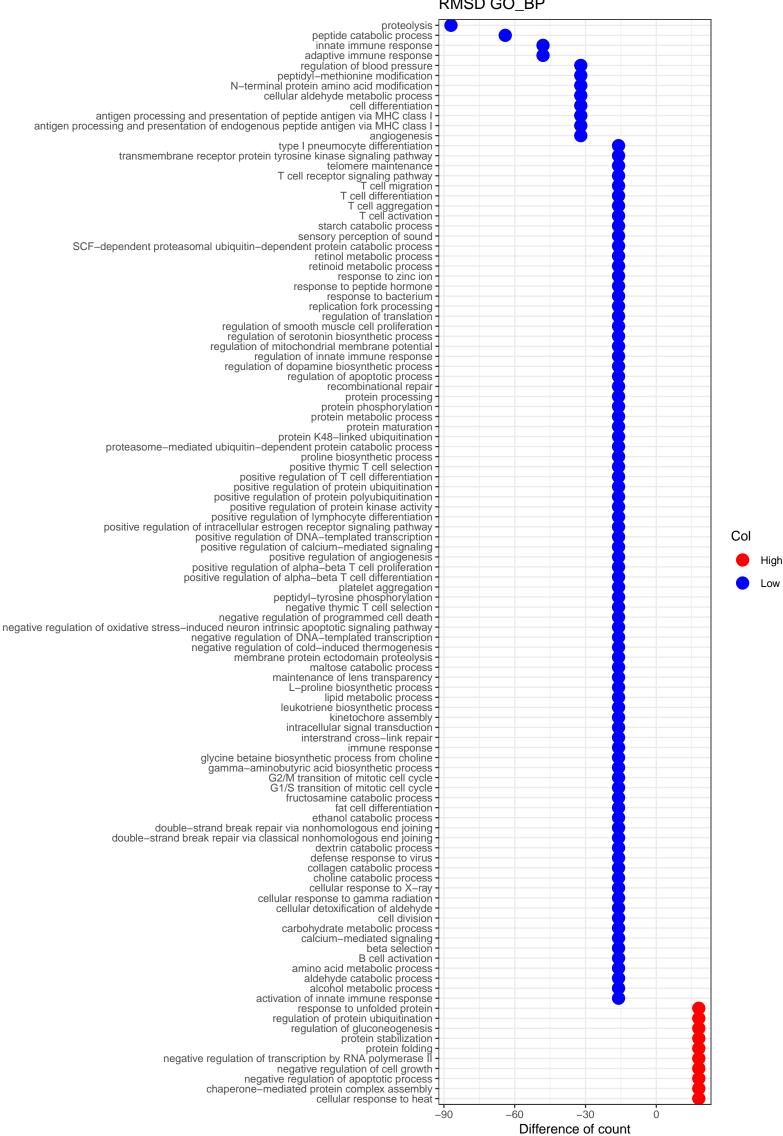
RMSD GO_BP



RMSD GO_CC cytosol extracellular exosome plasma membrane cytoplasm nucleus endoplasmic reticulum membrane endoplasmic reticulum lumen mitochondrial matrix extracellular region extracellular space transcription regulator complex tertiary granule membrane tertiary granule lumen T cell receptor complex secretory granule membrane SCF ubiquitin ligase complex protein-DNA complex nuclear telomere cap complex nonhomologous end joining complex lysosomal membrane Ku70:Ku80 complex Col inner kinetochore High Low immunological synapse ficolin-1-rich granule membrane Fanconi anaemia nuclear complex FANCM-MHF complex extrinsic component of cytoplasmic side of plasma membrane external side of plasma membrane endoplasmic reticulum-Golgi intermediate compartment -DNA-dependent protein kinase-DNA ligase 4 complex DNA-dependent protein kinase complex chromosome, telomeric region chromatin cell-cell junction apical plasma membrane nucleolus ficolin-1-rich granule lumen mitochondrion protein-containing complex perinuclear region of cytoplasm focal adhesion ribonucleoprotein complex -**5**0 -100

Difference of count

RMSD GO_MF metalloaminopeptidase activity aminopeptidase activity zinc ion binding glyceraldehyde-3-phosphate dehydrogenase (NAD+) (non-phosphorylating) activity aldehyde dehydrogenase (NAD+) activity peptide binding metalloexopeptidase activity peptidase activity NAD binding metallopeptidase activity initiator methionyl aminopeptidase activity endopeptidase activity metal ion binding DNA binding identical protein binding tripeptide aminopeptidase activity transcription cis-regulatory region binding telomeric DNA binding signaling receptor activity scaffold protein binding retinal dehydrogenase activity pyrroline-5-carboxylate reductase activity protein tyrosine kinase activity protein-containing complex binding proline dipeptidase activity phosphotyrosine residue binding phenylacetaldehyde dehydrogenase activity non-membrane spanning protein tyrosine kinase activity nitroglycerin reductase activity metallocarboxypeptidase activity maltose alpha-glucosidase activity leukotriene-A4 hydrolase activity Col L-aminoadipate-semialdehyde dehydrogenase activity interleukin-6 receptor binding interleukin-1, type II receptor binding GTPase activator activity glucan 1,4-alpha-glucosidase activity epoxide hydrolase activity electron transfer activity double-stranded DNA binding DNA helicase activity damaged DNA binding cyclin binding catalytic activity carboxylesterase activity carbohydrate binding betaine-aldehyde dehydrogenase activity benzaldehyde dehydrogenase (NAD+) activity androgen binding amylase activity aminobutyraldehyde dehydrogenase activity alpha-1,4-glucosidase activity aldehyde dehydrogenase [NAD(P)+] activity 5'-deoxyribose-5-phosphate lyase activity 3-deoxyglucosone dehydrogenase activity ATP hydrolysis activity ATP binding ubiquitin protein ligase binding protein kinase binding magnesium ion binding histone deacetylase binding heat shock protein binding disordered domain specific binding cadherin binding unfolded protein binding ATP-dependent protein folding chaperone protein homodimerization activity -80 -40 Difference of count

High

Low

