Name	pValue	FDR B&H	FDR B&Y	Bonferroni
regulation of transcription from RNA polymerase II promoter	1.47E-21	4.73E-18	4.32E-17	7.63E-18
positive regulation of gene expression	1.82E-21	4.73E-18	4.32E-17	9.46E-18
positive regulation of nucleobase-containing compound metabolic process	3.20E-21	5.53E-18	5.05E-17	1.66E-17
positive regulation of transcription, DNA-templated	1.34E-20	1.74E-17	1.59E-16	6.96E-17
positive regulation of nitrogen compound metabolic process	2.17E-20	1.96E-17	1.79E-16	1.13E-16
transcription from RNA polymerase II promoter	2.27E-20	1.96E-17	1.79E-16	1.18E-16
positive regulation of cellular biosynthetic process	5.81E-20	4.31E-17	3.94E-16	3.02E-16
positive regulation of biosynthetic process	9.05E-20	5.87E-17	5.36E-16	4.70E-16
positive regulation of RNA biosynthetic process	1.40E-19	7.68E-17	7.01E-16	7.29E-16
positive regulation of RNA metabolic process	1.48E-19	7.68E-17	7.01E-16	7.68E-16
positive regulation of macromolecule biosynthetic process	4.55E-18	2.15E-15	1.96E-14	2.36E-14
positive regulation oftranscription from RNA polymerase II promoter	7.79E-18	3.37E-15	3.08E-14	4.05E-14
negative regulation of macromolecule biosynthetic process	1.76E-16	7.02E-14	6.41E-13	9.12E-13
negative regulation of metabolic process	3.56E-16	1.31E-13	1.19E-12	1.85E-12
enzyme linked receptor protein signaling pathway	3.77E-16	1.31E-13	1.19E-12	1.96E-12
negative regulation of biosynthetic process	7.68E-16	2.49E-13	2.28E-12	3.99E-12
negative regulation of cellular macromolecule biosynthetic process	9.45E-16	2.89E-13	2.64E-12	4.91E-12
negative regulation of cellular biosynthetic process	2.34E-15	6.74E-13	6.16E-12	1.21E-11
regulation of developmental process	3.15E-15	8.04E-13	7.35E-12	1.64E-11
cellular response to organic substance	3.21E-15	8.04E-13	7.35E-12	1.67E-11
negative regulation of macromolecule metabolic process	3.25E-15	8.04E-13	7.35E-12	1.69E-11
negative regulation of cellular metabolic process	3.52E-15	8.32E-13	7.60E-12	1.83E-11
regulation of cell differentiation	4.70E-15	1.06E-12	9.70E-12	2.44E-11
cell proliferation	7.67E-15	1.66E-12	1.52E-11	3.98E-11
negative regulation of gene expression	5.18E-14	1.08E-11	9.83E-11	2.69E-10
cell development	6.48E-14	1.30E-11	1.18E-10	3.37E-10
phosphorylation	1.21E-13	2.33E-11	2.13E-10	6.29E-10
transmembrane receptor proteintyrosine kinase signaling pathway	1.52E-13	2.82E-11	2.57E-10	7.89E-10
protein phosphorylation	3.98E-13	7.13E-11	6.51E-10	2.07E-09
positive regulation of molecular function	5.81E-13	1.01E-10	9.19E-10	3.02E-09
regulation of cellular protein metabolic process	6.75E-13	1.13E-10	1.03E-09	3.51E-09
positive regulation of signaling	1.04E-12	1.68E-10	1.53E-09	5.38E-09
regulation of multicellular organismal development	1.23E-12	1.93E-10	1.76E-09	6.38E-09
positive regulation of cell communication	1.47E-12	2.24E-10	2.05E-09	7.63E-09
negative regulation of RNA biosynthetic process	2.20E-12	3.26E-10	2.98E-09	1.14E-08
positive regulation of protein metabolic process	2.30E-12	3.31E-10	3.02E-09	1.19E-08
negative regulation of transcription, DNA-templated	2.39E-12	3.35E-10	3.06E-09	1.24E-08
regulation of cellular component organization	2.89E-12	3.95E-10	3.61E-09	1.50E-08
negative regulation of nitrogen compound metabolic process	3.10E-12	4.12E-10	3.76E-09	1.61E-08
developmental process involved in reproduction	4.36E-12	5.66E-10	5.17E-09	2.26E-08
generation of neurons	4.66E-12	5.90E-10	5.39E-09	2.42E-08
cellular response to endogenous stimulus	5.33E-12	6.59E-10	6.02E-09	2.77E-08
neurogenesis	6.42E-12	7.75E-10	7.08E-09	3.33E-08
positive regulation of signal transduction	6.66E-12	7.86E-10	7.18E-09	3.46E-08
negative regulation of nucleobase-containing compound metabolic process	8.06E-12	9.31E-10	8.50E-09	4.19E-08
positive regulation of phosphorus metabolic process	8.83E-12	9.75E-10	8.91E-09	4.58E-08
positive regulation of phosphate metabolic process	8.83E-12	9.75E-10	8.91E-09	4.58E-08
negative regulation of RNA metabolic process	1.06E-11	1.14E-09	1.04E-08	5.48E-08
regulation of protein modification process	1.09E-11	1.15E-09	1.05E-08	5.64E-08
regulation of phosphorylation	1.30E-11	1.35E-09	1.23E-08	6.73E-08
cellular response to stress	1.57E-11	1.60E-09	1.46E-08	8.17E-08
regulation of cell death	1.63E-11	1.63E-09	1.49E-08	8.48E-08
positive regulation of phosphorylation	1.92E-11	1.88E-09	1.71E-08	9.95E-08
tissue development	2.28E-11	2.19E-09	2.00E-08	1.18E-07
programmed cell death	3.47E-11	3.22E-09	2.94E-08	1.80E-07
positive regulation of response to stimulus	3.48E-11	3.22E-09	2.94E-08	1.81E-07
reproductive structure development	8.37E-11	7.62E-09	6.96E-08	4.35E-07
single-organism organelle organization	8.83E-11	7.91E-09	7.22E-08	4.59E-07
positive regulation of catalytic activity	9.68E-11	8.52E-09	7.78E-08	5.03E-07
peptidyl-amino acid modification	1.10E-10	9.35E-09	8.54E-08	5.69E-07
reproductive system development	1.10E-10	9.35E-09	8.54E-08	5.70E-07
response to endogenous stimulus	1.16E-10	9.70E-09	8.86E-08	6.01E-07
embryo development	1.32E-10	1.08E-08	9.90E-08	6.83E-07
positive regulation of cellular protein metabolic process	1.97E-10	1.58E-08	1.45E-07	1.02E-06
cell cycle	1.98E-10	1.58E-08	1.45E-07	1.03E-06
positive regulation of cell differentiation	2.09E-10	1.65E-08	1.50E-07	1.09E-06
positive regulation of protein modification process	2.17E-10	1.68E-08	1.54E-07	1.13E-06
regulation of intracellular signal transduction	2.40E-10	1.83E-08	1.67E-07	1.24E-06
neuron differentiation	2.79E-10	2.10E-08	1.92E-07	1.45E-06
gland development	3.48E-10	2.58E-08	2.36E-07	1.81E-06
apoptotic process	3.64E-10	2.66E-08	2.43E-07	1.89E-06
regulation of phosphate metabolic process	4.81E-10	3.42E-08	3.13E-07	2.50E-06
positive regulation of kinase activity	4.81E-10	3.42E-08	3.13E-07	2.50E-06
blood vessel development	5.35E-10	3.76E-08	3.43E-07	2.78E-06
regulation of protein phosphorylation	5.60E-10	3.88E-08	3.54E-07	2.91E-06
positive regulation of protein phosphorylation	6.57E-10	4.49E-08	4.10E-07	3.41E-06
positive regulation of developmental process	6.88E-10	4.64E-08	4.24E-07	3.57E-06
regulation of phosphorus metabolic process	7.03E-10	4.68E-08	4.28E-07	3.65E-06
vasculature development	8.77E-10	5.77E-08	5.27E-07	4.56E-06
embryonic morphogenesis	9.96E-10	6.47E-08	5.91E-07	5.17E-06
regulation of cell proliferation	1.04E-09	6.65E-08	6.07E-07	5.39E-06
regulation of programmed cell death	1.11E-09	7.01E-08	6.40E-07	5.75E-06
chromatin modification	1.20E-09	7.48E-08	6.83E-07	6.20E-06
epithelium development	1.32E-09	8.15E-08	7.44E-07	6.85E-06
regulation of kinase activity	1.56E-09	9.52E-08	8.69E-07	8.09E-06
signal transduction by protein phosphorylation	1.88E-09	1.14E-07	1.04E-06	9.78E-06
cellular response to nitrogen compound	2.24E-09	1.33E-07	1.22E-06	1.16E-05
negative regulation of cell proliferation	2.33E-09	1.37E-07	1.25E-06	1.21E-05
cellular response to oxygen-containing compound	2.46E-09	1.43E-07	1.31E-06	1.28E-05
establishment of protein localization	2.61E-09	1.51E-07	1.37E-06	1.35E-05
response to growth factor	3.11E-09	1.78E-07	1.62E-06	1.62E-05
positive regulation of transferase activity	3.27E-09	1.85E-07	1.69E-06	1.70E-05
central nervous system development	3.44E-09	1.92E-07	1.75E-06	1.78E-05
circulatory system development	3.58E-09	1.96E-07	1.79E-06	1.86E-05
cardiovascular system development	3.58E-09	1.96E-07	1.79E-06	1.86E-05
blood vessel morphogenesis	3.74E-09	2.02E-07	1.85E-06	1.94E-05
cellular response to growth factor stimulus	3.83E-09	2.05E-07	1.87E-06	1.99E-05
response to oxygen-containing compound	4.86E-09	2.58E-07	2.35E-06	2.53E-05
single-organism intracellular transport	5.27E-09	2.76E-07	2.52E-06	2.74E-05
organ morphogenesis	6.60E-09	3.43E-07	3.13E-06	3.43E-05
cellular response to organonitrogen compound	7.38E-09	3.78E-07	3.45E-06	3.83E-05
regulation of apoptotic process	7.42E-09	3.78E-07	3.45E-06	3.85E-05
neuron projection development	7.61E-09	3.84E-07	3.50E-06	3.95E-05
regulation of protein kinase activity	8.17E-09	4.08E-07	3.73E-06	4.24E-05
intracellular transport	9.00E-09	4.45E-07	4.06E-06	4.67E-05
regulation of transferase activity	9.33E-09	4.57E-07	4.17E-06	4.85E-05
cell migration	1.10E-08	5.35E-07	4.88E-06	5.72E-05
brain development	1.21E-08	5.80E-07	5.29E-06	6.26E-05
positive regulation of protein kinase activity	1.24E-08	5.91E-07	5.40E-06	6.45E-05
protein localization	2.50E-08	1.18E-06	1.08E-05	1.30E-04
embryo development ending in birth or egg hatching	2.81E-08	1.31E-06	1.20E-05	1.46E-04
muscle structure development	2.88E-08	1.34E-06	1.22E-05	1.50E-04
vesicle-mediated transport	4.22E-08	1.94E-06	1.77E-05	2.19E-04
positive regulation of intracellular signal transduction	4.37E-08	1.99E-06	1.82E-05	2.27E-04
chordate embryonic development	5.02E-08	2.27E-06	2.07E-05	2.61E-04
response to nitrogen compound	5.49E-08	2.46E-06	2.24E-05	2.85E-04
tissue morphogenesis	5.78E-08	2.56E-06	2.34E-05	3.00E-04
positive regulation of cellular component organization	6.12E-08	2.70E-06	2.46E-05	3.18E-04
response to organonitrogen compound	6.25E-08	2.73E-06	2.49E-05	3.25E-04
negative regulation of transcription from RNA polymerase II promoter	7.52E-08	3.25E-06	2.97E-05	3.91E-04
neuron development	7.76E-08	3.30E-06	3.02E-05	4.03E-04
anatomical structure formation involved in morphogenesis	7.76E-08	3.30E-06	3.02E-05	4.03E-04
tube development	8.09E-08	3.42E-06	3.12E-05	4.20E-04
protein transport	8.69E-08	3.64E-06	3.32E-05	4.51E-04
morphogenesis of an epithelium	1.11E-07	4.62E-06	4.22E-05	5.78E-04
MAPK cascade	1.22E-07	5.03E-06	4.59E-05	6.34E-04
locomotion	1.28E-07	5.24E-06	4.79E-05	6.66E-04
localization of cell	1.31E-07	5.26E-06	4.81E-05	6.79E-04
cell motility	1.31E-07	5.26E-06	4.81E-05	6.79E-04
tube morphogenesis	1.44E-07	5.75E-06	5.25E-05	7.47E-04
activation of protein kinase activity	1.74E-07	6.89E-06	6.29E-05	9.03E-04
response to nutrient levels	2.07E-07	8.13E-06	7.43E-05	1.07E-03
regulation of transport	2.26E-07	8.84E-06	8.07E-05	1.18E-03
cellular response to hormone stimulus	2.32E-07	8.96E-06	8.18E-05	1.20E-03
chromatin organization	2.33E-07	8.96E-06	8.18E-05	1.21E-03
sex differentiation	2.41E-07	9.18E-06	8.39E-05	1.25E-03
response to peptide	2.67E-07	1.01E-05	9.24E-05	1.39E-03
reproductive process	2.76E-07	1.04E-05	9.47E-05	1.43E-03
response to peptide hormone	2.89E-07	1.08E-05	9.86E-05	1.50E-03
regulation of cellular component movement	2.91E-07	1.08E-05	9.86E-05	1.51E-03
neurotrophin TRK receptor signaling pathway	3.06E-07	1.13E-05	1.03E-04	1.59E-03
cell cycle process	3.11E-07	1.14E-05	1.04E-04	1.62E-03
cell projection organization	3.41E-07	1.24E-05	1.13E-04	1.77E-03
response to extracellular stimulus	3.51E-07	1.26E-05	1.16E-04	1.82E-03
embryonic organ development	3.58E-07	1.28E-05	1.17E-04	1.86E-03
neurotrophin signaling pathway	3.76E-07	1.34E-05	1.22E-04	1.95E-03
epidermal growth factor receptor signaling pathway	4.45E-07	1.57E-05	1.44E-04	2.31E-03
histone modification	4.90E-07	1.72E-05	1.57E-04	2.54E-03
cellular response to starvation	5.40E-07	1.88E-05	1.72E-04	2.81E-03
response to starvation	5.68E-07	1.97E-05	1.80E-04	2.95E-03
regulation of cell projection organization	5.74E-07	1.98E-05	1.80E-04	2.98E-03
ERBB signaling pathway	6.48E-07	2.21E-05	2.02E-04	3.36E-03
covalent chromatin modification	6.90E-07	2.34E-05	2.14E-04	3.59E-03
muscle tissue development	7.73E-07	2.61E-05	2.38E-04	4.01E-03
cellular response to external stimulus	7.96E-07	2.67E-05	2.44E-04	4.13E-03
cerebral cortex development	8.27E-07	2.75E-05	2.52E-04	4.30E-03
movement of cell or subcellular component	9.17E-07	3.03E-05	2.77E-04	4.76E-03
cytoskeleton organization	9.44E-07	3.10E-05	2.83E-04	4.90E-03
single organism reproductive process	9.68E-07	3.16E-05	2.89E-04	5.03E-03
regulation of cell migration	9.93E-07	3.22E-05	2.94E-04	5.16E-03
forebrain development	1.08E-06	3.47E-05	3.17E-04	5.59E-03
skeletal system development	1.09E-06	3.49E-05	3.19E-04	5.66E-03
growth	1.13E-06	3.57E-05	3.26E-04	5.88E-03
regulation of locomotion	1.13E-06	3.57E-05	3.26E-04	5.89E-03
regulation of neurogenesis	1.13E-06	3.57E-05	3.26E-04	5.89E-03
regulation of nervous system development	1.18E-06	3.69E-05	3.37E-04	6.13E-03
urogenital system development	1.26E-06	3.90E-05	3.57E-04	6.52E-03
cellular response to peptide hormone stimulus	1.33E-06	4.12E-05	3.76E-04	6.92E-03
regulation of cell motility	1.53E-06	4.70E-05	4.29E-04	7.94E-03
negative regulation of cell death	1.58E-06	4.83E-05	4.42E-04	8.22E-03
intracellular protein transport	1.65E-06	5.01E-05	4.58E-04	8.57E-03
rhythmic process	1.67E-06	5.05E-05	4.61E-04	8.69E-03
cellular response to nutrient levels	1.74E-06	5.23E-05	4.78E-04	9.05E-03
regulation of anatomical structure morphogenesis	1.77E-06	5.29E-05	4.83E-04	9.21E-03
epithelial tube morphogenesis	1.80E-06	5.34E-05	4.87E-04	9.34E-03
angiogenesis	1.87E-06	5.52E-05	5.04E-04	9.72E-03
pallium development	2.15E-06	6.32E-05	5.77E-04	1.12E-02
epithelial cell differentiation	2.32E-06	6.72E-05	6.14E-04	1.20E-02
cell morphogenesis involvedin differentiation	2.32E-06	6.72E-05	6.14E-04	1.20E-02
cellular macromolecule localization	2.34E-06	6.76E-05	6.18E-04	1.22E-02
neuron projection morphogenesis	2.40E-06	6.88E-05	6.28E-04	1.25E-02
response to hormone	2.47E-06	7.05E-05	6.44E-04	1.28E-02
cellular response to peptide	2.52E-06	7.15E-05	6.53E-04	1.31E-02
regulation of cell development	2.53E-06	7.15E-05	6.53E-04	1.32E-02
prostate gland development	2.85E-06	8.01E-05	7.31E-04	1.48E-02
response to abiotic stimulus	3.06E-06	8.53E-05	7.79E-04	1.59E-02
positive regulation of cell projection organization	3.22E-06	8.93E-05	8.16E-04	1.67E-02
cell-cell signaling	3.26E-06	9.00E-05	8.22E-04	1.69E-02
regulation of MAPK cascade	3.55E-06	9.75E-05	8.91E-04	1.84E-02
embryonic organ morphogenesis	3.69E-06	1.01E-04	9.21E-04	1.92E-02
nucleocytoplasmic transport	3.76E-06	1.02E-04	9.32E-04	1.95E-02
cellular response to extracellular stimulus	3.96E-06	1.07E-04	9.73E-04	2.06E-02
cellular protein localization	3.98E-06	1.07E-04	9.73E-04	2.07E-02
cell morphogenesis involved in neuron differentiation	4.09E-06	1.09E-04	9.94E-04	2.12E-02
cellular component morphogenesis	4.54E-06	1.20E-04	1.10E-03	2.36E-02
nuclear transport	4.80E-06	1.27E-04	1.16E-03	2.49E-02
muscle organ development	4.99E-06	1.31E-04	1.20E-03	2.59E-02
positive regulation of MAPK cascade	5.05E-06	1.32E-04	1.20E-03	2.62E-02
regulation of organelle organization	5.69E-06	1.48E-04	1.35E-03	2.95E-02

GO: Cellular Component

Name	pValue	FDR B&H	FDR B&Y	Bonferroni
early endosome	4.16E-10	2.29E-07	1.58E-06	2.33E-07
endosome	8.17E-10	2.29E-07	1.58E-06	4.58E-07
neuron part	2.90E-09	4.71E-07	3.26E-06	1.62E-06
neuron projection	3.36E-09	4.71E-07	3.26E-06	1.89E-06
somatodendritic compartment	4.80E-09	5.39E-07	3.72E-06	2.69E-06
cell body	1.54E-08	1.44E-06	9.97E-06	8.66E-06
neuronal cell body	5.86E-08	4.70E-06	3.25E-05	3.29E-05
cell projection	2.47E-07	1.73E-05	1.19E-04	1.38E-04
early endosome membrane	1.82E-06	1.13E-04	7.84E-04	1.02E-03
nuclear chromatin	3.11E-06	1.59E-04	1.10E-03	1.74E-03
nucleoplasm	3.12E-06	1.59E-04	1.10E-03	1.75E-03
dendrite	6.89E-06	3.22E-04	2.22E-03	3.86E-03
transcription factor complex	8.91E-06	3.85E-04	2.66E-03	5.00E-03
growth cone	1.58E-05	6.32E-04	4.36E-03	8.84E-03
site of polarized growth	2.20E-05	8.22E-04	5.68E-03	1.23E-02
chromosome	4.03E-05	1.42E-03	9.77E-03	2.26E-02
nucleoplasm part	4.29E-05	1.42E-03	9.77E-03	2.41E-02
ribonucleoprotein granule	5.72E-05	1.69E-03	1.17E-02	3.21E-02
cytoplasmic ribonucleoprotein granule	5.72E-05	1.69E-03	1.17E-02	3.21E-02
endosomal part	6.51E-05	1.82E-03	1.26E-02	3.65E-02
nuclear chromosome part	6.81E-05	1.82E-03	1.26E-02	3.82E-02

GO: Pathway

Name	Source	pValue	FDR B&H	FDR B&Y
Signalling by NGF	BioSystems: REACTOME	2.69E-06	1.93E-03	1.55E-02
NGF signalling via TRKA from the plasma membrane	BioSystems: REACTOME	3.22E-06	1.93E-03	1.55E-02
TGF-beta Receptor Signaling Pathway	BioSystems: WikiPathways	3.36E-06	1.93E-03	1.55E-02
Endocytosis	BioSystems: KEGG	1.34E-05	5.61E-03	4.50E-02
Signaling by EGFR	BioSystems: REACTOME	2.18E-05	5.61E-03	4.50E-02
BMAL1:CLOCK/NPAS2 Activates Circadian Expression	BioSystems: REACTOME	2.27E-05	5.61E-03	4.50E-02
Signaling by EGFR in Cancer	BioSystems: REACTOME	2.54E-05	5.61E-03	4.50E-02
Adherens junction	BioSystems: KEGG	2.61E-05	5.61E-03	4.50E-02

GO: Molecular Function

Name	pValue	FDR B&H	FDR B&Y	Bonferroni
regulatory region nucleic acid binding	3.82E-12	1.94E-09	1.45E-08	3.88E-09
regulatory region DNA binding	3.82E-12	1.94E-09	1.45E-08	3.88E-09
transcription regulatory region DNA binding	8.37E-12	2.83E-09	2.13E-08	8.50E-09
nucleic acid binding transcription factor activity	2.22E-10	4.76E-08	3.57E-07	2.25E-07
sequence-specific DNA binding	2.34E-10	4.76E-08	3.57E-07	2.38E-07
transcription factor activity, sequence-specific DNA binding	5.20E-10	8.80E-08	6.60E-07	5.28E-07
protein kinase activity	6.50E-10	9.43E-08	7.08E-07	6.60E-07
receptor signaling protein activity	2.19E-09	2.78E-07	2.09E-06	2.22E-06
phosphotransferase activity, alcohol group as acceptor	8.82E-09	9.95E-07	7.47E-06	8.96E-06
kinase activity	1.54E-08	1.57E-06	1.18E-05	1.57E-05
receptor signaling protein serine/threonine kinase activity	1.85E-08	1.71E-06	1.28E-05	1.88E-05
enzyme binding	2.10E-08	1.78E-06	1.34E-05	2.14E-05
transcription regulatory region sequence-specific DNA binding	3.21E-08	2.51E-06	1.88E-05	3.26E-05
RNA polymerase II transcription factor activity, sequence-specific DNA binding	1.32E-07	9.08E-06	6.81E-05	1.34E-04
RNA polymerase II regulatory region DNA binding	1.34E-07	9.08E-06	6.81E-05	1.36E-04
protein serine/threonine kinase activity	1.83E-07	1.16E-05	8.72E-05	1.86E-04
purine ribonucleotide binding	2.92E-07	1.65E-05	1.24E-04	2.96E-04
RNA polymerase II regulatory region sequence-specific DNA binding	2.93E-07	1.65E-05	1.24E-04	2.97E-04
ribonucleotide binding	4.28E-07	2.16E-05	1.62E-04	4.35E-04
transmembrane receptor proteinkinase activity	4.57E-07	2.16E-05	1.62E-04	4.65E-04
purine ribonucleoside binding	4.64E-07	2.16E-05	1.62E-04	4.71E-04
purine nucleoside binding	4.98E-07	2.16E-05	1.62E-04	5.06E-04
purine nucleotide binding	5.05E-07	2.16E-05	1.62E-04	5.13E-04
ribonucleoside binding	5.10E-07	2.16E-05	1.62E-04	5.19E-04
purine ribonucleoside triphosphate binding	6.43E-07	2.53E-05	1.90E-04	6.53E-04
nucleoside binding	6.47E-07	2.53E-05	1.90E-04	6.58E-04
transcriptional activator activity, RNA polymerase II transcription regulatory region sequence-specific binding	7.64E-07	2.87E-05	2.16E-04	7.76E-04
transcription factor binding	8.06E-07	2.92E-05	2.19E-04	8.19E-04
adenyl ribonucleotide binding	1.15E-06	4.02E-05	3.01E-04	1.16E-03
transferase activity, transferring phosphorus-containing groups	1.51E-06	5.12E-05	3.84E-04	1.53E-03
transcription factor activity, transcription factor binding	1.65E-06	5.40E-05	4.05E-04	1.68E-03
adenyl nucleotide binding	1.85E-06	5.86E-05	4.40E-04	1.88E-03
transcription factor activity, protein binding	1.96E-06	6.03E-05	4.52E-04	1.99E-03
ATP binding	2.93E-06	8.75E-05	6.57E-04	2.98E-03
transcriptional activator activity, RNA polymerase II transcription factor binding	5.72E-06	1.66E-04	1.25E-03	5.81E-03
transcription factor activity, RNA polymerase II transcription factor binding	9.72E-06	2.74E-04	2.06E-03	9.87E-03
transcriptional activator activity, RNA polymerase II core promoter proximal region sequence-specific binding	1.29E-05	3.53E-04	2.65E-03	1.31E-02
RNA polymerase II transcription coactivator activity	1.73E-05	4.54E-04	3.41E-03	1.76E-02
transcription cofactor activity	1.74E-05	4.54E-04	3.41E-03	1.77E-02
chromatin binding	1.81E-05	4.59E-04	3.44E-03	1.83E-02
RNA polymerase II transcription cofactor activity	2.97E-05	7.35E-04	5.51E-03	3.01E-02
protein tyrosine kinase activity	3.81E-05	9.22E-04	6.91E-03	3.87E-02
transcription factor activity, RNA polymerase II core promoter proximal region sequence-specific binding	4.19E-05	9.89E-04	7.42E-03	4.25E-02