

mitochondrion organization, GO:0007005

- metallopeptidase activity, GO:0008237
- mitochondrial transport, GO:0006839
- cristae formation, GO:0042407
- mitochondrial ATP synthesis coupled proton transport, GO:0042776
- RNA polymerase II transcription cofactor activity, GO:0001104
- GTP-dependent protein binding, GO:0030742
- NAD+ ADP-ribosyltransferase activity, GO:0003950
- cartilage development, GO:0051216
- negative regulation of cell cycle, GO:0045786
- heme biosynthetic process, GO:0006783
- response to cold, GO:0009409
- iron-sulfur cluster assembly, GO:0016226
- regulation of nucleic acid-templated transcription, GO:1903506
- extrinsic component of plasma membrane, GO:0019897
- mitochondrial calcium ion homeostasis, GO:0051560
- excitatory postsynaptic potential, GO:0060079
- collagen metabolic process, GO:0032963
- iron ion homeostasis, GO:0055072
- blood vessel remodeling, GO:0001974
- regulation of multicellular organism growth, GO:0040014
- positive regulation of calcium ion transport into cytosol, GO:0010524
- macrophage differentiation, GO:0030225
- neuromuscular junction development, GO:0007528
- response to zinc ion, GO:0010043
- cellular response to interleukin-6, GO:0071354
- developmental process, GO:0032502
- positive regulation of dendrite development, GO:1900006
- membrane depolarization, GO:0051899
- metallocarboxypeptidase activity, GO:0004181
- negative regulation of megakaryocyte differentiation, GO:0045653
- negative regulation of smooth muscle cell migration, GO:0014912
- protein ADP-ribosylation, GO:0006471
- positive regulation of protein dephosphorylation, GO:0035307