T_cells_CD8_KLRG1 - IMM - Colon - ActiveCD_vs_Control phosphorylation - GO:0016310 - p: 2.12e-04 *** response to nitrogen compound – GO:1901698 – p: 6.18e–04 *** cellular response to nitrogen compound – GO:1901699 – p: 3.12e–05 *** positive regulation of transcription by RNA polyme... - GO:0045944 - p: 3.84e-05 *** negative regulation of RNA metabolic process – GO:0051253 – p: 2.86e–07 *** negative regulation of nucleobase-containing compo... - GO:0045934 - p: 1.06e-07 *** negative regulation of DNA-templated transcription - GO:0045892 - p: 3.62e-07 *** negative regulation of RNA biosynthetic process – GO:1902679 – p: 2.12e–07 *** negative regulation of transcription by RNA polyme... - GO:0000122 - p: 3.84e-06 *** chromatin organization - GO:0006325 - p: 1.00e-10 *** chromatin remodeling - GO:0006338 - p: 1.00e-10 *** perinuclear region of cytoplasm - GO:0048471 - p: 1.94e-04 *** Gene Count chromatin - GO:0000785 - p: 3.44e-09 *** ribonucleotide binding - GO:0032553 - p: 1.67e-08 *** purine ribonucleotide binding - GO:0032555 - p: 7.50e-08 *** purine ribonucleoside triphosphate binding - GO:0035639 - p: 8.02e-08 *** kinase activity - GO:0016301 - p: 3.77e-06 *** Cluster adenyl nucleotide binding - GO:0030554 - p: 1.00e-10 *** phosphotransferase activity, alcohol group as acce... - GO:0016773 - p: 2.53e-06 *** histone modifying activity - GO:0140993 - p: 1.38e-07 *** adenyl ribonucleotide binding - GO:0032559 - p: 1.00e-10 *** protein kinase activity - GO:0004672 - p: 7.85e-06 *** ATP binding - GO:0005524 - p: 1.00e-10 *** histone H3 kinase activity - GO:0140996 - p: 1.91e-07 *** histone kinase activity - GO:0035173 - p: 1.91e-07 *** histone H2AX kinase activity - GO:0141003 - p: 1.25e-08 *** transcription regulator activity - GO:0140110 - p: 5.83e-07 *** sequence-specific double-stranded DNA binding - GO:1990837 - p: 4.04e-06 *** sequence-specific DNA binding - GO:0043565 - p: 3.11e-07 *** double-stranded DNA binding - GO:0003690 - p: 1.80e-07 *** histone binding - GO:0042393 - p: 3.70e-06 *** chromatin binding - GO:0003682 - p: 1.00e-10 *** 1.3 1.4 1.5 1.6 1.7

Absolute NES

GO Term