

GeDiPNet Cluster 91 -- 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 18:42:46

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
cellular response to estradiol stimulus	GO:0071392	4	EGFR, ESR1, GPER1, SFRP1	36	24	86.51	1.199e-7	1.405e-5
collagen-activated tyrosine kinase receptor signaling pathway	GO:0038063	3	COL4A3, COL4A5, COL4A6	12	24	194.66	4.064e-7	3.928e-5
positive regulation of cell migration	GO:0030335	6	WNT5B, F7, PLAU, EGFR, GPER1, SMAD3	292	24	16.00	1.469e-6	1.126e-4
response to genistein	GO:0033595	2	CYP1A1, F7	3	24	519.08	4.739e-6	2.878e-4
positive regulation of canonical Wnt signaling pathway	GO:0090263	4	WNT3A, EGFR, SFRP1, SMAD3	115	24	27.08	1.315e-5	6.465e-4
response to 2,3,7,8-tetrachlorodibenzodioxine	GO:1904612	2	CYP1A1, F7	5	24	311.45	1.577e-5	7.482e-4
regulation of branching involved in prostate gland morphogenesis	GO:0060687	2	ESR1, SFRP1	5	24	311.45	1.577e-5	7.482e-4
negative regulation of B cell differentiation	GO:0045578	2	INHBA, SFRP1	5	24	311.45	1.577e-5	7.482e-4
negative regulation of cell population proliferation	GO:0008285	6	COL4A3, GPER1, INHBA, SFRP1, SMAD3, TSC2	444	24	10.52	1.628e-5	7.661e-4
steroid hormone receptor signaling pathway	GO:0043401	2	ESR1, GPER1	6	24	259.54	2.364e-5	1.019e-3
prostate epithelial cord arborization involved in prostate glandular acinus morphogenesis	GO:0060527	2	ESR1, SFRP1	7	24	222.46	3.307e-5	1.316e-3
somitogenesis	GO:0001756	3	WNT3A, SFRP1, SMAD3	50	24	46.72	3.506e-5	1.378e-3
positive regulation of non-canonical Wnt signaling pathway	GO:2000052	2	WNT5B, SFRP1	8	24	194.66	4.406e-5	1.639e-3
negative regulation of fat cell differentiation	GO:0045599	3	WNT3A, GPER1, SMAD3	57	24	40.98	5.204e-5	1.858e-3
extrinsic apoptotic signaling pathway	GO:0097191	3	INHBA, SFRP1, SMAD3	57	24	40.98	5.204e-5	1.858e-3