response to hydrogen peroxide GO:0042542	p=9.7E−04	n=9
tail−anchored membrane protein insertion... GO:0071816	p=2.4E−03	n=2
negative regulation of intrinsic apoptot... GO:1903751	p=2.4E−03	n=2
actin polymerization−dependent cell moti... GO:0070358	p=2.4E−03	n=2
purine ribonucleotide transport GO:0015868	p=2.4E−03	n=2
oxygen homeostasis GO:0032364	p=2.4E−03	n=2
cellular response to antibiotic GO:0071236	p=2.9E−03	n=7
mRNA transcription GO:0009299	p=3.5E−03	n=3
negative regulation of neuron apoptotic ... GO:0043524	p=4.4E−03	n=7
regulation of response to drug GO:2001023	p=4.4E−03	n=5
response to axon injury GO:0048678	p=4.7E−03	n=6
cellular response to mechanical stimulus GO:0071260	p=5.0E−03	n=4
primary neural tube formation GO:0014020	p=6.4E−03	n=6
negative regulation of cellular response... GO:1900408	p=6.5E−03	n=4
negative regulation of establishment of ... GO:1903748	p=7.0E−03	n=2
elastin metabolic process GO:0051541	p=7.0E−03	n=2
purine−containing compound transmembrane... GO:0072530	p=7.0E−03	n=2
negative regulation of vascular associat... GO:1904706	p=7.0E−03	n=2
antibiotic biosynthetic process GO:0017000	p=7.0E−03	n=2
negative regulation of blood vessel endo... GO:0043537	p=7.0E−03	n=2
compartment pattern specification GO:0007386	p=7.0E−03	n=2
protein O−linked mannosylation GO:0035269	p=7.0E−03	n=2
cellular response to electrical stimulus GO:0071257	p=7.0E−03	n=2
negative regulation of cellular respirat... GO:1901856	p=7.0E−03	n=2
response to lipopolysaccharide GO:0032496	p=7.2E−03	n=7
positive regulation of nucleic acid−temp... GO:1903508	p=7.5E−03	n=25
sterol metabolic process GO:0016125	p=7.7E−03	n=5
regulation of ERAD pathway GO:1904292	p=7.9E−03	n=3
response to parathyroid hormone GO:0071107	p=7.9E−03	n=3
positive regulation of execution phase o... GO:1900119	p=1.1E−02	n=3

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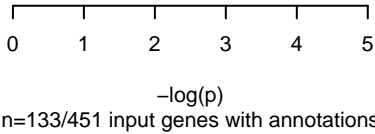
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DNA−binding transcription activator acti... GO:0001228	p=1.1E−03	n=11
purine ribonucleotide transmembrane tran... GO:0005346	p=2.6E−03	n=2
histone acetyltransferase binding GO:0035035	p=3.2E−03	n=4
RNA polymerase II cis−regulatory region ... GO:0000978	p=4.1E−03	n=10
mRNA 3'−UTR binding GO:0003730	p=7.3E−03	n=4
adenyl−nucleotide exchange factor activi... GO:0000774	p=7.5E−03	n=2
small ribosomal subunit rRNA binding GO:0070181	p=7.5E−03	n=2
DNA secondary structure binding GO:0000217	p=8.7E−03	n=3
xylosyltransferase activity GO:0042285	p=1.5E−02	n=2
UDP−xylosyltransferase activity GO:0035252	p=1.5E−02	n=2
minor groove of adenine−thymine−rich DNA... GO:0003680	p=1.5E−02	n=2
transcription coactivator activity GO:0003713	p=1.5E−02	n=9
transcription coregulator activity GO:0003712	p=1.6E−02	n=12
manganese ion binding GO:0030145	p=2.0E−02	n=4
proton transmembrane transporter activit... GO:0015078	p=2.0E−02	n=4
voltage−gated cation channel activity GO:0022843	p=2.3E−02	n=4
intronic transcription regulatory region... GO:0001161	p=2.3E−02	n=2
satellite DNA binding GO:0003696	p=2.3E−02	n=2
heat shock protein binding GO:0031072	p=3.0E−02	n=6
rDNA binding GO:0000182	p=3.4E−02	n=2
mRNA 5'−UTR binding GO:0048027	p=3.4E−02	n=2
protein self−association GO:0043621	p=3.8E−02	n=3
protein homodimerization activity GO:0042803	p=3.9E−02	n=18
histone deacetylase binding GO:0042826	p=4.1E−02	n=4
SMAD binding GO:0046332	p=4.5E−02	n=3
HMG box domain binding GO:0071837	p=4.6E−02	n=2
cyclin binding GO:0030332	p=4.6E−02	n=2
polynucleotide adenylyltransferase activ... GO:0004652	p=4.6E−02	n=2
purine ribonucleoside triphosphate bindi... GO:0035639	p=5.0E−02	n=12
magnesium ion binding GO:0000287	p=5.0E−02	n=6

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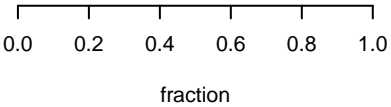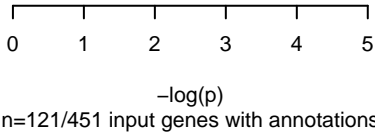
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septin complex GO:0031105	p=7.0E−03	n=2
septin ring GO:0005940	p=7.0E−03	n=2
pronucleus GO:0045120	p=1.4E−02	n=3
extracellular space GO:0005615	p=1.8E−02	n=9
rough endoplasmic reticulum GO:0005791	p=2.1E−02	n=4
integral component of Golgi membrane GO:0030173	p=2.3E−02	n=3
transcription regulator complex GO:0005667	p=2.3E−02	n=10
heterochromatin GO:0000792	p=2.8E−02	n=4
transcription factor TFTC complex GO:0033276	p=3.2E−02	n=2
rough endoplasmic reticulum membrane GO:0030867	p=3.2E−02	n=2
intrinsic component of Golgi membrane GO:0031228	p=3.4E−02	n=3
actin cytoskeleton GO:0015629	p=4.3E−02	n=8
actomyosin GO:0042641	p=4.8E−02	n=3
polytene chromosome band GO:0005704	p=4.9E−02	n=1
septin filament array GO:0032160	p=4.9E−02	n=1
ER membrane insertion complex GO:0072379	p=4.9E−02	n=1
NF−kappaB complex GO:0071159	p=4.9E−02	n=1
growth cone leading edge GO:0061850	p=4.9E−02	n=1
BAT3 complex GO:0071818	p=4.9E−02	n=1
DNA topoisomerase type II (double strand... GO:0009330	p=4.9E−02	n=1
endocytic vesicle lumen GO:0071682	p=4.9E−02	n=1
integral component of pigment granule me... GO:0090740	p=4.9E−02	n=1
pigment granule membrane GO:0090741	p=4.9E−02	n=1
Sec61 translocon complex GO:0005784	p=4.9E−02	n=1
translocon complex GO:0071256	p=4.9E−02	n=1
CCAAT−binding factor complex GO:0016602	p=4.9E−02	n=1
extracellular region GO:0005576	p=5.1E−02	n=15
RNA polymerase II transcription regulato... GO:0090575	p=5.3E−02	n=5
contractile ring GO:0070938	p=5.5E−02	n=2

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