

GeDiPNet Cluster 305 -- 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 13:24:04

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
ether lipid biosynthetic process	GO:0008611	3	PEX7, AGPS, GNPAT	8	18	389.31	4.190e-8	5.834e-6
chondrocyte development	GO:0002063	3	BPNT2, CHST11, BMPR1B	21	18	148.31	9.873e-7	8.211e-5
skeletal system development	GO:0001501	4	BPNT2, PTH1R, SFRP4, ARSL	151	18	27.50	1.148e-5	5.795e-4
chondroitin sulfate proteoglycan metabolic process	GO:0050654	2	BPNT2, CHST11	6	18	346.06	1.311e-5	6.450e-4
chondrocyte differentiation	GO:0002062	3	GDF5, PTH1R, BMPR1B	61	18	51.06	2.608e-5	1.099e-3
protein targeting to peroxisome	GO:0006625	2	PEX7, PEX5	10	18	207.63	3.925e-5	1.499e-3
protein import into peroxisome matrix	GO:0016558	2	PEX7, PEX5	14	18	148.31	7.920e-5	2.540e-3
cartilage development	GO:0051216	3	CHST11, GDF5, BMPR1B	89	18	34.99	8.092e-5	2.587e-3
positive regulation of chondrocyte differentiation	GO:0032332	2	GDF5, BMPR1B	20	18	103.82	1.648e-4	4.391e-3
proteoglycan biosynthetic process	GO:0030166	2	CHST11, BMPR1B	21	18	98.87	1.820e-4	4.738e-3
peroxisome organization	GO:0007031	2	PEX7, PEX5	23	18	90.28	2.191e-4	5.374e-3
endochondral ossification	GO:0001958	2	BPNT2, PEX7	31	18	66.98	4.008e-4	8.215e-3
cell surface receptor protein serine/threonine kinase signaling pathway	GO:0007178	2	GDF5, BMPR1B	33	18	62.92	4.546e-4	8.966e-3
negative regulation of protein-containing complex assembly	GO:0031333	2	PEX5, HDAC6	36	18	57.68	5.415e-4	1.006e-2
fatty acid beta-oxidation	GO:0006635	2	PEX7, PEX5	48	18	43.26	9.629e-4	1.467e-2