

GeDiPNet Cluster 314 -- 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 16:30:15

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
positive regulation of epidermal growth factor receptor signaling pathway	GO:0045742	2	AGT, PLAU	32	3	389.31	8.514e-6	4.600e-4
regulation of smooth muscle cell-matrix adhesion	GO:2000097	1	PLAU	1	3	6229.00	1.605e-4	4.313e-3
regulation of renal output by angiotensin	GO:0002019	1	AGT	2	3	3114.50	3.211e-4	7.027e-3
regulation of blood volume by renin-angiotensin	GO:0002016	1	AGT	2	3	3114.50	3.211e-4	7.027e-3
G protein-coupled receptor signaling pathway coupled to cGMP nucleotide second messenger	GO:0007199	1	AGT	2	3	3114.50	3.211e-4	7.027e-3
positive regulation of membrane hyperpolarization	GO:1902632	1	AGT	2	3	3114.50	3.211e-4	7.027e-3
regulation of cell population proliferation	GO:0042127	2	AGT, PLAU	201	3	61.98	3.429e-4	7.362e-3
renin-angiotensin regulation of aldosterone production	GO:0002018	1	AGT	3	3	2076.33	4.816e-4	9.305e-3
regulation of renal sodium excretion	GO:0035813	1	AGT	3	3	2076.33	4.816e-4	9.305e-3
positive regulation of angiotensin-activated signaling pathway	GO:0110063	1	AGT	3	3	2076.33	4.816e-4	9.305e-3
regulation of plasminogen activation	GO:0010755	1	PLAU	3	3	2076.33	4.816e-4	9.305e-3
urokinase plasminogen activator signaling pathway	GO:0038195	1	PLAU	3	3	2076.33	4.816e-4	9.305e-3
response to muscle activity involved in regulation of muscle adaptation	GO:0014873	1	AGT	4	3	1557.25	6.421e-4	1.127e-2
negative regulation of neurotrophin TRK receptor signaling pathway	GO:0051387	1	AGT	4	3	1557.25	6.421e-4	1.127e-2
regulation of extracellular matrix assembly	GO:1901201	1	AGT	4	3	1557.25	6.421e-4	1.127e-2