

GeDiPNet Cluster 264 -- 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: 2026-10-08 03:23:04. · Rows: 15 · Generated: 2026-10-07 21:59:20

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
ERBB signaling pathway	GO:0038127	2	MAPK1, PTPN11	4	14	667.39	3.125e-6	2.102e-4
Bergmann glial cell differentiation	GO:0060020	2	MAPK1, PTPN11	11	14	242.69	2.856e-5	1.191e-3
positive regulation of cell differentiation	GO:0045597	3	ARID1A, GHR, RPS6KA3	83	14	48.25	2.969e-5	1.227e-3
hormone metabolic process	GO:0042445	2	GHR, PTPN11	25	14	106.78	1.548e-4	4.282e-3
insulin-like growth factor receptor signaling pathway	GO:0048009	2	GHR, MAPK1	33	14	80.90	2.716e-4	6.373e-3
hormone-mediated signaling pathway	GO:0009755	2	GHR, PTPN11	42	14	63.56	4.411e-4	8.958e-3
regulation of response to nutrient levels	GO:0032107	1	GHR	1	14	1334.79	7.492e-4	1.282e-2
negative regulation of cortisol secretion	GO:0051463	1	PTPN11	1	14	1334.79	7.492e-4	1.282e-2
negative regulation of growth hormone secretion	GO:0060125	1	PTPN11	1	14	1334.79	7.492e-4	1.282e-2
intestinal epithelial cell migration	GO:0061582	1	PTPN11	1	14	1334.79	7.492e-4	1.282e-2
cellular response to amino acid starvation	GO:0034198	2	MAPK1, YWHAG	60	14	44.49	8.999e-4	1.449e-2
epidermal growth factor receptor signaling pathway	GO:0007173	2	MAPK1, PTPN11	64	14	41.71	1.023e-3	1.562e-2
TORC1 signaling	GO:0038202	2	RPS6KA3, YWHAG	67	14	39.84	1.121e-3	1.656e-2
cytosine metabolic process	GO:0019858	1	MAPK1	2	14	667.39	1.498e-3	1.953e-2
microvillus organization	GO:0032528	1	PTPN11	2	14	667.39	1.498e-3	1.953e-2