










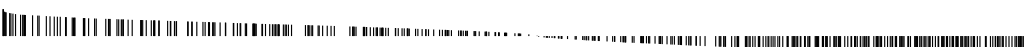










Pathway	Gene ranks	NES	pval	padj
ENKEPHALIN RELEASE%PANTHER PATHWAY%P05913		2.03	2.2e-04	2.8e-03
PRC2 METHYLATES HISTONES AND DNA%REACTOME DATABASE ID RELEASE 74%212300		2.35	2.2e-04	2.8e-03
CONDENSATION OF PROPHASE CHROMOSOMES%REACTOME%R-HSA-2299718.1		2.17	2.2e-04	2.8e-03
REGULATION OF MRNA POLYADENYLATION%GOBP%GO:1900363		2.08	2.2e-04	2.8e-03
CHROMATIN DISASSEMBLY%GOBP%GO:0031498		2.17	2.2e-04	2.8e-03
NUCLEOSOME DISASSEMBLY%GOBP%GO:0006337		2.17	2.2e-04	2.8e-03
PROTEIN-DNA COMPLEX DISASSEMBLY%GOBP%GO:0032986		2.15	2.3e-04	2.8e-03
INHIBITION OF DNA RECOMBINATION AT TELOMERE%REACTOME%R-HSA-9670095.2		2.00	2.3e-04	2.8e-03
TRANSCRIPTIONAL REGULATION OF GRANULOPOIESIS%REACTOME DATABASE ID RELEASE 74%9616222		2.02	2.3e-04	2.8e-03
PROCESSING OF INTRONLESS PRE-MRNAS%REACTOME%R-HSA-77595.2		2.41	2.3e-04	2.8e-03
ORGANIC ACID METABOLIC PROCESS%GOBP%GO:0006082		-1.62	1.2e-04	2.3e-03
SECRETION%GOBP%GO:0046903		-1.58	1.2e-04	2.3e-03
CELL ACTIVATION%GOBP%GO:0001775		-1.69	1.2e-04	2.3e-03
OXOACID METABOLIC PROCESS%GOBP%GO:0043436		-1.59	1.2e-04	2.3e-03
SECRETION BY CELL%GOBP%GO:0032940		-1.58	1.2e-04	2.3e-03
VESICLE-MEDIATED TRANSPORT%REACTOME DATABASE ID RELEASE 74%5653656		-1.80	1.2e-04	2.3e-03
MOVEMENT OF CELL OR SUBCELLULAR COMPONENT%GOBP%GO:0006928		-1.56	1.2e-04	2.3e-03
ORGANOPHOSPHATE METABOLIC PROCESS%GOBP%GO:0019637		-1.74	1.2e-04	2.3e-03
REGULATION OF CELLULAR COMPONENT BIOGENESIS%GOBP%GO:0044087		-1.67	1.2e-04	2.3e-03
NEGATIVE REGULATION OF SIGNAL TRANSDUCTION%GOBP%GO:0009968		-1.53	1.2e-04	2.3e-03