

dephosphorylation, GO:0016311

- phosphoprotein phosphatase activity, GO:0004721
- phosphatase activity, GO:0016791
- protein tyrosine phosphatase activity, GO:0004725
- peptidyl-tyrosine dephosphorylation, GO:0035335
- hematopoietic progenitor cell differentiation, GO:0002244
- inositol phosphate metabolic process, GO:0043647
- carbohydrate phosphorylation, GO:0046835
- megakaryocyte development, GO:0035855
- protein tyrosine/serine/threonine phosphatase activity, GO:0008138
- gluconeogenesis, GO:0006094
- phosphatidylinositol-3-phosphatase activity, GO:0004438
- negative regulation of T cell activation, GO:0050868
- lipoxygenase pathway, GO:0019372
- drug metabolic process, GO:0017144
- phosphate-containing compound metabolic process, GO:0006796
- C-terminal protein lipidation, GO:0006501
- metalloexopeptidase activity, GO:0008235
- myelin assembly, GO:0032288
- negative regulation of glycolytic process, GO:0045820
- 3'-phosphoadenosine 5'-phosphosulfate metabolic process, GO:0050427
- negative regulation of PERK-mediated unfolded protein response, GO:1903898
- positive regulation of regulatory T cell differentiation, GO:0045591
- response to growth factor, GO:0070848
- negative regulation of receptor activity, GO:2000272
- purine nucleotide catabolic process, GO:0006195
- adenosine metabolic process, GO:0046085
- response to denervation involved in regulation of muscle adaptation, GO:0014894
- negative regulation of epithelial cell migration, GO:0010633
- nucleobase-containing small molecule catabolic process, GO:0034656
- regulation of acetyl-CoA biosynthetic process from pyruvate, GO:0010510
- acid phosphatase activity, GO:0003993