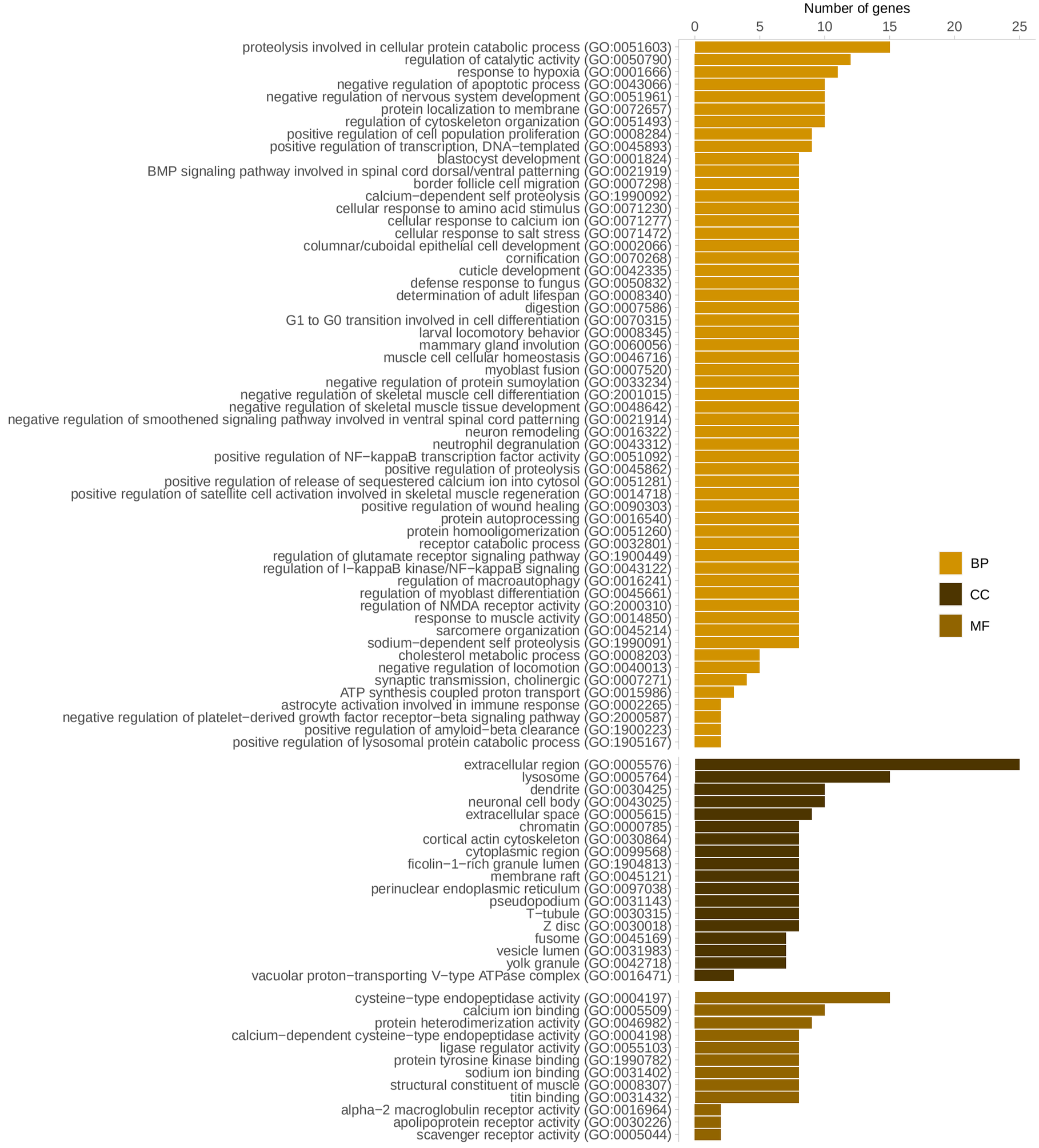
Number of genes
0
5
10
15
20
25
proteolysis involved in cellular protein catabolic process (GO:0051603)
regulation of catalytic activity (GO:0050790)
response to hypoxia (GO:0001666)
negative regulation of apoptotic process (GO:0043066)
negative regulation of nervous system development (GO:0051961)
protein localization to membrane (GO:0072657)
regulation of cytoskeleton organization (GO:0051493)
positive regulation of cell population proliferation (GO:0008284)
positive regulation of transcription, DNA−templated (GO:0045893)
blastocyst development (GO:0001824)
BMP signaling pathway involved in spinal cord dorsal/ventral patterning (GO:0021919)
border follicle cell migration (GO:0007298)
calcium−dependent self proteolysis (GO:1990092)
cellular response to amino acid stimulus (GO:0071230)
cellular response to calcium ion (GO:0071277)
cellular response to salt stress (GO:0071472)
columnar/cuboidal epithelial cell development (GO:0002066)
cornification (GO:0070268)
cuticle development (GO:0042335)
defense response to fungus (GO:0050832)
determination of adult lifespan (GO:0008340)
digestion (GO:0007586)
G1 to G0 transition involved in cell differentiation (GO:0070315)
larval locomotory behavior (GO:0008345)
mammary gland involution (GO:0060056)
muscle cell cellular homeostasis (GO:0046716)
myoblast fusion (GO:0007520)
negative regulation of protein sumoylation (GO:0033234)
negative regulation of skeletal muscle cell differentiation (GO:2001015)
negative regulation of skeletal muscle tissue development (GO:0048642)
negative regulation of smoothened signaling pathway involved in ventral spinal cord patterning (GO:0021914)
neuron remodeling (GO:0016322)
neutrophil degranulation (GO:0043312)
positive regulation of NF−kappaB transcription factor activity (GO:0051092)
positive regulation of proteolysis (GO:0045862)
positive regulation of release of sequestered calcium ion into cytosol (GO:0051281)
positive regulation of satellite cell activation involved in skeletal muscle regeneration (GO:0014718)
positive regulation of wound healing (GO:0090303)
protein autoprocessing (GO:0016540)
protein homooligomerization (GO:0051260)
receptor catabolic process (GO:0032801)
regulation of glutamate receptor signaling pathway (GO:1900449)
regulation of I−kappaB kinase/NF−kappaB signaling (GO:0043122)
regulation of macroautophagy (GO:0016241)
regulation of myoblast differentiation (GO:0045661)
regulation of NMDA receptor activity (GO:2000310)
response to muscle activity (GO:0014850)
sarcomere organization (GO:0045214)
sodium−dependent self proteolysis (GO:1990091)
cholesterol metabolic process (GO:0008203)
negative regulation of locomotion (GO:0040013)
synaptic transmission, cholinergic (GO:0007271)
ATP synthesis coupled proton transport (GO:0015986)
astrocyte activation involved in immune response (GO:0002265)
negative regulation of platelet−derived growth factor receptor−beta signaling pathway (GO:2000587)
positive regulation of amyloid−beta clearance (GO:1900223)
positive regulation of lysosomal protein catabolic process (GO:1905167)
extracellular region (GO:0005576)
lysosome (GO:0005764)
dendrite (GO:0030425)
neuronal cell body (GO:0043025)
extracellular space (GO:0005615)
chromatin (GO:0000785)
cortical actin cytoskeleton (GO:0030864)
cytoplasmic region (GO:0099568)
ficolin−1−rich granule lumen (GO:1904813)
membrane raft (GO:0045121)
perinuclear endoplasmic reticulum (GO:0097038)
pseudopodium (GO:0031143)
T−tubule (GO:0030315)
Z disc (GO:0030018)
fusome (GO:0045169)
vesicle lumen (GO:0031983)
yolk granule (GO:0042718)
vacuolar proton−transporting V−type ATPase complex (GO:0016471)
cysteine−type endopeptidase activity (GO:0004197)
calcium ion binding (GO:0005509)
protein heterodimerization activity (GO:0046982)
calcium−dependent cysteine−type endopeptidase activity (GO:0004198)
ligase regulator activity (GO:0055103)
protein tyrosine kinase binding (GO:1990782)
sodium ion binding (GO:0031402)
structural constituent of muscle (GO:0008307)
titin binding (GO:0031432)
alpha−2 macroglobulin receptor activity (GO:0016964)
apolipoprotein receptor activity (GO:0030226)
scavenger receptor activity (GO:0005044)
BP
CC
MF