GO Term

## Monocyte - CD\_vs\_Control antimicrobial humoral response = G0:0019730 = p-val: humoral immune response = G0:0006959 = p-val: granulocyte migration = G0:0097530 = p-val: granulocyte migration = G0:0097530 = p-val: granulocyte chemiotaxis = G0:0071621 = p-val: granulocyte chemiotaxis = G0:0071621 = p-val: granulocyte chemiotaxis = G0:0042742 = p-val: granulocyte chemiotaxis = G0:0042742 = p-val: cell chemotaxis = G0:0045765 = p-val: granulocyte chemiotaxis = G0:005729 = p-val: granulocyte chemiotaxis = G0:005729 = p-val: granulocyte chemiotaxis = G0:005729 = p-val: granulocyte chemiotaxis = G0:0001806 = p-val: granulocyte chemiotaxis = G0:0001806 = p-val: granulocyte chemiotaxis = G0:0001806 = p-val: granulocyte chemiotaxis = G0:0002449 = p-val: granulocyte chemiotaxis = G0:000835 = p-val: granulocyt Down Up 14e-06 immune response-regulation of anatomical structure morphogenesis = G0:005260 pc. leukocyte mediated immunity = G0:0002460 pc. circulatory system development = G0:0002460 pc. circulatory system development = G0:0002660 pc. circulatory system development = G0:0002660 pc. circulatory system development = G0:0002768 pc. vasculature development = G0:0001944 pc. locomotion = G0:0001944 pc. circulatory system development = G0:0001944 pc. locomotion = G0:0001944 pc. circulatory system development = G0:0001968 pc. locomotion = G0:0007267 pc. tube morphogenesis = G0:0035239 pc. leukocyte mediated immunity = G0:0002433 pc. regulation of anatomical structure morphogenesis = G0:0035234 pc. regulation of cell motility = G0:0002434 pc. regulation of cell motility = G0:000144 pc. immune response = regulation of locomotion = G0:000144 pc. positive regulation of locomotion = G0:000144 pc. positive regulation of immune response = G0:0002764 pc. positive regulation of immune response = G0:0001767 pc. response to cytokine = G0:0001767 pc. response to cytokine = G0:0001767 pc. regulation of intracellular signal transduction = G0:0001764 pc. response to cytokine = G0:0001764 pc. regulation of cell motility = G0:0001764 pc. response to cytokine = G0:00017676 pc. regulation of cell dahesion = G0:0050778 pc. regulation of cell dahesion = G0:005133 pc. regulation of cellular component biogenesis = G0:0001652 pc. regulation of cellular component biogenesis = G0:0001652 pc. regulation of cellular component biogenesis = G0:0001130 pc. regulation of cellular component biogenesis = G0: .01e-08 .97e-08 .79e-07 .13e-07 Gene Count 100 200 1.60e-07 9.78e-07 1.20e-08 3.98e-08 6.44e-09 4.58e-08 6.15e-07 300 400 Cluster plasma membrane signaling receptor complex – GO:0051130 – p-val: 1 plasma membrane signaling receptor complex – GO:0043292 – p-val: 9 leading edge membrane – GO:0043291 – p-val: 9 specific granule – GO:0042581 – p-val: 5 tertiary granule – GO:0070820 – p-val: 9 perinuclear region of cytoplasm – GO:0030667 – p-val: 9 perinuclear region of cytoplasm – GO:0030414 – p-val: 9 secretory granule – GO:0030141 – p-val: 9 external encapsulating structure – GO:0030112 – p-val: 2 external encapsulating structure – GO:0030312 – p-val: 2 endoplasmic reticulum lumen – GO:005788 – p-val: 2 collagen-containing extracellular matrix – GO:0062023 – p-val: 4 cytosolic large ribosomal subunit – GO:0022625 – p-val: 1 cytosolic small ribosomal subunit – GO:0022627 – p-val: 2 small ribosomal subunit – GO:0044391 – p-val: 1 blood microparticle – GO:0079262 – p-val: 1 blood microparticle – GO:0009986 – p-val: 7 1. 1.30e-03 9.61e-04 1. 1.88e-03 5.07e-04 6.53e-04 9.99e-04 5.04e-05 1. 1.62 1.75e-03 \*\* 1.00e-10 \*\*\* cell surface – GO:0009986 – p-val: 3.00e-06 \*\*\* lyase activity – GO:0016829 – p-val: 4.08e-04 \*\*\* growth factor activity – GO:0008083 – p-val: 3.33e-08 \*\*\* growth factor receptor binding – GO:0070851 – p-val: 2.11e-05 \*\*\* protein kinase activator activity – GO:0030296 – p-val: 1.12e-03 \*\*- protein kinase activator activity – GO:0030296 – p-val: 7.31e-04 \*\*\* kinase activator activity – GO:0030296 – p-val: 7.31e-04 \*\*\* kinase activator activity – GO:0030295 – p-val: 7.31e-04 \*\*\* glycosaminoglycan binding – GO:0005201 – p-val: 9.51e-06 \*\*\* glycosaminoglycan binding – GO:0005201 – p-val: 2.83e-06 \*\*\* glycosaminoglycan binding – GO:0005201 – p-val: 2.42e-04 \*\*\* extracellular matrix binding – GO:00050840 – p-val: 2.42e-04 \*\*\* growth factor binding – GO:0019838 – p-val: 1.92e-04 \*\*\* heparin binding – GO:0008201 – p-val: 1.74e-03 \*\* calcium ion binding – GO:0008201 – p-val: 1.74e-03 \*\* cytokine activity – GO:0005125 – p-val: 1.09e-03 \*\* cytokine activity – GO:0005125 – p-val: 1.00e-10 \*\*\* signaling receptor regulator activity – GO:0030545 – p-val: 1.00e-10 \*\*\* signaling receptor activator activity – GO:0030546 – p-val: 1.44e-10 \*\*\* cytokine receptor binding – GO:0005126 – p-val: 1.28e-07 \*\*\* antigen binding – GO:0008209 – p-val: 1.28e-07 \*\*\* chemokine receptor binding – GO:000809 – p-val: 1.28e-07 \*\*\* chemokine receptor binding – GO:0008009 – p-val: 1.28e-07 \*\*\* chemokine receptor binding – GO:0008009 – p-val: 1.26e-04 \*\*\* chemokine receptor binding – GO:0008009 – p-val: 1.26e-04 \*\*\* chemokine receptor binding – GO:0008009 – p-val: 1.26e-04 \*\*\* chemokine receptor binding – GO:0008009 – p-val: 1.26e-04 \*\*\* chemokine receptor binding – GO:0008009 – p-val: 1.26e-04 \*\*\* chemokine receptor binding – GO:0008009 – p-val: 1.26e-04 \*\*\* chemokine receptor binding – GO:0008009 – p-val: 1.26e-04 \*\*\* chemokine receptor binding – GO:0008009 – p-val: 1.26e-04 \*\*\* chemokine receptor binding – GO:0008009 – p-val: 1.26e-04 \*\*\* chemokine receptor binding – GO:0008009 – p-val: 1.26e-04 \*\*\* chemokine receptor binding – GO:0008009 – p-val:

2.0 2.50.0

Absolute NES

0.5

1.0

1.5

0.5

1.0

1.5

2.0