

GeDiPNet Cluster 625 -- 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: 2026-10-19 23:18:37

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	7	1601.74	3.218e-10	8.693e-8
vitamin D metabolic process	GO:0042359	3	CYP27B1, CYP2R1, CYP3A4	12	7	667.39	7.071e-9	1.306e-6
vitamin D biosynthetic process	GO:0042368	2	CYP27B1, CYP2R1	2	7	2669.57	1.203e-7	1.482e-5
vitamin D catabolic process	GO:0042369	2	CYP27B1, CYP3A4	4	7	1334.79	7.214e-7	6.577e-5
positive regulation of vitamin D receptor signaling pathway	GO:0070564	2	CYP27B1, VDR	6	7	889.86	1.803e-6	1.394e-4
vitamin metabolic process	GO:0006766	2	CYP27B1, CYP2R1	6	7	889.86	1.803e-6	1.394e-4
positive regulation of keratinocyte differentiation	GO:0045618	2	CYP27B1, VDR	20	7	266.96	2.278e-5	1.019e-3
decidualization	GO:0046697	2	CYP27B1, VDR	25	7	213.57	3.594e-5	1.438e-3
response to cesium ion	GO:0010164	1	CYP2R1	1	7	2669.57	3.746e-4	7.813e-3
nuclear receptor-mediated bile acid signaling pathway	GO:0038185	1	VDR	2	7	1334.79	7.491e-4	1.230e-2
negative regulation of phosphate transmembrane transport	GO:2000186	1	VDR	2	7	1334.79	7.491e-4	1.230e-2
xenobiotic metabolic process	GO:0006805	2	CYP2R1, CYP3A4	120	7	44.49	8.409e-4	1.325e-2
apoptotic process involved in mammary gland involution	GO:0060057	1	VDR	3	7	889.86	1.123e-3	1.550e-2
alkaloid catabolic process	GO:0009822	1	CYP3A4	3	7	889.86	1.123e-3	1.550e-2
T cell mediated cytotoxicity directed against tumor cell target	GO:0002419	1	TRB	3	7	889.86	1.123e-3	1.550e-2