

GO terms associated with CEBPD downstream genes downregulated in the RNA-Seq Data

| Go terms | Gene count | Fold Enrichment | p-Value |
|--|------------|-----------------|----------|
| regulation of cell proliferation | 9 | 8,1 | 3,90E-06 |
| positive regulation of cellular process | 12 | 4,6 | 5,10E-06 |
| positive regulation of biological process | 12 | 4,2 | 1,30E-05 |
| system development | 12 | 3,6 | 5,00E-05 |
| anatomical structure development | 12 | 3,4 | 1,10E-04 |
| organ development | 10 | 4,1 | 1,80E-04 |
| positive regulation of immune system process | 5 | 14,8 | 2,50E-04 |
| multicellular organismal development | 12 | 3 | 3,50E-04 |
| positive regulation of cell activation | 4 | 25,4 | 4,20E-04 |
| regulation of response to stress | 5 | 12,9 | 4,30E-04 |
| response to wounding | 6 | 8 | 5,50E-04 |
| developmental process | 12 | 2,7 | 8,30E-04 |
| regulation of multicellular organismal process | 7 | 5,3 | 1,10E-03 |
| positive regulation of T cell proliferation | 3 | 54,3 | 1,20E-03 |
| regulation of leukocyte activation | 4 | 17 | 1,30E-03 |
| regulation of cellular process | 17 | 1,8 | 1,40E-03 |
| negative regulation of biological process | 9 | 3,5 | 1,50E-03 |
| regulation of cell activation | 4 | 16,1 | 1,60E-03 |
| regulation of cell division | 3 | 45,1 | 1,80E-03 |
| regulation of biological process | 17 | 1,7 | 2,40E-03 |
| reproduction | 6 | 5,5 | 2,90E-03 |
| regulation of response to stimulus | 5 | 7,6 | 3,00E-03 |
| multicellular organismal process | 13 | 2,1 | 3,10E-03 |
| negative regulation of cellular process | 8 | 3,4 | 4,30E-03 |
| response to stress | 8 | 3,4 | 4,70E-03 |
| biological regulation | 17 | 1,6 | 4,80E-03 |
| reproductive developmental process | 4 | 10,8 | 4,90E-03 |
| regulation of lymphocyte proliferation | 3 | 25,5 | 5,50E-03 |
| positive regulation of developmental process | 4 | 10,2 | 5,80E-03 |
| response to external stimulus | 6 | 4,6 | 6,10E-03 |
| signal transduction | 10 | 2,5 | 6,90E-03 |
| positive regulation of molecular function | 5 | 6 | 6,90E-03 |
| regulation of molecular function | 6 | 4,4 | 7,80E-03 |
| cell surface receptor linked signal transduction | 8 | 3 | 8,00E-03 |
| immune system process | 6 | 4,2 | 8,80E-03 |
| inflammatory response | 4 | 8,7 | 8,90E-03 |
| anatomical structure formation involved in morphogenesis | 4 | 8 | 1,10E-02 |
| negative regulation of apoptosis | 4 | 8 | 1,10E-02 |
| regulation of developmental process | 5 | 5,2 | 1,10E-02 |
| negative regulation of programmed cell death | 4 | 7,9 | 1,20E-02 |
| negative regulation of cell death | 4 | 7,8 | 1,20E-02 |
| negative regulation of cell proliferation | 4 | 7,8 | 1,20E-02 |
| positive regulation of alpha-beta T cell proliferation | 2 | 156,8 | 1,20E-02 |
| positive regulation of stress-activated MAPK cascade | 2 | 156,8 | 1,20E-02 |
| reproductive structure development | 3 | 16,8 | 1,20E-02 |
| nervous system development | 6 | 3,9 | 1,30E-02 |
| regulation of stress-activated MAPK cascade | 2 | 141,2 | 1,30E-02 |
| positive regulation of cell-cell adhesion | 2 | 128,3 | 1,50E-02 |
| regulation of defense response | 3 | 14,8 | 1,60E-02 |
| cell differentiation | 7 | 3 | 1,70E-02 |
| sex differentiation | 3 | 14 | 1,70E-02 |
| regulation of alpha-beta T cell proliferation | 2 | 108,6 | 1,70E-02 |
| regulation of binding | 3 | 13,8 | 1,80E-02 |
| anatomical structure morphogenesis | 6 | 3,5 | 1,80E-02 |
| regulation of response to external stimulus | 3 | 13,3 | 1,90E-02 |
| regulation of chemokine production | 2 | 94,1 | 2,00E-02 |
| cellular developmental process | 7 | 2,9 | 2,10E-02 |
| positive regulation of JNK cascade | 2 | 83 | 2,30E-02 |
| regulation of catalytic activity | 5 | 4,2 | 2,40E-02 |
| positive regulation of interleukin-6 production | 2 | 74,3 | 2,50E-02 |
| reproductive process in a multicellular organism | 4 | 5,8 | 2,60E-02 |
| multicellular organism reproduction | 4 | 5,8 | 2,60E-02 |
| wound healing | 3 | 11,1 | 2,70E-02 |
| regulation of cell differentiation | 4 | 5,7 | 2,70E-02 |
| positive regulation of stress-activated protein kinase signaling pathway | 2 | 67,2 | 2,80E-02 |
| regulation of cell-cell adhesion | 2 | 64,2 | 2,90E-02 |
| anti-apoptosis | 3 | 10,3 | 3,10E-02 |
| positive regulation of catalytic activity | 4 | 5,4 | 3,10E-02 |
| blood vessel morphogenesis | 3 | 10 | 3,20E-02 |

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|---|---|------|----------|
| heart development | 3 | 9,8 | 3,30E-02 |
| regulation of anatomical structure morphogenesis | 3 | 9,7 | 3,40E-02 |
| tube development | 3 | 9,6 | 3,50E-02 |
| regulation of immune response | 3 | 9,4 | 3,60E-02 |
| positive regulation of cell differentiation | 3 | 9,2 | 3,70E-02 |
| organ morphogenesis | 4 | 5 | 3,80E-02 |
| positive regulation of response to stimulus | 3 | 9 | 3,90E-02 |
| embryo implantation | 2 | 47,1 | 4,00E-02 |
| regulation of interleukin-2 production | 2 | 47,1 | 4,00E-02 |
| positive regulation of smooth muscle cell proliferation | 2 | 45,5 | 4,10E-02 |
| positive regulation of adaptive immune response | 2 | 45,5 | 4,10E-02 |
| positive regulation of multicellular organismal process | 3 | 8,7 | 4,20E-02 |
| blood vessel development | 3 | 8,6 | 4,20E-02 |
| vasculature development | 3 | 8,4 | 4,40E-02 |
| regulation of interleukin-6 production | 2 | 39,2 | 4,70E-02 |
| defense response | 4 | 4,6 | 4,70E-02 |
| pattern specification process | 3 | 7,9 | 4,90E-02 |

GO terms associated with BCL3 downstream genes downregulated in the RNA-Seq Data

| Go terms | Gene count | Fold Enrichment | p-Value |
|---|------------|-----------------|----------|
| response to external stimulus | 15 | 3,6 | 4,70E-05 |
| regulation of molecular function | 15 | 3,4 | 8,80E-05 |
| defense response | 12 | 4,2 | 8,90E-05 |
| response to stimulus | 31 | 1,9 | 1,00E-04 |
| response to stress | 20 | 2,6 | 1,10E-04 |
| response to wounding | 11 | 4,5 | 1,20E-04 |
| response to chemical stimulus | 17 | 2,9 | 1,40E-04 |
| response to biotic stimulus | 9 | 5,1 | 3,30E-04 |
| positive regulation of biological process | 21 | 2,2 | 4,50E-04 |
| regulation of metabolic process | 30 | 1,8 | 5,00E-04 |
| regulation of cellular metabolic process | 29 | 1,8 | 5,80E-04 |
| regulation of primary metabolic process | 28 | 1,8 | 6,10E-04 |
| inflammatory response | 8 | 5,3 | 6,50E-04 |
| regulation of cell proliferation | 12 | 3,3 | 7,40E-04 |
| negative regulation of biological process | 19 | 2,3 | 8,60E-04 |
| positive regulation of cellular process | 19 | 2,2 | 1,10E-03 |
| regulation of response to stimulus | 9 | 4,2 | 1,10E-03 |
| pathway-restricted SMAD protein phosphorylation | 3 | 54,3 | 1,30E-03 |
| regulation of catalytic activity | 12 | 3,1 | 1,30E-03 |
| response to organic substance | 11 | 3,3 | 1,40E-03 |
| regulation of response to stress | 7 | 5,5 | 1,50E-03 |
| response to virus | 5 | 10 | 1,50E-03 |
| response to other organism | 7 | 5,2 | 2,00E-03 |
| negative regulation of cellular process | 17 | 2,2 | 2,50E-03 |
| multi-organism process | 10 | 3,2 | 3,40E-03 |
| negative regulation of molecular function | 7 | 4,6 | 4,00E-03 |
| regulation of muscle contraction | 4 | 12,1 | 4,20E-03 |
| regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process | 23 | 1,8 | 4,80E-03 |
| positive regulation of molecular function | 9 | 3,3 | 4,80E-03 |
| regulation of nitrogen compound metabolic process | 23 | 1,8 | 5,40E-03 |
| regulation of response to external stimulus | 5 | 6,8 | 5,80E-03 |
| response to hormone stimulus | 7 | 4,1 | 6,30E-03 |
| chemical homeostasis | 8 | 3,4 | 8,30E-03 |
| regulation of cellular biosynthetic process | 23 | 1,7 | 8,40E-03 |
| positive regulation of smooth muscle cell proliferation | 3 | 21 | 8,60E-03 |
| regulation of biosynthetic process | 23 | 1,7 | 9,10E-03 |
| regulation of biological process | 43 | 1,3 | 9,60E-03 |
| response to endogenous stimulus | 7 | 3,8 | 9,90E-03 |
| transmembrane receptor protein serine/threonine kinase signaling pathway | 4 | 8,4 | 1,10E-02 |
| regulation of transcription factor activity | 4 | 8,4 | 1,10E-02 |
| regulation of system process | 6 | 4,2 | 1,30E-02 |
| regulation of macromolecule metabolic process | 24 | 1,6 | 1,40E-02 |
| biological regulation | 44 | 1,3 | 1,50E-02 |
| negative regulation of cellular metabolic process | 9 | 2,7 | 1,60E-02 |
| regulation of nucleotide metabolic process | 4 | 7,5 | 1,60E-02 |
| regulation of DNA binding | 4 | 7,2 | 1,80E-02 |
| response to glucose stimulus | 3 | 14,5 | 1,80E-02 |
| regulation of smooth muscle cell proliferation | 3 | 14,2 | 1,80E-02 |
| regulation of phosphorylation | 7 | 3,3 | 1,90E-02 |
| response to hexose stimulus | 3 | 13,9 | 1,90E-02 |
| response to monosaccharide stimulus | 3 | 13,9 | 1,90E-02 |
| homeostatic process | 9 | 2,6 | 2,00E-02 |
| regulation of phosphorus metabolic process | 7 | 3,1 | 2,20E-02 |
| regulation of phosphate metabolic process | 7 | 3,1 | 2,20E-02 |
| mesenchymal cell development | 3 | 12,8 | 2,20E-02 |
| mesenchymal cell differentiation | 3 | 12,8 | 2,20E-02 |
| regulation of macromolecule biosynthetic process | 21 | 1,6 | 2,20E-02 |
| regulation of kinase activity | 6 | 3,6 | 2,30E-02 |
| mesenchyme development | 3 | 12,5 | 2,30E-02 |
| negative regulation of metabolic process | 9 | 2,5 | 2,40E-02 |
| regulation of multicellular organismal process | 10 | 2,3 | 2,50E-02 |
| peptide transport | 3 | 12,1 | 2,50E-02 |
| response to nutrient | 4 | 6,2 | 2,60E-02 |
| regulation of transferase activity | 6 | 3,5 | 2,70E-02 |
| response to mechanical stimulus | 3 | 11,6 | 2,70E-02 |
| B cell mediated immunity | 3 | 11,6 | 2,70E-02 |
| cellular cation homeostasis | 5 | 4,3 | 2,80E-02 |
| positive regulation of catalytic activity | 7 | 2,9 | 3,00E-02 |
| transforming growth factor beta receptor signaling pathway | 3 | 10,9 | 3,00E-02 |

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| response to carbohydrate stimulus | 3 | 10,9 | 3,00E-02 |
| regulation of binding | 4 | 5,7 | 3,20E-02 |
| positive regulation of cellular biosynthetic process | 8 | 2,5 | 3,50E-02 |
| taxis | 4 | 5,4 | 3,60E-02 |
| chemotaxis | 4 | 5,4 | 3,60E-02 |
| regulation of protein metabolic process | 7 | 2,8 | 3,70E-02 |
| negative regulation of catalytic activity | 5 | 3,9 | 3,70E-02 |
| positive regulation of biosynthetic process | 8 | 2,5 | 3,70E-02 |
| regulation of transcription | 19 | 1,6 | 3,70E-02 |
| regeneration | 3 | 9,4 | 3,90E-02 |
| positive regulation of cell proliferation | 6 | 3,1 | 3,90E-02 |
| cation homeostasis | 5 | 3,8 | 4,10E-02 |
| negative regulation of nucleotide metabolic process | 2 | 43,4 | 4,40E-02 |
| positive regulation of cellular metabolic process | 9 | 2,2 | 4,40E-02 |
| regulation of protein modification process | 5 | 3,7 | 4,50E-02 |
| regulation of gene expression | 20 | 1,5 | 4,60E-02 |
| negative regulation of macromolecule metabolic process | 8 | 2,4 | 4,80E-02 |
| adaptive immune response | 3 | 8,5 | 4,80E-02 |
| adaptive immune response based on somatic recombination of immune receptors built from ir | 3 | 8,5 | 4,80E-02 |
| regulation of cellular process | 39 | 1,2 | 4,90E-02 |

GO terms associated with HIF1A downstream genes upregulated in the RNA-Seq Data

| Go terms | Gene count | Fold Enrichment | p-Value |
|--|------------|-----------------|----------|
| response to hypoxia | 5 | 32,9 | 9,80E-06 |
| response to oxygen levels | 5 | 31,3 | 1,20E-05 |
| response to chemical stimulus | 8 | 5,5 | 1,70E-04 |
| negative regulation of biological process | 9 | 4,4 | 2,00E-04 |
| negative regulation of cellular process | 8 | 4,3 | 8,40E-04 |
| response to stress | 8 | 4,2 | 9,20E-04 |
| regulation of cell proliferation | 5 | 5,6 | 8,00E-03 |
| response to endogenous stimulus | 4 | 8,7 | 8,30E-03 |
| regulation of apoptosis | 5 | 5,5 | 8,60E-03 |
| regulation of programmed cell death | 5 | 5,4 | 8,90E-03 |
| regulation of cell death | 5 | 5,4 | 9,00E-03 |
| protein oligomerization | 3 | 15,2 | 1,40E-02 |
| regulation of multicellular organismal process | 5 | 4,7 | 1,50E-02 |
| response to stimulus | 9 | 2,3 | 1,60E-02 |
| organ regeneration | 2 | 67,9 | 2,70E-02 |
| response to organic substance | 4 | 4,9 | 3,80E-02 |
| negative regulation of phosphorylation | 2 | 39,2 | 4,70E-02 |