
G0:0051386	1	regulation of neurotrophin TRK receptor signaling pathway
G0:0004170	1	dUTP diphosphatase activity
G0:0051389	1	inactivation of MAPKK activity
G0:0051388	1	positive regulation of neurotrophin TRK receptor signaling pathway
G0:0046958	1	nonassociative learning
G0:2001111	1	positive regulation of lens epithelial cell proliferation
G0:0036303	1	lymph vessel morphogenesis
G0:0036306	1	embryonic heart tube elongation
G0:0035226	1	glutamate-cysteine ligase catalytic subunit binding
G0:0018872	1	arsonoacetate metabolic process
G0:0055065	1	metal ion homeostasis
G0:0050703	1	interleukin-1 alpha secretion
G0:0036363	1	transforming growth factor beta activation
G0:0032023	1	trypsinogen activation
G0:0032029	1	myosin tail binding
G0:0032028	1	myosin head/neck binding
G0:0031547	1	brain-derived neurotrophic factor receptor signaling pathway
G0:0008460	1	dTDP-glucose 4,6-dehydratase activity
G0:0003342	1	proepicardium development
G0:0000921	1	septin ring assembly
G0:0000920	1	cytokinetic cell separation
G0:0097494	1	regulation of vesicle size
G0:0070002	1	glutamic-type peptidase activity
G0:0035101	1	FACT complex
G0:0072719	1	cellular response to cisplatin
G0:0047444	1	N-acylneuraminate-9-phosphate synthase activity
G0:0047442	1	17-alpha-hydroxyprogesterone aldolase activity
G0:0015659	1	formate uptake transmembrane transporter activity
G0:0036327	1	VEGF-B-activated receptor activity
G0:1901881	1	positive regulation of protein depolymerization
G0:0042007	1	interleukin-18 binding
G0:0003002	1	regionalization
G0:0043538	1	regulation of actin phosphorylation
G0:0045795	1	positive regulation of cell volume
G0:0045799	1	positive regulation of chromatin assembly or disassembly
G0:0060981	1	cell migration involved in coronary angiogenesis
G0:0032532	1	regulation of microvillus length
G0:0032535	1	regulation of cellular component size
G0:0033778	1	7alpha-hydroxycholest-4-en-3-one 12alpha-hydroxylase activity
G0:0034276	1	kynurenic acid biosynthetic process
G0:0002113	1	interleukin-33 binding
G0:0021703	1	locus ceruleus development
G0:0030975	1	thiamine binding
G0:0002432	1	granuloma formation
G0:0046314	1	phosphocreatine biosynthetic process
G0:0046318	1	negative regulation of glucosylceramide biosynthetic process
G0:0051608	1	histamine transport
G0:0002758	1	innate immune response-activating signal transduction
G0:0002759	1	regulation of antimicrobial humoral response
G0:0051169	1	nuclear transport
G0:0006430	1	lysyl-tRNA aminoacylation
G0:0006438	1	valyl-tRNA aminoacylation
G0:1900827	1	positive regulation of membrane depolarization during cardiac muscle cell action potential
G0:1990166	1	protein localization to site of double-strand break
G0:1990167	1	protein K27-linked deubiquitination
G0:0016990	1	arginine deiminase activity
G0:0075521	1	microtubule-dependent intracellular transport of viral material towards nucleus
G0:0019391	1	glucuronoside catabolic process
G0:0060565	1	inhibition of mitotic anaphase-promoting complex activity
G0:0008419	1	RNA lariat debranching enzyme activity
G0:0008418	1	protein-N-terminal asparagine amidohydrolase activity
G0:0030791	1	arsenite methyltransferase activity
G0:0061618	1	sublamina densa
G0:0030792	1	methylarsonite methyltransferase activity
G0:0035325	1	Toll-like receptor binding

G0:0061628	1	H3K27me3 modified histone binding
G0:0002399	1	MHC class II protein complex assembly
G0:0086092	1	regulation of the force of heart contraction by cardiac conduction
G0:0086097	1	phospholipase C-activating angiotensin-activated signaling pathway
G0:0060695	1	negative regulation of cholesterol transporter activity
G0:0060694	1	regulation of cholesterol transporter activity
G0:0060697	1	positive regulation of phospholipid catabolic process
G0:0060691	1	epithelial cell maturation involved in salivary gland development
G0:0033477	1	S-methylmethionine metabolic process
G0:0072046	1	establishment of planar polarity involved in nephron morphogenesis
G0:0005169	1	neurotrophin TRKB receptor binding
G0:0005163	1	nerve growth factor receptor binding
G0:0008127	1	quercetin 2,3-dioxygenase activity
G0:0005166	1	neurotrophin p75 receptor binding
G0:0048757	1	pigment granule maturation
G0:0000105	1	histidine biosynthetic process
G0:0070821	1	tertiary granule membrane
G0:0042466	1	chemokinesis
G0:0070826	1	paraferitin complex
G0:0047945	1	L-glutamine:pyruvate aminotransferase activity
G0:0070829	1	heterochromatin maintenance
G0:0004346	1	glucose-6-phosphatase activity
G0:0004341	1	gluconolactonase activity
G0:0004343	1	glucosamine 6-phosphate N-acetyltransferase activity
G0:0004342	1	glucosamine-6-phosphate deaminase activity
G0:0035572	1	N-terminal peptidyl-serine dimethylation
G0:0001828	1	inner cell mass cellular morphogenesis
G0:1902750	1	negative regulation of cell cycle G2/M phase transition
G0:0050129	1	N-formylglutamate deformylase activity
G0:0050124	1	N-acylneuraminate-9-phosphatase activity
G0:0070926	1	regulation of ATP:ADP antiporter activity
G0:0090158	1	endoplasmic reticulum membrane organization
G0:0031440	1	regulation of mRNA 3'-end processing
G0:0031441	1	negative regulation of mRNA 3'-end processing
G0:0031448	1	positive regulation of fast-twitch skeletal muscle fiber contraction
G0:0050648	1	5(S)-hydroxyperoxy-6E,8Z,11Z,14Z-icosatetraenoic acid binding
G0:0022018	1	lateral ganglionic eminence cell proliferation
G0:0015334	1	high affinity oligopeptide transporter activity
G0:0033612	1	receptor serine/threonine kinase binding
G0:0085018	1	maintenance of symbiont-containing vacuole by host
G0:0004778	1	succinyl-CoA hydrolase activity
G0:0018467	1	formaldehyde dehydrogenase activity
G0:0014820	1	tonic smooth muscle contraction
G0:0014822	1	detection of wounding
G0:0019481	1	L-alanine catabolic process, by transamination
G0:0019482	1	beta-alanine metabolic process
G0:0051595	1	response to methylglyoxal
G0:0044140	1	negative regulation of growth of symbiont on or near host surface
G0:0044146	1	negative regulation of growth of symbiont involved in interaction with host
G0:0071529	1	cementum mineralization
G0:0031857	1	type 1 parathyroid hormone receptor binding
G0:0032427	1	GBD domain binding
G0:2000439	1	positive regulation of monocyte extravasation
G0:2000438	1	negative regulation of monocyte extravasation
G0:0060979	1	vasculogenesis involved in coronary vascular morphogenesis
G0:0019153	1	protein-disulfide reductase (glutathione) activity
G0:0032498	1	detection of muramyl dipeptide
G0:0007066	1	female meiosis sister chromatid cohesion
G0:0032490	1	detection of molecule of bacterial origin
G0:0007060	1	male meiosis chromosome segregation
G0:0007063	1	regulation of sister chromatid cohesion
G0:0032370	1	positive regulation of lipid transport
G0:0043132	1	NAD transport
G0:0071298	1	cellular response to L-ascorbic acid
G0:0033013	1	tetrapyrrole metabolic process
G0:0033011	1	perinuclear theca
G0:0021934	1	hindbrain tangential cell migration
G0:0030895	1	apolipoprotein B mRNA editing enzyme complex
G0:0043134	1	regulation of hindgut contraction
G0:1901581	1	negative regulation of telomeric RNA transcription from RNA pol II promoter
G0:0047783	1	corticosterone 18-monooxygenase activity
G0:0016901	1	oxidoreductase activity, acting on the CH-OH group of donors, quinone or similar compound as acceptor

G0:0043492	1	ATPase activity, coupled to movement of substances
G0:0060961	1	phospholipase D inhibitor activity
G0:0047166	1	1-alkenylglycerophosphoethanolamine 0-acyltransferase activity
G0:0050080	1	malonyl-CoA decarboxylase activity
G0:0006225	1	UDP biosynthetic process
G0:0006226	1	dUMP biosynthetic process
G0:0046789	1	host cell surface receptor binding
G0:0071393	1	cellular response to progesterone stimulus
G0:0006083	1	acetate metabolic process
G0:1900122	1	positive regulation of receptor binding
G0:1900128	1	regulation of G-protein activated inward rectifier potassium channel activity
G0:0030504	1	inorganic diphosphate transmembrane transporter activity
G0:0031858	1	pituitary adenylate cyclase-activating polypeptide receptor binding
G0:0070869	1	heterochromatin assembly involved in chromatin silencing
G0:0031328	1	positive regulation of cellular biosynthetic process
G0:0031851	1	kappa-type opioid receptor binding
G0:0031323	1	regulation of cellular metabolic process
G0:1903168	1	positive regulation of pyrroline-5-carboxylate reductase activity
G0:1903169	1	regulation of calcium ion transmembrane transport
G0:0072176	1	nephric duct development
G0:0072175	1	epithelial tube formation
G0:0072173	1	metanephric tubule morphogenesis
G0:0060730	1	regulation of intestinal epithelial structure maintenance
G0:0010232	1	vascular transport
G0:0090308	1	regulation of methylation-dependent chromatin silencing
G0:0033343	1	positive regulation of collagen binding
G0:0060739	1	mesenchymal-epithelial cell signaling involved in prostate gland development
G0:0001193	1	maintenance of transcriptional fidelity during DNA-templated transcription elongation from RNA polymerase II promoter
G0:0022840	1	leak channel activity
G0:0022848	1	acetylcholine-gated cation channel activity
G0:0004486	1	methylenetetrahydrofolate dehydrogenase [NAD(P)+] activity
G0:0004487	1	methylenetetrahydrofolate dehydrogenase (NAD+) activity
G0:0004484	1	mRNA guanylyltransferase activity
G0:0004482	1	mRNA (guanine-N7-)-methyltransferase activity
G0:0004483	1	mRNA (nucleoside-2'-O-)-methyltransferase activity
G0:0004489	1	methylenetetrahydrofolate reductase (NAD(P)H) activity
G0:1903178	1	positive regulation of tyrosine 3-monooxygenase activity
G0:2001287	1	negative regulation of caveolin-mediated endocytosis
G0:0048698	1	negative regulation of collateral sprouting in absence of injury
G0:0005283	1	sodium:amino acid symporter activity
G0:1990390	1	protein K33-linked ubiquitination
G0:0048691	1	positive regulation of axon extension involved in regeneration
G0:0005914	1	spot adherens junction
G0:0002253	1	activation of immune response
G0:1902564	1	negative regulation of neutrophil activation
G0:1902567	1	negative regulation of eosinophil activation
G0:2001135	1	regulation of endocytic recycling
G0:0046977	1	TAP binding
G0:0005586	1	collagen type III trimer
G0:1902569	1	negative regulation of activation of JAK2 kinase activity
G0:0000719	1	photoreactive repair
G0:0034224	1	cellular response to zinc ion starvation
G0:0000711	1	meiotic DNA repair synthesis
G0:0000717	1	nucleotide-excision repair, DNA duplex unwinding
G0:0004151	1	dihydroorotase activity
G0:0004155	1	6,7-dihydropteridine reductase activity
G0:0042697	1	menopause
G0:0008482	1	sulfite oxidase activity
G0:0008480	1	sarcosine dehydrogenase activity
G0:0008488	1	gamma-glutamyl carboxylase activity
G0:0008489	1	UDP-galactose:glucosylceramide beta-1,4-galactosyltransferase activity
G0:0045403	1	negative regulation of interleukin-4 biosynthetic process
G0:0045407	1	positive regulation of interleukin-5 biosynthetic process
G0:0070026	1	nitric oxide binding
G0:0033320	1	UDP-D-xylose biosynthetic process
G0:0060578	1	superior vena cava morphogenesis
G0:1902206	1	negative regulation of interleukin-2-mediated signaling pathway
G0:1901639	1	XDP catabolic process
G0:1901860	1	positive regulation of mitochondrial DNA metabolic process
G0:1901863	1	positive regulation of muscle tissue development
G0:2000376	1	positive regulation of oxygen metabolic process
G0:0021541	1	ammon gyrus development

G0:0021547	1	midbrain-hindbrain boundary initiation
G0:0021548	1	pons development
G0:1902203	1	negative regulation of hepatocyte growth factor receptor signaling pathway
G0:0043412	1	macromolecule modification
G0:1901249	1	regulation of lung goblet cell differentiation
G0:0090481	1	pyrimidine nucleotide-sugar transmembrane transport
G0:1901248	1	positive regulation of lung ciliated cell differentiation
G0:0032557	1	pyrimidine ribonucleotide binding
G0:0032003	1	interleukin-28 receptor binding
G0:0030038	1	contractile actin filament bundle assembly
G0:0072040	1	negative regulation of mesenchymal cell apoptotic process involved in nephron morphogenesis
G0:0047856	1	dihydrocoumarin hydrolase activity
G0:0021767	1	mammillary body development
G0:0021764	1	amygdala development
G0:0021763	1	subthalamic nucleus development
G0:0019811	1	cocaine binding
G0:0002416	1	IgG immunoglobulin transcytosis in epithelial cells mediated by FcRn immunoglobulin receptor
G0:0002418	1	immune response to tumor cell
G0:0071882	1	phospholipase C-activating adrenergic receptor signaling pathway
G0:0015675	1	nickel cation transport
G0:0071881	1	adenylate cyclase-inhibiting adrenergic receptor signaling pathway
G0:0047316	1	glutamine-phenylpyruvate transaminase activity
G0:0071884	1	vitamin D receptor activator activity
G0:0015926	1	glucosidase activity
G0:0050973	1	detection of mechanical stimulus involved in equilibrioception
G0:0046370	1	fructose biosynthetic process
G0:0015928	1	fucosidase activity
G0:0002739	1	regulation of cytokine secretion involved in immune response
G0:0002737	1	negative regulation of plasmacytoid dendritic cell cytokine production
G0:0002732	1	positive regulation of dendritic cell cytokine production
G0:0002731	1	negative regulation of dendritic cell cytokine production
G0:0051622	1	negative regulation of norepinephrine uptake
G0:2000556	1	positive regulation of T-helper 1 cell cytokine production
G0:0061044	1	negative regulation of vascular wound healing
G0:0035692	1	macrophage migration inhibitory factor receptor complex
G0:0035691	1	macrophage migration inhibitory factor signaling pathway
G0:1990147	1	talin binding
G0:0035696	1	monocyte extravasation
G0:0035695	1	mitochondrion degradation by induced vacuole formation
G0:0030409	1	glutamate formimidoyltransferase activity
G0:0060503	1	bud dilation involved in lung branching
G0:0060502	1	epithelial cell proliferation involved in lung morphogenesis
G0:2000558	1	positive regulation of immunoglobulin production in mucosal tissue
G0:0035349	1	coenzyme A transmembrane transport
G0:0052829	1	inositol-1,3,4-trisphosphate 1-phosphatase activity
G0:0042501	1	serine phosphorylation of STAT protein
G0:0052826	1	inositol hexakisphosphate 2-phosphatase activity
G0:0052825	1	inositol-1,3,4,5,6-pentakisphosphate 1-phosphatase activity
G0:0003429	1	growth plate cartilage chondrocyte morphogenesis
G0:0006148	1	inosine catabolic process
G0:0009855	1	determination of bilateral symmetry
G0:0043111	1	replication fork arrest
G0:0043112	1	receptor metabolic process
G0:0006145	1	purine nucleobase catabolic process
G0:0006147	1	guanine catabolic process
G0:0005144	1	interleukin-13 receptor binding
G0:0005147	1	oncostatin-M receptor binding
G0:0005140	1	interleukin-9 receptor binding
G0:0005141	1	interleukin-10 receptor binding
G0:0005142	1	interleukin-11 receptor binding
G0:0004367	1	glycerol-3-phosphate dehydrogenase [NAD+] activity
G0:0070846	1	Hsp90 deacetylation
G0:0004362	1	glutathione-disulfide reductase activity
G0:0004361	1	glutaryl-CoA dehydrogenase activity
G0:0047963	1	glycine N-choloyltransferase activity
G0:0004819	1	glutamine-tRNA ligase activity
G0:0047969	1	glyoxylate oxidase activity
G0:0060803	1	BMP signaling pathway involved in mesodermal cell fate specification
G0:1902771	1	positive regulation of choline O-acetyltransferase activity
G0:1902959	1	regulation of aspartic-type endopeptidase activity involved in amyloid precursor protein catabolic process
G0:0019135	1	deoxyhypusine monooxygenase activity
G0:1902955	1	positive regulation of early endosome to recycling endosome transport

G0:1902951	1	negative regulation of dendritic spine maintenance
G0:1902952	1	positive regulation of dendritic spine maintenance
G0:1902953	1	positive regulation of ER to Golgi vesicle-mediated transport
G0:0008817	1	cob(I)yrinic acid a,c-diamide adenosyltransferase activity
G0:0008812	1	choline dehydrogenase activity
G0:0070905	1	serine binding
G0:0042996	1	regulation of Golgi to plasma membrane protein transport
G0:0061196	1	fungiform papilla development
G0:0008700	1	4-hydroxy-2-oxoglutarate aldolase activity
G0:0033798	1	thyroxine 5-deiodinase activity
G0:0008705	1	methionine synthase activity
G0:0043914	1	NADPH:sulfur oxidoreductase activity
G0:0033204	1	ribonuclease P RNA binding
G0:0051022	1	Rho GDP-dissociation inhibitor binding
G0:0008709	1	cholate 7-alpha-dehydrogenase activity
G0:0090094	1	metanephric cap mesenchymal cell proliferation involved in metanephros development
G0:0051029	1	rRNA transport
G0:0050211	1	procollagen galactosyltransferase activity
G0:0009673	1	low affinity phosphate transmembrane transporter activity
G0:0044268	1	multicellular organismal protein metabolic process
G0:0085032	1	modulation by symbiont of host I-kappaB kinase/NF-kappaB cascade
G0:0010536	1	positive regulation of activation of Janus kinase activity
G0:0014805	1	smooth muscle adaptation
G0:0014804	1	terminal cisterna lumen
G0:0060887	1	limb epidermis development
G0:0036119	1	response to platelet-derived growth factor
G0:0035248	1	alpha-1,4-N-acetylgalactosaminyltransferase activity
G0:0001851	1	complement component C3b binding
G0:0036111	1	very long-chain fatty-acyl-CoA metabolic process
G0:0036112	1	medium-chain fatty-acyl-CoA metabolic process
G0:0036114	1	medium-chain fatty-acyl-CoA catabolic process
G0:0036116	1	long-chain fatty-acyl-CoA catabolic process
G0:2000417	1	negative regulation of eosinophil migration
G0:2000415	1	positive regulation of fibronectin-dependent thymocyte migration
G0:2000142	1	regulation of DNA-templated transcription, initiation
G0:2000144	1	positive regulation of DNA-templated transcription, initiation
G0:2000149	1	negative regulation of planar cell polarity pathway involved in ventricular septum morphogenesis
G0:0003205	1	cardiac chamber development
G0:0001207	1	histone displacement
G0:0003296	1	regulation of inositol trisphosphate biosynthetic process
G0:0001206	1	RNA polymerase II distal enhancer sequence-specific DNA binding transcription factor activity involved in negative regulation of transcription
G0:0052591	1	sn-glycerol-3-phosphate:ubiquinone-8 oxidoreductase activity
G0:0052590	1	sn-glycerol-3-phosphate:ubiquinone oxidoreductase activity
G0:0052597	1	diamine oxidase activity
G0:0046105	1	thymidine biosynthetic process
G0:0052598	1	histamine oxidase activity
G0:0033567	1	DNA replication, Okazaki fragment processing
G0:0033566	1	gamma-tubulin complex localization
G0:0035973	1	aggrephagy
G0:0035971	1	peptidyl-histidine dephosphorylation
G0:0035978	1	histone H2A-S139 phosphorylation
G0:0032618	1	interleukin-15 production
G0:0042017	1	interleukin-22 binding
G0:0072697	1	protein localization to cell cortex
G0:0033699	1	DNA 5'-adenosine monophosphate hydrolase activity
G0:0048855	1	adenohypophysis morphogenesis
G0:0019171	1	3-hydroxyacyl-[acyl-carrier-protein] dehydratase activity
G0:0032615	1	interleukin-12 production
G0:0047105	1	4-trimethylammonibutyraldehyde dehydrogenase activity
G0:0052106	1	quorum sensing involved in interaction with host
G0:0043221	1	SMC family protein binding
G0:0006067	1	ethanol metabolic process
G0:0048213	1	Golgi vesicle prefusion complex stabilization
G0:0006797	1	polyphosphate metabolic process
G0:0006062	1	sorbitol catabolic process
G0:0031129	1	inductive cell-cell signaling
G0:0031128	1	developmental induction
G0:0031125	1	rRNA 3'-end processing
G0:0034752	1	cytosolic aryl hydrocarbon receptor complex
G0:0097115	1	neurexin clustering
G0:0097117	1	guanylate kinase-associated protein clustering
G0:0035594	1	ganglioside binding

G0:0097111	1	endoplasmic reticulum-Golgi intermediate compartment organization
G0:1900142	1	negative regulation of oligodendrocyte apoptotic process
G0:0032900	1	negative regulation of neurotrophin production
G0:0031871	1	proteinase activated receptor binding
G0:0031877	1	somatostatin receptor binding
G0:0060248	1	detection of cell density by contact stimulus involved in contact inhibition
G0:0031690	1	adrenergic receptor binding
G0:0035003	1	subapical complex
G0:0090367	1	negative regulation of mRNA modification
G0:0090361	1	regulation of platelet-derived growth factor production
G0:0010968	1	regulation of microtubule nucleation
G0:0010965	1	regulation of mitotic sister chromatid separation
G0:1902891	1	negative regulation of root hair elongation
G0:0010961	1	cellular magnesium ion homeostasis
G0:0010963	1	regulation of L-arginine import
G0:0000089	1	mitotic metaphase
G0:0097374	1	sensory neuron axon guidance
G0:0005775	1	vacuolar lumen
G0:0097045	1	phosphatidylserine exposure on blood platelet
G0:0006608	1	snRNP protein import into nucleus
G0:0001896	1	autolysis
G0:0048679	1	regulation of axon regeneration
G0:0009443	1	pyridoxal 5'-phosphate salvage
G0:0036470	1	tyrosine 3-monooxygenase activator activity
G0:1902093	1	positive regulation of sperm motility
G0:0036478	1	L-dopa decarboxylase activator activity
G0:1902098	1	calcitriol binding
G0:0030616	1	transforming growth factor beta receptor, common-partner cytoplasmic mediator activity
G0:0005550	1	pheromone binding
G0:1903141	1	negative regulation of establishment of endothelial barrier
G0:1903142	1	positive regulation of establishment of endothelial barrier
G0:1902239	1	negative regulation of intrinsic apoptotic signaling pathway in response to osmotic stress by p53 class mediator
G0:0019310	1	inositol catabolic process
G0:0060807	1	regulation of transcription from RNA polymerase II promoter involved in definitive endodermal cell fate specification
G0:1902548	1	negative regulation of cellular response to vascular endothelial growth factor stimulus
G0:1902546	1	positive regulation of DNA N-glycosylase activity
G0:1902233	1	negative regulation of positive thymic T cell selection
G0:0004799	1	thymidylate synthase activity
G0:0030379	1	neurotensin receptor activity, non-G-protein coupled
G0:1902237	1	positive regulation of intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress
G0:0044594	1	17-beta-hydroxysteroid dehydrogenase (NAD+) activity
G0:0004796	1	thromboxane-A synthase activity
G0:0035258	1	steroid hormone receptor binding
G0:2001153	1	positive regulation of renal water transport
G0:0045054	1	constitutive secretory pathway
G0:0035252	1	UDP-xylosyltransferase activity
G0:0035251	1	UDP-glucosyltransferase activity
G0:0030377	1	urokinase plasminogen activator receptor activity
G0:0055024	1	regulation of cardiac muscle tissue development
G0:0060302	1	negative regulation of cytokine activity
G0:0055020	1	positive regulation of cardiac muscle fiber development
G0:0004608	1	phosphatidylethanolamine N-methyltransferase activity
G0:0008465	1	glycerate dehydrogenase activity
G0:0004607	1	phosphatidylcholine-sterol O-acyltransferase activity
G0:0004603	1	phenylethanolamine N-methyltransferase activity
G0:0052692	1	raffinose alpha-galactosidase activity
G0:0018169	1	ribosomal S6-glutamic acid ligase activity
G0:0018160	1	peptidyl-pyrromethane cofactor linkage
G0:2000612	1	regulation of thyroid-stimulating hormone secretion
G0:0045423	1	regulation of granulocyte macrophage colony-stimulating factor biosynthetic process
G0:0050725	1	positive regulation of interleukin-1 beta biosynthetic process
G0:0036332	1	placental growth factor-activated receptor activity
G0:0019783	1	small conjugating protein-specific protease activity
G0:0019782	1	ISG15 activating enzyme activity
G0:0019780	1	FAT10 activating enzyme activity
G0:0051984	1	positive regulation of chromosome segregation
G0:2000349	1	negative regulation of CD40 signaling pathway
G0:2000358	1	positive regulation of kidney smooth muscle cell differentiation

G0:2000607	1	negative regulation of cell proliferation involved in mesonephros development
G0:2000354	1	regulation of ovarian follicle development
G0:2000357	1	negative regulation of kidney smooth muscle cell differentiation
G0:2000350	1	positive regulation of CD40 signaling pathway
G0:2000351	1	regulation of endothelial cell apoptotic process
G0:0021564	1	vagus nerve development
G0:0021561	1	facial nerve development
G0:0021563	1	glossopharyngeal nerve development
G0:0008265	1	Mo-molybdopterin cofactor sulfurase activity
G0:0051251	1	positive regulation of lymphocyte activation
G0:0051252	1	regulation of RNA metabolic process
G0:0051255	1	spindle midzone assembly
G0:0051257	1	spindle midzone assembly involved in meiosis
G0:0098640	1	integrin binding involved in cell-matrix adhesion
G0:0032575	1	ATP-dependent 5'-3' RNA helicase activity
G0:0010771	1	negative regulation of cell morphogenesis involved in differentiation
G0:0010770	1	positive regulation of cell morphogenesis involved in differentiation
G0:0032579	1	apical lamina of hyaline layer
G0:0033737	1	l-pyrroline dehydrogenase activity
G0:0034506	1	chromosome, centromeric core region
G0:2000502	1	negative regulation of natural killer cell chemotaxis
G0:0007388	1	posterior compartment specification
G0:0002476	1	antigen processing and presentation of endogenous peptide antigen via MHC class Ib
G0:0007387	1	anterior compartment pattern formation
G0:0001928	1	regulation of exocyst assembly
G0:2000382	1	positive regulation of mesoderm development
G0:0071317	1	cellular response to isoquinoline alkaloid
G0:0001923	1	B-1 B cell differentiation
G0:1901846	1	positive regulation of cell communication by electrical coupling involved in cardiac conduction
G0:0021966	1	corticospinal neuron axon guidance
G0:0046359	1	butyrate catabolic process
G0:0061369	1	negative regulation of testicular blood vessel morphogenesis
G0:0002710	1	negative regulation of T cell mediated immunity
G0:0051643	1	endoplasmic reticulum localization
G0:0038192	1	gastric inhibitory peptide signaling pathway
G0:0038195	1	urokinase plasminogen activator signaling pathway
G0:0009032	1	thymidine phosphorylase activity
G0:1901303	1	negative regulation of cargo loading into COPII-coated vesicle
G0:0008521	1	acetyl-CoA transporter activity
G0:0060408	1	regulation of acetylcholine metabolic process
G0:0035659	1	Wnt signaling pathway involved in wound healing, spreading of epidermal cells
G0:0030429	1	kynureninase activity
G0:0030421	1	defecation
G0:0035105	1	sterol regulatory element binding protein import into nucleus
G0:0061433	1	cellular response to caloric restriction
G0:0061386	1	closure of optic fissure
G0:0061381	1	cell migration in diencephalon
G0:0061383	1	trabecula morphogenesis
G0:0047598	1	7-dehydrocholesterol reductase activity
G0:0060365	1	coronal suture morphogenesis
G0:0045993	1	negative regulation of translational initiation by iron
G0:0045992	1	negative regulation of embryonic development
G0:0045994	1	positive regulation of translational initiation by iron
G0:0042527	1	negative regulation of tyrosine phosphorylation of Stat6 protein
G0:0042526	1	positive regulation of tyrosine phosphorylation of Stat6 protein
G0:0031855	1	oxytocin receptor binding
G0:0003404	1	optic vesicle morphogenesis
G0:0003409	1	optic cup structural organization
G0:0005124	1	scavenger receptor binding
G0:0005129	1	granulocyte macrophage colony-stimulating factor receptor binding
G0:0004838	1	L-tyrosine:2-oxoglutarate aminotransferase activity
G0:0004832	1	valine-tRNA ligase activity
G0:0070861	1	regulation of protein exit from endoplasmic reticulum
G0:0070860	1	RNA polymerase I core factor complex
G0:0060383	1	positive regulation of DNA strand elongation
G0:0060381	1	positive regulation of single-stranded telomeric DNA binding
G0:0010848	1	regulation of chromatin disassembly
G0:0035262	1	gonad morphogenesis
G0:0009386	1	translational attenuation
G0:0030026	1	cellular manganese ion homeostasis
G0:0047747	1	cholate-CoA ligase activity

G0:0005983	1	starch catabolic process
G0:0097433	1	dense body
G0:0047291	1	lactosylceramide alpha-2,3-sialyltransferase activity
G0:0009128	1	purine nucleoside monophosphate catabolic process
G0:0010857	1	calcium-dependent protein kinase activity
G0:0010164	1	response to cesium ion
G0:0008389	1	coumarin 7-hydroxylase activity
G0:0044736	1	acid-sensing ion channel activity
G0:0008387	1	steroid 7-alpha-hydroxylase activity
G0:0008386	1	cholesterol monooxygenase (side-chain-cleaving) activity
G0:0008832	1	dGTPase activity
G0:0014866	1	skeletal myofibril assembly
G0:0014861	1	regulation of skeletal muscle contraction via regulation of action potential
G0:0006507	1	GPI anchor release
G0:0043004	1	cytoplasmic sequestering of CFTR protein
G0:0015195	1	L-threonine transmembrane transporter activity
G0:0036131	1	prostaglandin D2 11-ketoreductase activity
G0:2000168	1	negative regulation of planar cell polarity pathway involved in neural tube closure
G0:0060404	1	axonemal microtubule depolymerization
G0:0003837	1	beta-ureidopropionase activity
G0:2000162	1	negative regulation of planar cell polarity pathway involved in cardiac right atrium morphogenesis
G0:0036139	1	peptidyl-histidine dioxygenase activity
G0:0036138	1	peptidyl-histidine hydroxylation
G0:2000167	1	regulation of planar cell polarity pathway involved in neural tube closure
G0:2000166	1	negative regulation of planar cell polarity pathway involved in pericardium morphogenesis
G0:2000164	1	negative regulation of planar cell polarity pathway involved in outflow tract morphogenesis
G0:0003835	1	beta-galactoside alpha-2,6-sialyltransferase activity
G0:0010992	1	ubiquitin homeostasis
G0:0008310	1	single-stranded DNA 3'-5' exodeoxyribonuclease activity
G0:0032904	1	negative regulation of nerve growth factor production
G0:0032901	1	positive regulation of neurotrophin production
G0:0021686	1	cerebellar granular layer maturation
G0:0061609	1	fructose-1-phosphate aldolase activity
G0:1901307	1	positive regulation of spermidine biosynthetic process
G0:1901300	1	positive regulation of hydrogen peroxide-mediated programmed cell death
G0:0047341	1	fucose-1-phosphate guanylyltransferase activity
G0:0003241	1	growth involved in heart morphogenesis
G0:2000296	1	negative regulation of hydrogen peroxide catabolic process
G0:2000291	1	regulation of myoblast proliferation
G0:0021972	1	corticospinal neuron axon guidance through spinal cord
G0:0019376	1	galactolipid catabolic process
G0:0019377	1	glycolipid catabolic process
G0:0003839	1	gamma-glutamylcyclotransferase activity
G0:0021979	1	hypothalamus cell differentiation
G0:0015739	1	sialic acid transport
G0:0071307	1	cellular response to vitamin K
G0:0032637	1	interleukin-8 production
G0:0032632	1	interleukin-3 production
G0:0047293	1	4-hydroxybenzoate nonaprenyltransferase activity
G0:0047290	1	(alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-acetyl-galactosaminide 6-alpha-sialyltransferase activity
G0:0052066	1	entry of symbiont into host cell by promotion of host phagocytosis
G0:0052063	1	induction by symbiont of defense-related host nitric oxide production
G0:0047749	1	cholestanetriol 26-monooxygenase activity
G0:0009214	1	cyclic nucleotide catabolic process
G0:0043456	1	regulation of pentose-phosphate shunt
G0:0016429	1	tRNA (adenine-N1-)-methyltransferase activity
G0:0016427	1	tRNA (cytosine) methyltransferase activity
G0:0070526	1	threonylcarbamoyladenosine biosynthetic process
G0:0016422	1	mRNA (2'-O-methyladenosine-N6-)-methyltransferase activity
G0:0070625	1	zymogen granule exocytosis
G0:0070522	1	ERCC4-ERCC1 complex
G0:0070251	1	pristanate-CoA ligase activity
G0:0070252	1	actin-mediated cell contraction
G0:0070254	1	mucus secretion
G0:0070627	1	ferrous iron import
G0:0070524	1	11-beta-hydroxysteroid dehydrogenase (NADP+) activity