RMSD GO_BP

RMSD (High - Low) | Xlim (-100 to 100)

Count diff |6 & -25| are removed.



RMSD GO_CC RMSD (High - Low) | Xlim (-100 to 100) cytosol extracellular exosome plasma membrane cytoplasm nucleus endoplasmic reticulum membrane endoplasmic reticulum lumen mitochondrial matrix extracellular region vesicle small-subunit processome ribosome nuclear speck neuronal cell body mitochondrial pyruvate dehydrogenase complex mitochondrial intermembrane space mitochondrial inner membrane melanosome male germ cell nucleus Col inclusion body HSP90-CDC37 chaperone complex dynein axonemal particle DNA topoisomerase type II (double strand cut, ATP-hydrolyzing) complex dendritic growth cone cytosolic small ribosomal subunit cytosolic ribosome condensed chromosome chromosome, centromeric region centrosome centriole cell surface cell periphery blood microparticle axonal growth cone aryl hydrocarbon receptor complex aggresome protein-containing complex perinuclear region of cytoplasm focal adhesion ribonucleoprotein complex

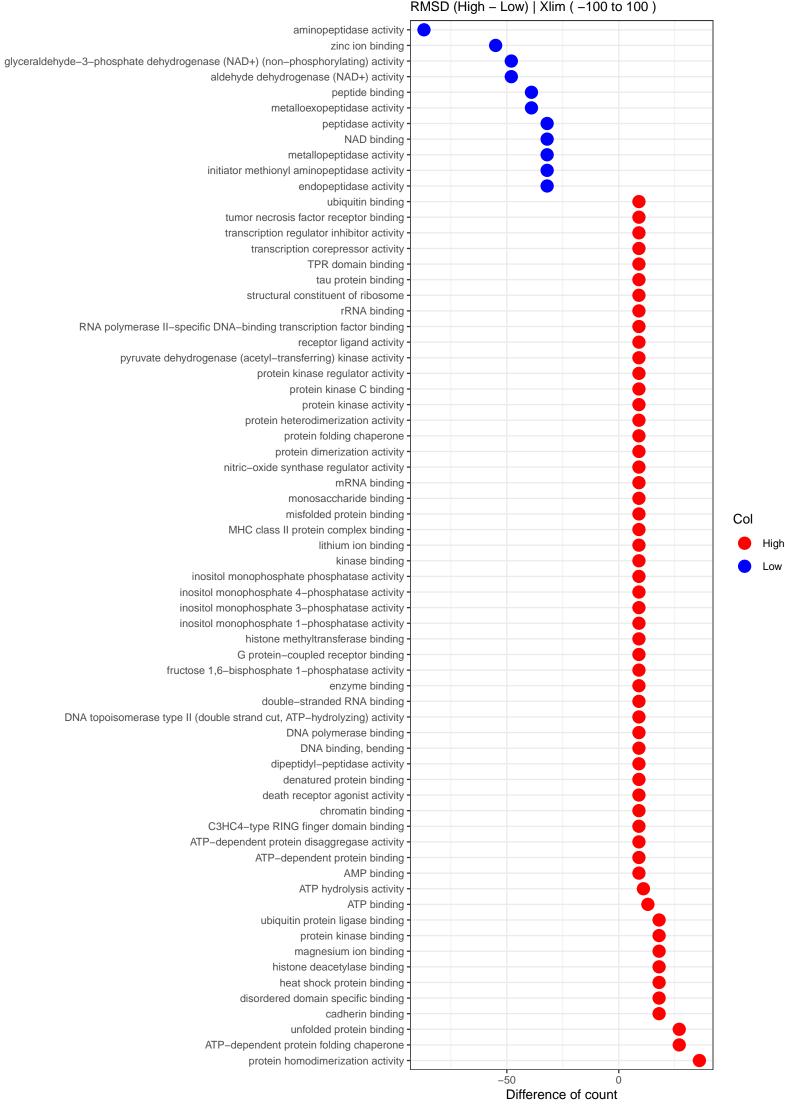
-100

Count diff |6 & -25| are removed.

Difference of count

High

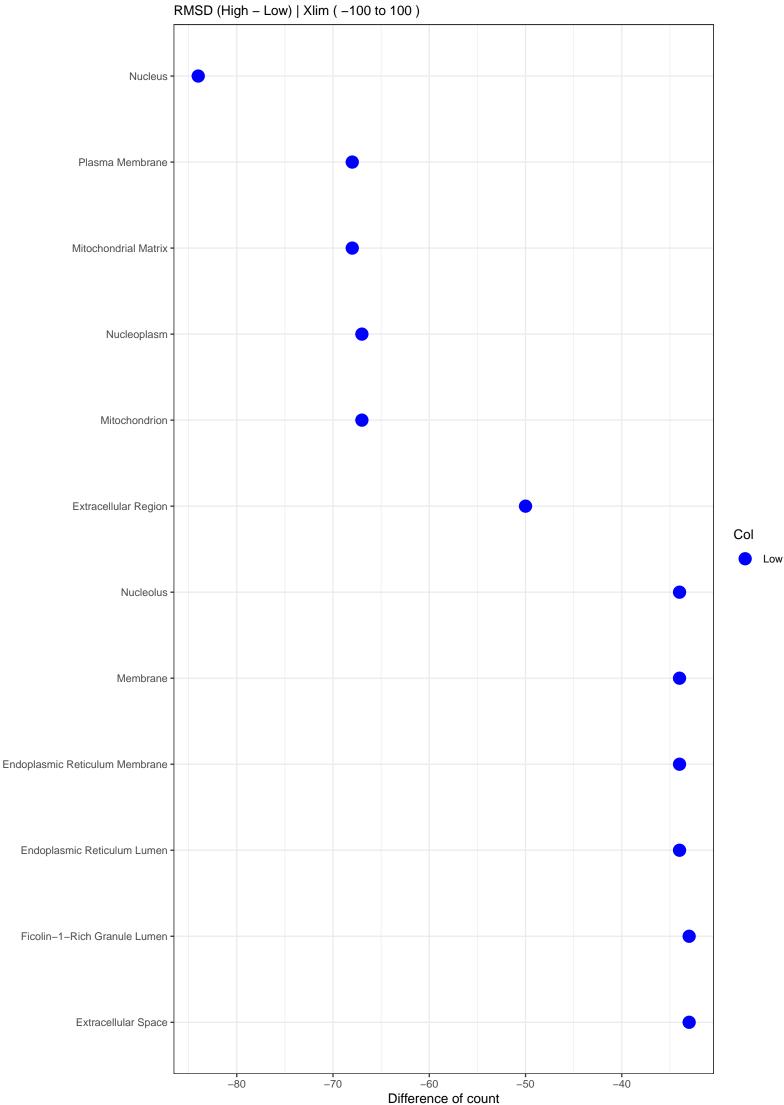
RMSD GO_MF RMSD (High – Low) | Xlim (–100 to 100)



Count diff |6 & -25| are removed.

FCrmsd GO_BP RMSD (High - Low) | Xlim (-100 to 100) Peptide Catabolic Process Response To Zinc Ion Membrane Potential Peptidyl-Methionine Modification Col Low Modification Process Cell Differentiation

FCrmsd GO_CC



FCrmsd GO_MF RMSD (High - Low) | Xlim (-100 to 100) Zinc Ion Binding Identical Protein Binding Peptide Binding Metalloexopeptidase Activity Glyceraldehyde-3-Phosphate Dehydrogenase (Nad+) (Non–Phosphorylating) Activity Dna Binding Aldehyde Dehydrogenase (Nad+) Activity Rna Binding Col Peptidase Activity Nad Binding Metallopeptidase Activity Metal Ion Binding Manganese Ion Binding Initiator Methionyl Aminopeptidase Activity Endopeptidase Activity Atp Binding -60 -50 -40

Difference of count

Low