

GeDiPNet Cluster 123 -- Enriched GO Terms (Biological Process)

GO term enrichment: Biological Process terms (gene2go, human/tax_id=9606 only), upper-tail hypergeometric test, fold enrichment = (overlap / cluster gene count) / (term gene count / universe size), Benjamini-Hochberg FDR-corrected. Top 15 terms per cluster by q-value. See scripts/build_cluster_go_enrichment.php on gedipnet.bicnirrh.res.in. Data as of: 2026-10-07 03:23:06. · Rows: 15 · Generated: 2026-10-07 02:51:59

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
canonical Wnt signaling pathway	GO:0060070	3	LRP5, TGFB1, SOST	105	9	59.32	1.413e-5	6.843e-4
retina vasculature development in camera-type eye	GO:0061298	2	LRP5, TGFB1	15	9	276.84	2.158e-5	9.541e-4
positive regulation of branching involved in ureteric bud morphogenesis	GO:0090190	2	LGR4, TGFB1	18	9	230.70	3.142e-5	1.265e-3
bone remodeling	GO:0046849	2	LRP5, LGR4	18	9	230.70	3.142e-5	1.265e-3
negative regulation of ossification	GO:0030279	2	TGFB1, SOST	27	9	153.80	7.192e-5	2.365e-3
digestive tract development	GO:0048565	2	LGR4, TGFB1	34	9	122.14	1.148e-4	3.353e-3
Wnt signaling pathway	GO:0016055	3	LRP5, LGR4, SOST	232	9	26.85	1.502e-4	4.099e-3
gene expression	GO:0010467	3	LRP5, TGFB1, LRP2	269	9	23.16	2.324e-4	5.610e-3
diol metabolic process	GO:0034311	1	LRP2	1	9	2076.33	4.816e-4	9.305e-3
columnar/cuboidal epithelial cell maturation	GO:0002069	1	TGFB1	1	9	2076.33	4.816e-4	9.305e-3
adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	GO:0002460	1	TGFB1	1	9	2076.33	4.816e-4	9.305e-3
positive regulation of microglia differentiation	GO:0014008	1	TGFB1	1	9	2076.33	4.816e-4	9.305e-3
regulation of interleukin-23 production	GO:0032667	1	TGFB1	1	9	2076.33	4.816e-4	9.305e-3
branch elongation involved in mammary gland duct branching	GO:0060751	1	TGFB1	1	9	2076.33	4.816e-4	9.305e-3
cellular response to acetaldehyde	GO:1905641	1	TGFB1	1	9	2076.33	4.816e-4	9.305e-3