

GeDiPNet Cluster 281 -- 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 06:49:17

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
face morphogenesis	GO:0060325	2	ANKRD11, ARID5B	33	7	161.79	6.316e-5	2.142e-3
skeletal system morphogenesis	GO:0048705	2	ANKRD11, ARID5B	45	7	118.65	1.182e-4	3.430e-3
negative regulation of neuroblast migration	GO:0061855	1	ABCC8	1	7	2669.57	3.746e-4	7.813e-3
positive regulation of uterine smooth muscle relaxation	GO:1900721	1	ABCC8	1	7	2669.57	3.746e-4	7.813e-3
atrial septum secundum morphogenesis	GO:0003290	1	NSD2	2	7	1334.79	7.491e-4	1.251e-2
positive regulation of sodium ion transmembrane transporter activity	GO:2000651	1	WNK3	2	7	1334.79	7.491e-4	1.251e-2
glutamate secretion, neurotransmission	GO:0061535	1	ABCC8	3	7	889.86	1.123e-3	1.623e-2
negative regulation of blood-brain barrier permeability	GO:1905604	1	ABCC8	3	7	889.86	1.123e-3	1.623e-2
atrial septum primum morphogenesis	GO:0003289	1	NSD2	5	7	533.91	1.872e-3	2.187e-2
positive regulation of tight junction disassembly	GO:1905075	1	ABCC8	5	7	533.91	1.872e-3	2.187e-2
negative regulation of pancreatic juice secretion	GO:0090188	1	WNK3	5	7	533.91	1.872e-3	2.187e-2
positive regulation of isotype switching to IgA isotypes	GO:0048298	1	NSD2	6	7	444.93	2.246e-3	2.412e-2
response to pH	GO:0009268	1	ABCC8	7	7	381.37	2.620e-3	2.622e-2
regulation of double-strand break repair via nonhomologous end joining	GO:2001032	1	NSD2	8	7	333.70	2.993e-3	2.816e-2
neutrophil differentiation	GO:0030223	1	LBR	8	7	333.70	2.993e-3	2.816e-2