

chaperone binding, GO:0051087

- protein targeting to mitochondrion, GO:0006626
- potassium ion transport, GO:0006813
- toxin transport, GO:1901998
- protein localization to nucleus, GO:0034504
- positive regulation of cell cycle, GO:0045787
- chaperone-mediated protein folding, GO:0061077
- cellular response to organic substance, GO:0071310
- signal transducer activity, GO:0005057
- negative regulation of TOR signaling, GO:0032007
- chaperone mediated protein folding requiring cofactor, GO:0051085
- positive regulation of pri-miRNA transcription from RNA polymerase II promoter, GO:1902895
- ventricular septum development, GO:0003281
- misfolded protein binding, GO:0051787
- protein folding in endoplasmic reticulum, GO:0034975
- regulation of mitochondrial membrane permeability, GO:0046902
- sodium:potassium-exchanging ATPase complex, GO:0005890
- protein insertion into mitochondrial membrane involved in apoptotic signaling pathway, GO:0001844
- pore complex, GO:0046930
- tissue remodeling, GO:0048771
- cell communication by electrical coupling involved in cardiac conduction, GO:0086064
- chaperone cofactor-dependent protein refolding, GO:0070389
- regulation of cysteine-type endopeptidase activity involved in apoptotic process, GO:0043281
- membrane depolarization during cardiac muscle cell action potential, GO:0086012
- negative regulation of peptidyl-serine phosphorylation, GO:0033137
- striatum development, GO:0021756
- sodium ion binding, GO:0031402
- vagina development, GO:0060068