

GeDiPNet Cluster 588 -- 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: 2026-10-20 03:23:14. · Rows: 15 · Generated: 2026-10-20 00:01:13

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
bone mineralization	GO:0030282	3	PTH1R, CYP27B1, PTH	56	6	166.85	5.066e-7	4.930e-5
positive regulation of vitamin D receptor signaling pathway	GO:0070564	2	CYP27B1, VDR	6	6	1038.17	1.288e-6	1.057e-4
positive regulation of inositol phosphate biosynthetic process	GO:0060732	2	PTH1R, PTH	7	6	889.86	1.803e-6	1.394e-4
intracellular calcium ion homeostasis	GO:0006874	3	PTH1R, PTH, VDR	113	6	82.69	4.249e-6	2.783e-4
skeletal system development	GO:0001501	3	PTH1R, PTH, VDR	151	6	61.88	1.016e-5	5.504e-4
positive regulation of keratinocyte differentiation	GO:0045618	2	CYP27B1, VDR	20	6	311.45	1.628e-5	7.922e-4
response to vitamin D	GO:0033280	2	CYP27B1, PTH	21	6	296.62	1.799e-5	8.552e-4
decidualization	GO:0046697	2	CYP27B1, VDR	25	6	249.16	2.569e-5	1.111e-3
bone resorption	GO:0045453	2	PTH1R, PTH	26	6	239.58	2.783e-5	1.181e-3
calcium ion homeostasis	GO:0055074	2	CYP27B1, PTH	42	6	148.31	7.355e-5	2.461e-3
positive regulation of bone mineralization	GO:0030501	2	PTH, VDR	42	6	148.31	7.355e-5	2.461e-3
negative regulation of cell population proliferation	GO:0008285	3	PTH1R, CYP27B1, VDR	444	6	21.04	2.526e-4	5.994e-3
macromolecule biosynthetic process	GO:0009059	1	PTH	1	6	3114.50	3.211e-4	7.044e-3
nuclear receptor-mediated bile acid signaling pathway	GO:0038185	1	VDR	2	6	1557.25	6.421e-4	1.113e-2
negative regulation of phosphate transmembrane transport	GO:2000186	1	VDR	2	6	1557.25	6.421e-4	1.113e-2