RNA polymerase II general transcriptio NAD-dependent histone deacetylase iron ion transmembran inositol monophosphate pho activin acetyltransi 3',5'–nucleotide bisphosphare 0.0364795901722606 endoplasmic reticulum-plasma memb transcription fag MOZ/MORF histone ac core TFIIH complex portion of hold alpha DNA polymerase:p positive regulation of transcrip negative regulation of N cellular response to transcription initiation from RNA p regulation of anatomic positive regulation of extrinsic apoptotic si plasma membrane boun embryo development ending in birth o cellular response to platelet de ludar cellular response to fibrob ontology regulation of peroxisome proliferator activa regulation of MyD88-dependent toll-like i regulation of branch elongation regulat protein transport to vacuole involved in ubiquitin–dependent protein catabolic process via the m protein transport from ciliary progression of morphogenetic furrow in positive regulation of malate dehydron positive regulation of positive regulation of positive regulation of positive regulation of humoral immune res positive regulation positive regulation of dengriting positive regulation of cell growth involve positive regulation of cell growth involve positive regulation of cell provides positive regulation of biosynthetic process of antibacterial peptides negative regulation of intrinsic apoptotic signaling pathway in response to D negative regulation of interferon—generative regulation of interferon—generative regulation mesenchymal to epithelial transition involved mesenchymal stem cell maintenance ii mesenchymal cell differentiat maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRN maintenance o DNA replication of DNA replication of temperature stimulus involve detection of chemical stimulus involve condensed n chondr chitin-based embryoni cardiac neural crest cell development inv carbon catabolite repression calcium ion transm branch fr