

GeDiPNet Cluster 342 -- 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 00:26:36

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
calcitriol biosynthetic process from calciol	GO:0036378	3	CYP27B1, CYP2R1, CYP3A4	5	11	1019.29	1.516e-9	3.258e-7
vitamin D metabolic process	GO:0042359	3	CYP27B1, CYP2R1, CYP3A4	12	11	424.70	3.329e-8	4.803e-6
vitamin D biosynthetic process	GO:0042368	2	CYP27B1, CYP2R1	2	11	1698.82	3.150e-7	3.172e-5
vitamin D catabolic process	GO:0042369	2	CYP27B1, CYP3A4	4	11	849.41	1.889e-6	1.375e-4
bone mineralization	GO:0030282	3	CYP27B1, PTH, PTH1R	56	11	91.01	4.135e-6	2.576e-4
positive regulation of vitamin D receptor signaling pathway	GO:0070564	2	CYP27B1, VDR	6	11	566.27	4.719e-6	2.870e-4
vitamin metabolic process	GO:0006766	2	CYP27B1, CYP2R1	6	11	566.27	4.719e-6	2.870e-4
positive regulation of inositol phosphate biosynthetic process	GO:0060732	2	PTH, PTH1R	7	11	485.38	6.605e-6	3.740e-4
intracellular calcium ion homeostasis	GO:0006874	3	VDR, PTH, PTH1R	113	11	45.10	3.429e-5	1.354e-3
positive regulation of keratinocyte differentiation	GO:0045618	2	CYP27B1, VDR	20	11	169.88	5.951e-5	2.043e-3
response to vitamin D	GO:0033280	2	CYP27B1, PTH	21	11	161.79	6.575e-5	2.207e-3
skeletal system development	GO:0001501	3	VDR, PTH, PTH1R	151	11	33.75	8.138e-5	2.593e-3
decidualization	GO:0046697	2	CYP27B1, VDR	25	11	135.91	9.381e-5	2.882e-3
bone resorption	GO:0045453	2	PTH, PTH1R	26	11	130.68	1.016e-4	3.059e-3
calcium ion homeostasis	GO:0055074	2	CYP27B1, PTH	42	11	80.90	2.678e-4	6.202e-3